2-66 To determine which bacterial cells have been transformed when making the recombinant DNA an antibiotic resistance gene is inserted into the plasmid with the target gene. When the bacterial cells are cultured, an antibiotic is added and only those bacteria with the resistance gene will survive.

2-67

Advantage	Disadvantage
• Ability to produce large quantities of proteins/peptides that can't be produced by other means. • Production of useful bacteria that can yield valuable products such as insulin. • The exact protein required is produced so no rejection problems.	• Complicated and expensive on a commercial scale. • Hard to identify useful genes in a large genome. • Not all eukaryotic genes will be expressed in bacterial plasmids. • Use of restriction enzymes with DNA produces millions of useless fragments.

2-68 Diagram 2.

A genetically modified organism (GMO) is an organism whose genome has been altered by genetic engineering. The alteration maybe an addition of a gene or the silencing of a gene. Transgenic organisms are a subset of GMOs. Transgenic organisms are GMOs that have gained DNA from a different species.

2-69 Transformation is when foreign DNA is incorporated into a prokaryotic cell whereas transfection is when foreign DNA is incorporated into a eukaryotic cell.

2-70 Ways foreign DNA can be inserted into host cells:

- liposomes
- plasmid vectors
- viral vectors
- pronuclear injection
- ballistic DNA injection.

2-71 The Ti plasmid is found naturally in *Agrobacterium*. *Agrobacterium* infect plants and cause disease by inserting their Ti plasmids into plant cells. The Ti plasmid then inserts tumour-forming genes into the plant's chromosomes. When these genes are expressed, a tumour or gall forms. In genetic engineering, the tumour forming genes are replaced with genes the scientist wants the plant to express. In this way, the introduced genes are inserted into the plant's genome.

2-72

Use of GMO	Example	Advantage
To provide resistance to insect predation	The introduction of the Bt toxin gene from Bacillus thuringiensis into cotton. The cotton produces the Bt toxin protecting the cotton from insect pests.	Less use of pesticides.
To provide resistance to disease	The introduction of the R gene from peppers into tomatoes. The tomatoes produce the R protein, which breaks down the toxin causing Bacterial spot.	Less use of chemical sprays and increased productivity.

2-73

For	Against
Increase crop yields/food production	May have unknown effects
Promote efficient land use	Recombinant plasmids are usually genetically engineered to contain genes coding for antibiotic resistance. The recombinant plasmids ae selected by growing bacteria on antibiotics. There is a risk that these recombinant plasmids could be taken up by disease-causing bacteria. These would then be resistant to antibiotics and therefore treatment of infections would be less.
Reduce the use of pesticides/herbicides	Risk of GMOs escaping into the natural environment where they may out-compete native species reducing biodiversity.

Chapter 2: Multiple-choice questions

2-74 [VCAA 2015 SA Q3]

A single DNA nucleotide is shown by sub-unit(s)

D X, Y and Z together. (A nucleotide consists of a nitrogenous base, a phosphate and a sugar subunit.)

2-75 [VCAA 2015 SA Q4]

A feature of DNA that can be seen in the diagram above is

A the anti-parallel arrangement of the two strands of nucleotides. (One chain runs 5´to 3´ and the other 3´ to 5´ - hence anti-parallel.)

2-76 [VCAA 2018 SA Q4]

The genetic code is described as a degenerate code. This means that

B some amino acids may be encoded by more than one codon. (Fact: in a number of cases it is just that the first 2 bases of a codon that determine an amino acid – so coding for some amino acids is not unique.)

2-77 [VCAA 2020 SA Q7]

It is correct to state that

D the DNA template sequence GAA codes for Leu. (Identical amino acid sequences are found in all organisms is not true. The genetic code for Met is not degenerate as only one codon codes for MET. GGU codes for Gly, not Trp. The RNA codon is the complement of the DNA triplet; therefore, the complement of CUU is GAA.)

2-78 [VCAA 2015 SA Q23]

Using the table provided, the DNA template sequence that could code for this amino acid sequence is

A TTG / CCC / GGT / GCT / TCG (To answer the question determine the mRNA sequence –therefore – AAU or C, GG_, CC_, CG_, and AGU or C. The complement with T replacing U gives the DNA template sequence.)

2-79 [VCAA 2014 SA Q5]

The part of a molecule referred to as an anticodon can be found in

B transfer RNA. (Triplets are found in DNA and codons in mRNA.)

2-80 [VCAA 2011 E2 SA Q24]
The first step of gene expression is
B transcription of DNA. (You need a detailed understanding of protein synthesis and the location of each step. The order for the steps given is transcription, translation, modification and then packaging of proteins.)

2-81 [VCAA 2011 E1 SA Q44]
A molecule of transfer RNA could include the nucleotide sequence
B GGCUUUAAA (In RNA T (thymine) is replaced by U (uracil).)

2-82 [Adapted VCAA 2020 SA Q26]
The trp operon in prokaryotes illustrates the switching off and on of genes.
The operator within the trp operon
D is the binding site for the repressor protein and tryptophan. (The regulatory gene codes for the production of a repressor protein. The repressor protein binds to tryptophan and the resulting molecule binds to the operator stopping RNA polymerase from reading the gene.)

2-83 [Adapted VCAA 2019 SA Q3]
Transcription of the structural genes within the *trp* operon will occur when
B RNA polymerase is attached to the promoter. (When tryptophan is present in high concentration it binds to the repressor protein. The resulting molecule binds to the operator stopping transcription.)

2-84 [Adapted VCAA 2019 SA Q4]
Transcription of the structural genes within the *trp* operon results in the production of molecules of
D mRNA (The transcription of the structural genes results in mRNA complements of the trp E, trp D, trp B and trp A genes. Translation of the mRNA molecules results in the production of enzymes that result in the production of tryptophan.)

2-85 [VCAA 2019 SA Q11]
Which one of the following is a correct conclusion to reach when comparing the two cells?
A At any given time, the genes expressed in each cell may be different. (Within an organism, all somatic cells have the same genome. In different cells, the differences in function and structure are determined by which genes have been switched on as this determines what proteins are produced.)

2-86 [VCAA 2020 SA Q8]
The primary structure of a protein is important because it
C influences the way that the polypeptide folds. (The functional form of the protein is due to the tertiary and quaternary structure which gives the protein its three-dimensional shape.)

2-87 [VCAA 2019 SA Q5]
Which one of the following statements about proteins is correct?
A The activity of a protein may be affected by the temperature and pH of its environment. (Proteins are affected by temperature and pH. Primary structure refers to the amino acid order in a chain before folding so is not 3-dimensional. Proteins e.g. immunoglobulins are involved in the immune response and not all proteins with quaternary structure are proteins.)

2-88 [VCAA 2018 SA Q3]
The joining of adjacent amino acids
D is a condensation reaction. (The reaction results in the production of water therefore condensation. Nucleic acids are not produced, and the reaction requires energy rather than releasing it. Ligase joins pieces of DNA.)

2-89 [VCAA 2017 SA Q1]
Which one of the following statements about proteins is correct?
A A change in the tertiary structure of a protein may result in the protein becoming biologically inactive. (The tertiary structure of a protein determines its shape, and the shape of a protein determines its function. Two different proteins may have the same amino acid sequence, but the chains maybe folded in different ways therefore they will have different shapes and different functions.)

2-90 [VCAA 2018 SA Q2]
The proteome is
C the entire set of proteins expressed by an organism at a given time. (Fact. A and B refer to the DNA content rather than protein.)

2-91 [VCAA 2015 SA Q8]
Which one of the following conclusions is supported by the data?
C The rate of uptake of this protein by Cell type 2 is faster at 37°C than at 25°C. (A is incorrect as cell type does influence rate as shown by Cell type 1 at 25°C compared with Cell type 1 at 37°C. B is incorrect as temperature in Cell type 1 does influence uptake as shown by Cell type 1 at 25°C and at 37°C. There is evidence that uptake has levelled off as shown by last two measurements for Cell type 1 at 37°C. C is supported by the data.)

2-92 [VCAA 2016 SA Q7]
One pathway for the production of protein for these junctions is
B nucleus – ribosome – endoplasmic reticulum – vesicle – Golgi apparatus. (The question asks for an understanding of protein production. The nucleus is involved in coding for proteins, the ribosomes on the ER are the site of protein production and the vesicles and Golgi apparatus are involved in export from the cell.)

2-93 [VCAA 2019 SA Q1]
What type of transport is shown?
C endocytosis. (The process shown shows bulk materials being taken into a cell by an active process so is not an example of diffusion.)

2-94 [VCAA 2014 SA Q3]
Process R is an example of
A exocytosis. (The bulk release of molecules from a cell is called exocytosis. Phagocytosis and pinocytosis are forms of endocytosis where molecules are taken into a cell.)

2-95 [VCAA 2014 SA Q4]
Organelle X
B packages protein molecules for export from the cell. (Organelle X is a Golgi Apparatus. Mitochondria are the sites of aerobic respiration and chloroplasts are the sites of photosynthesis.)

2-96 [VCAA 2019 SA Q2]
Which one of the following organelles has the role of synthesising proteins from their monomers?
B ribosomes. (Fact. Ribosomes are the site of protein synthesis.)

2-97 [VCAA 2013 SA Q6]

The site of synthesis of protein M is the

B ribosomes. (Proteins are assembled at ribosomes, transported by the smooth endoplasmic reticulum and vesicles.)

2-98 [VCAA 2013 SA Q7]

The export of protein M by these cells would involve

C the Golgi apparatus. (Chromosomes store genetic information, centrioles are involved in cell division and lysosomes contain digestive enzymes.)

2-99 [VCAA 2012 E1 SA Q7]

The order in which the parts of the cell play a role in the production and secretion of proteins is

C J, T, E, M. (The instructions for the production of the protein are found in J, the nucleus. mRNA carries these instructions to T, the ribosome. The protein is packaged for secretion at E, the Golgi body. M- vesicles bud off the Golgi body and carry the secretion to the cell membrane.)

2-100 [VCAA 2019 SA Q38]

DNA ligase

A joins two DNA fragments together by forming phosphodiester bonds between the two fragments. (Definition. Ligases are enzymes that join pieces of DNA together.)

2-101 [VCAA 2015 SA Q28]

Which one of the following can be correctly concluded from the gel electrophoresis results?

B Eukaryote mitochondria contain the ribosomal sub-units of the smallest size. (Movement in gel electrophoresis depends on size – small units travel further. The sub-units of the eukaryote mitochondria have travelled the greatest distances and must be the smallest.)

2-102 [VCAA 2013 SA Q29]

Adding EcoRI to a solution containing one copy of this double-stranded DNA produces

A two fragments of double-stranded DNA, each with a sticky end. (There is only one recognition sequence for EcoRI in the sample, therefore one cut and two pieces. EcoRI cuts the DNA unevenly therefore, sticky ends will be produced.)

2-103 [VCAA 2013 SA Q30]

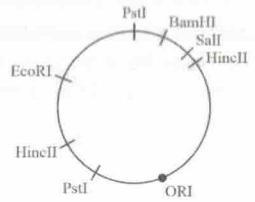
Which enzyme(s) will cut this piece of DNA?

C AluI and HindIII only. (Only the recognition sequences for these restriction enzymes are present in the sequence.)

2-104 [VCAA 2019 SA Q39]

Which of the following shows the number of restriction sites that have been cut and the resulting number of DNA fragments produced?

	Number of restriction sites cut	Number of DNA fragments produced
C	4	4



(Note the yellow mark – representing 4 restriction sites where a cut will occur – resulting in 4 DNA fragments.)

2-105 [VCAA 2020 SA Q29]

Which one of the following is a correct statement regarding the PCR process?

C Annealing and extension of the DNA occur at different temperatures. (Fact. Taq polymerase joins DNA nucleotide together and the number of copies of DNA double each cycle.)

2-106 [VCAA 2018 SA Q28]

The diagram represents a method of DNA manipulation. The method represented is

D polymerase chain reaction. (The diagram represents the polymerase chain reaction used to make multiple copies of a piece of DNA. It is not bacterial transformation as bacterial DNA is single stranded.)

2-107 [VCAA 2018 SA Q30]

Which lane represents a sample that was loaded with DNA fragments of four different lengths: 100 bp, 150 bp, 200 bp and 300 bp?

C Y (Useful to use a ruler to add in the missing figures. Doing so makes it easy to see that lane Y satisfies the criteria. All other lanes have samples of much greater length – 350 base pairs and greater.)

2-108 [VCAA 2018 SA Q31]

Which lane contains the band that is closest to the negative electrode?

B X (The DNA fragments are negatively charged. The negative electrode is at the loading well end. Fragments will move towards the opposite/positive end of the gel plate. Note the 500-base piece near the X well. S could have been answer but was not alternative.)

2-109 [VCAA 2014 SA Q25]

Which one of the following shows the enzymes required for the first and last steps of the process?

	Cuts plasmid	Inserts genes
A	**restriction enzyme**	**DNA ligase**

(Restriction enzymes cut plasmids and ligase joins double stranded DNA segments together. DNA polymerase joins DNA nucleotides together to form a single chain of nucleotides.)

2-110 [VCAA 2020 SA Q30]

In order to collect only bacterial cells that had taken up the plasmid successfully, a sample should be taken from

C Plate 3. (The aim of the process to produce cells that are resistant to ampicillin. Therefore, we need to look at a treated plate with ampicillin. Any bacterial cells that grow will have taken up the gene and be resistant.)

2-111 [VCAA 2020 SA Q31]

The process in which the bacterial cell takes up the plasmid is called

D transformation. (Fact. The other three processes are involved in normal cell processes – for example, preparation for cell division or production of proteins.)

2-112 [VCAA 2020 SA Q32]

Target DNA is to be inserted into a plasmid.

For a recombinant plasmid to be produced.

D DNA ligase is used to re-join the sugar-phosphate sections of the plasmid and the target DNA. (Ligase is used to join pieces of DNA with sticky ends. The DNA to be used can, in theory, come from any source. Blunt ends would not be useful – the pieces would not join.)

2-113 [VCAA 2015 SA Q25]

Bacteria are used in gene cloning because they

B can replicate non-bacterial sequences of DNA in a short time. (Bacteria do not have nuclei or divide by mitosis.)

2-114 [VCAA 2015 SA Q26]

Which plate would contain bacteria that fluoresce under UV light?

C plate Y (Only transformed bacteria can grow in the presence of ampicillin and the 'gfp' gene is only expressed if arabinose is present.)

2-115 [VCAA 2015 SA Q27]

Which one of the following statements is an accurate description for the purpose of plate W or X?

D Plate X shows that ampicillin was effective in killing the untransformed bacteria.

(Untransformed bacteria cannot grow in the presence of ampicillin therefore any growth on Y and Z must be of transformed bacteria.)

2-116 [VCAA 2013 SA Q34]

The correct sequence of steps when producing the insulin is

C R, Q, V, T, P, U, S. (The code for the amino acid sequence must be known before the gene can be synthesized therefore R must be first. The code can be worked out from the amino acid sequence in the protein therefore Q before V.)

2-117 [VCAA 2013 SA Q35]

The tool used for joining the artificial gene to plasmid DNA at step T is

B DNA ligase. (Gel electrophoresis is used to separate different lengths of DNA, a primer is used as an anchor to start the addition of DNA nucleotides and DNA polymerase joins DNA nucleotides into a single chain. DNA ligase is used to join doubled stranded DNA (plasmid) together.)

2-118 [VCAA 2013 SA Q36]

This is because the DNA code is

A redundant. (Redundant refers to the fact that a number of DNA triplets may code for the same amino acid.)

2-119 [VCAA 2013 SA Q28]

The person most likely to have been at the crime scene is suspect

B 2. (Only the bars for Suspect 2 sample match the bars for the sample found at the crime scene.)

2-120 [VCAA 2019 SA Q36]

S. cerevisiae can most accurately be described as a

A transgenic organism. (Definition. If a yeast is modified to include a human gene, it is a changed organism – that is transgenic.)

2-121

What is the best explanation for the successful development of transgenic species?

C DNA in the biosphere is composed of the same chemical components. (Transgenic species contain and express genes from another species. If DNA /the genetic code was not universal, the genes from another species could not be expressed.)

2-122 [VCAA 2020 SA Q36]

It is most likely that the main aim of this research and technology is to

D improve the nutrition of malnourished people. (Use the data! Look at the increase in Iron and Zinc levels in the biofortified rice – large increases. Also, in the question stem, there is a hint – rice supplies energy but is low in micronutrients such as iron and zinc.)

2-123 [VCAA 2020 SA Q37]

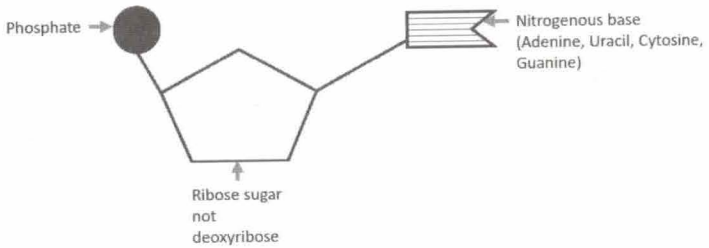
Which one of the following is the best description for this strain of biofortified rice?

B genetically modified and transgenic (The new strain is genetically modified because it has new genes inserted. It is transgenic because it contains genetic material from other species, i.e. soybeans.)

Chapter 2: Short-answer questions

2-124 [VCAA 2020 SB Q2]

a



b

Type of RNA	Role in a cell
tRNA	tRNA carries specific amino acids to the ribosome. Its anticodon is complementary to the mRNA codon.
mRNA	mRNA carries a transcript of the DNA template strand to the ribosome and therefore determines the order amino acids are assembled into a polypeptide chain at the ribosome.

c Any two of:

- Introns are removed.

Importance: only coding nucleotides remain in the mRNA. Only these are transcribed; therefore, the correct polypeptide chain is translated.

- Exons are spliced together: only coding nucleotides remain in the mRNA. Only these are transcribed; therefore, the correct polypeptide chain is translated.
- Exon shuffling.

Importance: allows many slightly different proteins to be coded for by one gene. This increases the variety of proteins produced by the cell.

- A 5' methyl cap is added to the RNA.

Importance: this protects the mRNA from degradation as it moves from the nucleus to the ribosome and allows the mRNA to bind to the ribosome.
- A poly-A tail is added to the RNA.
Importance: this protects the mRNA from degradation as it moves from the nucleus to the ribosome.

2-125 [VCAA 2019 SB Q1]

a Any two of:

	Molecule 1	Molecule 2
Difference	The pentose sugar present is ribose.	The pentose sugar present is deoxyribose.
Difference	The nitrogenous bases present are adenine, cytosine, guanine and uracil.	The nitrogenous bases present are adenine, cytosine, guanine and uracil.
Difference	Ribose sugar contains more oxygen.	Deoxyribose sugar contains less oxygen.

Note: the question asks for differences in the monomers, i.e. RNA nucleotide and DNA nucleotide not the molecules transfer RNA and DNA.

b Genes consist of introns and exons. These are both transcribed into pre mRNA. Pre mRNA introns are removed to form mRNA. Three mRNA molecules code for one amino acid.

2-126 [VCAA 2012 E1 SB Q3]

a proteins

b 'Primary structure' of the insulin macromolecules refers to the specific order of amino acids in each of the two polypeptide chains making up insulin.

c Animal: pig
Explanation: The order of amino acids in the alpha chain of the pig is more similar (identical) to humans than the other animals therefore its shape will be more similar to human insulin and it will be more likely to fit human insulin receptors on cells.

d i Human – thr Coding triplets: TGA TGG TGT TGC
Cow – ala Coding triplets: CGA CGG CGT CGC
The DNA triplets coding for the amino acid at position 30 differ in the first base. For humans the first nucleotide is T whereas for cows it is C.

ii The sequence of nucleotides in DNA coding for the amino acid at position 30 will not necessarily be identical in cows, pigs and sheep. The amino acid at position 30 is the same (ala) but there are 4 possible triplets (CGA, CGG, CGT and CGC) that code for this amino acid therefore any of these could be present and still result in the same amino acid at position 30.

2-127 [VCAA 2015 SB Q7]

a RNA polymerase

b Molecule S is pre-mRNA. Before it leaves the nucleus, introns are removed and a methyl cap and poly-A tail are added.

c The genetic sequence is identical but when expressed different proteins are produced because when pre-mRNA is edited different introns are spliced out. Therefore, the resulting mRNA is different and when translated a different protein is produced.

d The genetic code is universal. This means that the same three DNA bases code for the same amino acid in all living organisms.

2-128 [VCAA 2010 E1 SB Q6]

a The three components of a DNA nucleotide are a phosphate, deoxyribose and a nitrogenous base.

b TSD amino acid sequence: glu-his-phe
Explanation: a different amino acid sequence will change the primary structure of the protein, which will then affect how the protein chain folds and therefore the final shape of the enzyme. The shape of the active site of the enzyme is specific to the reactants it catalyses. If the active site is altered, the enzyme will no longer be able to catalyse the reaction.

2-129 [VCAA 2016 SB Q6]

a i Transfer RNA

ii tRNA carries specific amino acids to the ribosome. The anticodon on the tRNA attaches to a complementary to the mRNA codon. In this way, the amino acids are assembled and joined according to the order of bases on the mRNA that was formed from the transcription of the preproinsulin gene.

b Molecule W is mRNA and is formed when the preproinsulin gene is transcribed. Transcription begins when RNA polymerase binds to the preproinsulin gene promoter. The DNA unwinds and unzips. RNA polymerase then joins RNA nucleotides that are complementary (adenine with uracil, thymine with adenine, cytosine with guanine and guanine with cytosine) to the exposed DNA template, together to form pre mRNA. This continues until the terminator sequence is reached. The single-stranded pre mRNA is complementary to the DNA and contains uracil instead of thymine. The pre mRNA dissociates from the template strand and is edited. Introns are removed and a cap and a tail are added to form mRNA coding for preproinsulin.

2-130 [VCAA 2012 E2 SB Q1]

a Stage 1: Transcription
Stage 2: Translation

b RNA polymerase initiates transcription by binding to the promoter of the gene coding for the amyloid beta-protein gene. The DNA unwinds and unzips. RNA polymerase then joins RNA nucleotides that are complementary (adenine with uracil, thymine with adenine, cytosine with guanine and guanine with cytosine) to the exposed DNA template, together to form pre mRNA. This continues until the terminator sequence is reached. The pre mRNA dissociates from the template strand and is edited. Introns are removed and a cap and tail are added to form mRNA.

c Any three of the following:

Letter representing structure chosen	Role of structure in second stage of amyloid beta-protein synthesis
M	A chain of amino acids, when folded will form the amyloid beta-protein. (It is not correct to write amyloid beta-protein as the diagram shows a chain of amino acids not the final folded molecule.)

J	Nucleus Site of transcription where an mRNA complement of the gene for amyloid beta-protein is synthesised. This mRNA carries the information that determines the order amino acids are joined during translation to make the amyloid beta-protein.
R	Rough Endoplasmic Reticulum Site of translation where amino acids are assembled into a polypeptide. The order is determined by mRNA. tRNA brings specific amino acids to the ribosome where bonds form between the adjacent amino acids forming the chain of amino acids that will form the amyloid beta-protein.
L	Mitochondrion Site of aerobic respiration. Provides the energy required to assemble the amino acids together in translation.
K	Transfer RNA (tRNA) tRNA carries **specific** amino acids to the ribosome. The anticodon on the tRNA is complementary to the mRNA codon. In this way, the amino acids are assembled according to the order of bases on the mRNA.
S	Messenger RNA (mRNA) The order of bases on the mRNA is determined by the order of bases in DNA. Therefore, mRNA carries the instructions for assembling amino acids into the amyloid beta-protein from the nucleus to the ribosome.

2-131 [VCAA 2014 SB Q7]

a Translation occurs at the ribosome. mRNA attaches to the ribosome. The start codon is read. tRNA molecules bring specific amino acids to the complementary mRNA in the order determined by the mRNA. Three mRNA bases or a codon, code for one amino acid. The complementary bases on the tRNA are called an anticodon. The anticodon determines the type of amino acid carried to the ribosome and the order the amino acids are assembled as the anticodon pairs with the codon at the ribosome. Peptide bonds form between adjacent amino acids, tRNA molecules detach and translation ceases when a stop codon is reached. The chain of amino acids produced forms the polymer.

b Each monomer is coded for by three nucleotide bases therefore $3 \times 90 = 270$ nucleotide bases were involved in the coding of this polymer.

Or 3×90 plus 3 for the start codon and 3 for the stop codon = 276

2-132 [VCAA 2013 SB Q6]

a i Action X is transcription. RNA polymerase locates the gene by recognising the promoter. The DNA unwinds and unzips. Controlled by RNA polymerase, complementary RNA nucleotides (adenine and uracil, thymine and adenine, cytosine and guanine, guanine and cytosine) are added to the exposed DNA template. This continues until a termination sequence is reached. Pre mRNA is formed. This separates from the DNA and the DNA joins back together again.

ii P consists of exons (dark sections) and introns (pale sections). Introns are non-coding and are cut out. The exons are coding and join together to form mRNA. The mRNA then leaves the nucleus and moves to the ribosome for translation.

b mRNA moves out of the nucleus to the ribosome, structure S and site of translation. The start codon is read. Structure E is tRNA. tRNA molecules bring specific amino acids to the complementary mRNA in the order determined by the mRNA. Three mRNA bases or a codon, code for one amino acid. The complementary bases on the tRNA are called an anticodon, structure G. The anticodon determines the type of amino acid carried to the ribosome and the order the amino acids are assembled as the anticodon pairs with the codon at the ribosome. Peptide bonds form between adjacent amino acids, tRNA molecules detach and translation ceases when a stop codon is reached. The final product F is an amino acid chain or polypeptide. This forms the primary structure of a protein.

2-133 [VCAA 2011 E2 SB Q1]

a Nucleus

b RNA polymerase initiates transcription by binding to the promoter. The DNA unwinds and unzips. RNA polymerase then joins RNA nucleotides that are complementary to the exposed DNA template, together to form pre mRNA.

c Strand G is pre mRNA. It is an RNA complement of the template strand of the DNA for a gene including both introns and exons. The sections complementary to the introns are removed from the RNA, shortening the strand. A cap and tail is added to form the shorter mRNA which is strand H.

d Strand H: messenger RNA (mRNA)

The order of bases on the mRNA is determined by the order of bases in DNA. Therefore, mRNA carries the instructions for assembling amino acids into proteins from the nucleus to the ribosome.

Structure P: transfer RNA (tRNA)

tRNA carries specific amino acids to the ribosome. The anticodon of the tRNA is complementary to the mRNA codon. In this way, the amino acids are assembled according to the order of bases on the mRNA.

Structure M: ribosome

Site where amino acids are assembled into a polypeptide. The order is determined by mRNA. tRNA brings the amino acids to the ribosome where bonds form between the adjacent amino acids

2-134 [VCAA 2010 E2 SB Q2]

a i Transcription

ii RNA polymerase locates the gene by recognising the promoter. The DNA unwinds and unzips. Controlled by **RNA polymerase**, complementary RNA nucleotides (adenine and uracil, thymine and adenine, cytosine and guanine, guanine and cytosine) are added to the exposed **DNA template**. This continues until a termination sequences is reached.

Pre mRNA is formed. This is **edited**, introns are removed and a cap and tail added. The final **product** is **mRNA**.

b i Translation

ii mRNA moves out of the nucleus to the **ribosome**.

The start codon is read. Charged tRNA molecules bring **specific amino acids** to the complementary mRNA in the order determined by the mRNA. Three mRNA bases or a **codon** codes for one amino acid. The complementary bases on the tRNA are called an **anticodon**.

Peptide bonds form between adjacent amino acids. tRNA molecules detach and translation ceases when a stop codon is reached. The **final product** is an amino acid chain or **polypeptide**.

2-135 [Adapted VCAA 2018 SB Q6]

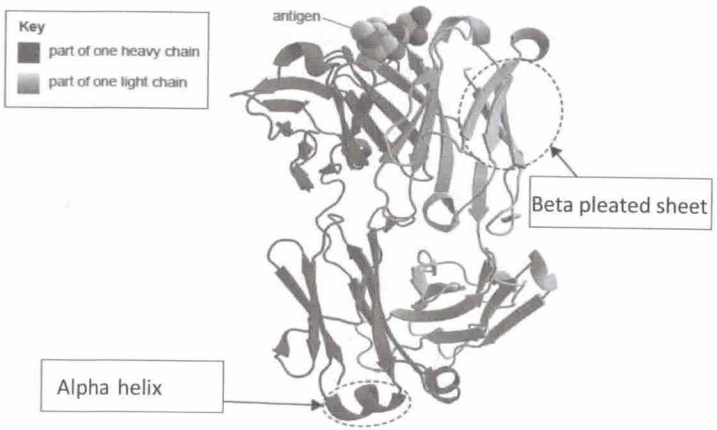
a Structural genes code for a protein that is part of an organism's structure whereas regulatory genes code for proteins that control the action of other genes by determining whether a gene is active or not.

b Any one of the following ways genes are regulated in different locations:
- different regulatory genes are expressed at different times at the different sites
- different regulatory sequences of on/off times at different sites
- different introns are removed during the production of mRNA from pre-mRNA resulting in different regulatory proteins at each site.

2-136 [VCAA 2016 SB Q1]

a amino acid

b



Source: Thomas Splettstoesser (www.scistyle.com)

c Quaternary structure refers to the structure that is formed by two or more polypeptide chains joined together. In this example, there are two polypeptide chains – one heavy and one light therefore it is a quaternary structure.

2-137 [VCAA 2018 SB Q1]

a mRNA that is the complement of the DNA coding for tryptase moves from the mast cell nucleus to the ribosome where it is read, and translation begins. The start codon is read. Charged tRNA molecules bring specific amino acids to the complementary mRNA in the order determined by the mRNA. Three mRNA bases or a codon codes for one amino acid. The complementary bases on the tRNA are called an anticodon. Peptide bonds form between adjacent amino acids. tRNA molecules detach and translation ceases when a stop codon is reached. The final product is the specific order of amino acids in a polypeptide chain of tryptase.

b

Organelle	Role
Rough endoplasmic reticulum or ribosome	Site where the tryptase-polypeptide chain, is folded and carbohydrates added and provides channels for movement of the tryptase through the cytoplasm within the cell.
Golgi apparatus	Site where the tryptase is packaged into vesicles ready for export out of the cell.
Vesicles	Vesicles containing tryptase bud off from the Golgi apparatus and transport the tryptase to the plasma membrane where they fuse with the membrane releasing the tryptase into the extracellular fluid.
Plasma membrane	Vesicles fuse with the plasma membrane releasing the tryptase into the extracellular fluid.
Mitochondria	Site of aerobic respiration which provides ATP (energy) for exocytosis of tryptase.

2-138 [Adapted VCAA 2011 E1 SB Q1]

a Hydrophilic molecules readily dissolve in water. In this molecule, the amino acid hydrophilic R groups are on the outside and are in close association with water whilst the amino acid hydrophobic R groups are on the inside of the molecule away from the surrounding water.

b

	Type of nucleic acid found in structure	Specific function of the nucleic acid
Structure N	DNA **or** mRNA **or** rRNA **or** tRNA	Codes for the proteins/enzymes that are produced inside the chloroplast **or** Carries a RNA complement of the DNA found in the chloroplast to the ribosomes where protein/enzymes are produced in the chloroplast **or** Site where proteins/enzymes are produced in the chloroplasts **or** Carry amino acids to the ribosomes in the chloroplast so that proteins/enzymes used in the chloroplast can be produced
Structure Q	mRNA	Carries a RNA complement of the DNA found in the nucleus to the ribosomes where protein/enzymes are produced

2-139 [VCAA 2015 SB Q1]

a i

Structure level of protein	Diagram (A, B or C)
primary	C
secondary	A
tertiary	B

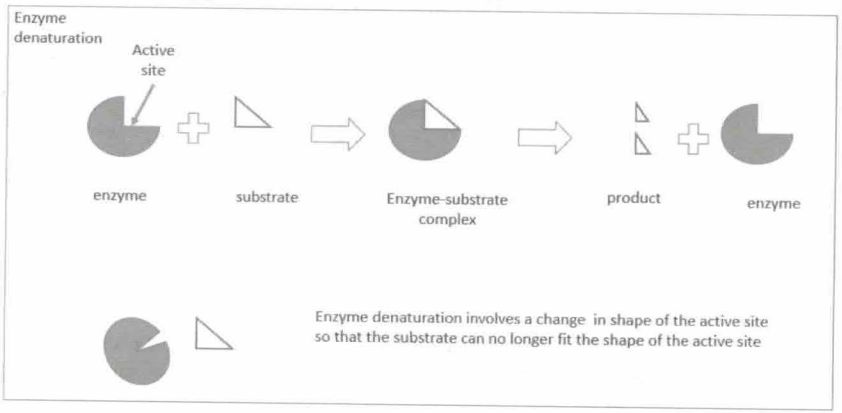
ii Amino acid

b Any two of the following:

- Piercing the membrane results in loss of cell contents disrupting metabolic reactions.
- Mitochondria are lost therefore, the cell has reduced aerobic respiration/ATP available to maintain life.
- Ribosomes are lost, translation and therefore protein synthesis will be reduced. The cell will not be able to produce enough enzymes to catalyse metabolic reactions at the speed required to maintain life.
- Piecing the membrane initiates apoptosis.
- Loss of contents/damage to membrane results in disruption of the cell's osmotic gradient.

c The specific shape of the molecular chaperone would need to be considered. The shape of the molecular chaperone determines its ability to bind to the protein and allow correct folding. The molecular chaperone must have a complementary shape to the protein it binds to. The rational drug must have the same shape as the molecular chaperone if it is to have the same function.

d



2-140 [VCAA 2013 SB Q2]

a Polymerise refers to the production of a large molecule from many repeating smaller units by condensation reactions. The protofilament molecule is formed from many repeating units of smaller alpha-tubulin and beta-tubulin.

b The primary structure of alpha-tubulin refers to the set/specific order of amino acids in its polypeptide chain whereas the secondary structure refers to the folding and twisting of the polypeptide chain (alpha helices/beta-pleated sheets) due to the formation of hydrogen bonds between amino acids within the chain.

c Tertiary structure refers to the folded 3-dimensional shape of the secondary structures of the protein molecule. In this example, this refers to the long chains that form the protofilaments. Quaternary structure refers to the structure that is formed by two or more polypeptide chains joined together. In this example, this refers to the microtubule made of 13 protofilaments.

2-141 [VCAA 2020 SB Q11]

a The results indicate the linear DNA:

- has one recognition site for BamHI cutting the DNA into 2 pieces, one 5500bp and one 4000bp long
- has 2 recognition sites for HindIII cutting the DNA into 3 pieces, one 500bp, one 1000bp and one 8000bp long
- when cut with both BamHI and HindIII, the DNA was cut into 4 pieces, one 500bp, one 1000bp, one 2500bp and one 5500bp long
- the recognition site for BamHI is located within the 8000bp piece produced by HindIII.

b Any one of the following:

- No bands are present in Tube 1. This suggests that no DNA is present due to the student not loading the buffered DNA correctly into the well
- Only 1 band not 3 bands are present in Tube 2. This suggests that the restriction enzymes have been denatured.

c Any two of the following

- the length of the DNA fragment
- the density of the agarose gel
- the type of agarose gel
- the voltage applied to the gel

Note: not charge as all fragments are DNA and will therefore have the same charge.

d Any two of the following safety guidelines:

- wear gloves to stop the contact of chemicals with the body
- wear glasses to stop chemical contact with eyes
- correct disposal of chemicals
- avoiding electrocution by ensuring the equipment is not touched when the current is turned on

2-142 [VCAA 2019 SB Q8]

a Many possible answers including sickle cell anaemia, Huntington disease, cystic fibrosis.

b

Stage	What is happening at this stage
1	Denaturing: the DNA is denatured by heating to around 95°C
2	Annealing: the sample is cooled to approximately 50°C. Primers – synthetic single strand pieces of DNA (usually) that are complementary to the DNA sequence either side of the target sequence are added and anneal to the exposed DNA strands. DNA nucleotides are added.
3	Extension: the sample is heated to approximately 72°C. Taq polymerase is added (heat tolerant enzyme from Taq bacteria). This joins nucleotides together starting at the primer and continuing to the end of the template DNA. The cycle is repeated many times resulting in a mixture of DNA strands including many copies of the desired sequence of DNA.

c Three factors affecting the migration of DNA fragments through agarose gel:
- the length of the DNA fragment. The shorter the fragment the easier the movement therefore the greater distance travelled.
- the charge on the DNA fragment. DNA has a negative charge, so it is attracted to the positive end of the gel.
- the consistency of the gel. Gels vary in density. The denser the gel the shorter the distance the DNA travels.

d Any one from each category:

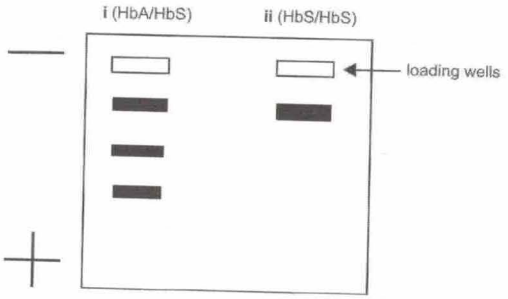
	Issue/implication
Ethical	Should the pregnancy be terminated? If only one parent carries the mutation, should they be told? Does the foetus have a right to live?
Social	Who should pay for the testing? May lead to increased costs for psychological therapy for known carriers

2-143 [VCAA 2004 SB Q7]

a The ends of the fragments are called sticky ends.

b The HbS mutation removes a *MstII* recognition sequence from the allele so the restriction enzyme cannot cut the section of DNA used in the test.

c



2-144

a CRISPR-Cas 9 defends bacteria from invading viruses by cutting the viral DNA into pieces.

b **(i)** RNA guide: guides the Cas 9 endonuclease to the target site.

(ii) Cas 9 endonuclease unwinds the DNA and cuts both strands at a specific site.

c CRISPR-Cas 9 can edit genes by:
- Gene knock in – where a new sequence of DNA is inserted into the DNA.
- Gene knock out – where a sequence of DNA is removed from the DNA.

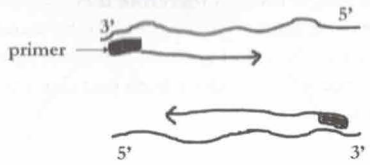
d Any two of the following:
- more precise
- fast
- low cost.

2-145 [VCAA 2007 SB Q2]

a Polymerase chain reaction.

b The DNA is heated to 90°C between stage 1 and stage 2. This breaks the hydrogen bonds between the bases and separates the strands.

c



Nucleotides are added to the primers by taq polymerase

d ↑ (Arrow pointing up the page.)

e The standards consist of DNA of known lengths. The size of the DNA in the other samples can be determined when they are compared with the known standard samples.

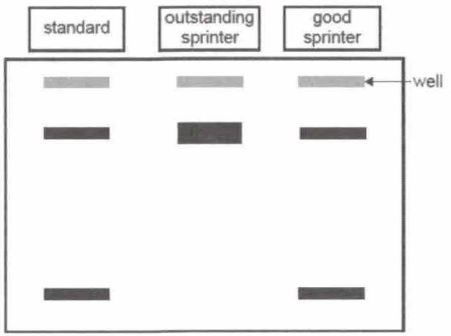
f The sample taken from the crime scene is not from the victim but could be from either suspect.

g Any one of the following:
- use different restriction enzymes to cut DNA from the victim, suspects and crime scene sample
- repeat the procedure for different gene loci
- compare suspects' fingerprints with those found at the scene of the crime
- DNA profiling of the sample and suspects.

2-146 [VCAA 2012 E2 SB Q3]

a - DNA **is denatured** by heating to around 95°C.
- The sample is cooled tot approximately 50°C. Primers – synthetic single strand pieces of DNA (usually) that are complementary to the DNA sequence either side of the target sequence are added and anneal to the exposed DNA strands.
- DNA nucleotides are added.
- The sample is heated to approximately 72°C. Taq polymerase is added (heat tolerant enzyme from *Taq* bacteria). This joins nucleotides together starting at the primer and continuing until the end of the template DNA.
- The cycle is repeated many times resulting in a mixture of DNA strands including many copies of the desired sequence of DNA.
- Gel electrophoresis is used to separate out the copies of the desired sequence of DNA.

b



The outstanding sprinter will have one bar corresponding to the standard band at the shortest distance from the well. This band should be slightly thicker. The good sprinter should have two bands corresponding to the standard bands.

Reason: The 577R and the 577X alleles code for proteins that are different length. The 577X allele codes for a short protein and the 577R allele codes for a

longer protein. The outstanding sprinter is homozygous for the 577R allele therefore only produces the longer protein therefore there will be only one band, and, as this is the longer protein, it must correspond to the standard band at the greatest distance from the well. The good sprinter is heterozygous therefore has both alleles and would be expected to produce both proteins and therefore show the same pattern as the standard.

2-147 [VCAA 2010 E2 SB Q8]

a STRs are found in introns which are non-coding sections of DNA.

b Polymerase chain reaction.

c Family Y is Ben's most recent common ancestor as there are more (four out of five) STR markers in common between Ben and Family Y than either other family.

2-148 [VCAA 2008 SB Q6]

a Each restriction enzyme cuts DNA at a specific and unique DNA sequence or recognition site. (Note referring to a recognition place or position is incorrect.) Using the same restriction enzyme on Individual 1 and Individual 2 will allow scientists to compare the genetic variation in the number and position of recognition sites.

b i The different lengths of DNA are sorted as the smaller the fragment the further and faster it will more through the gel.
Or
The DNA fragments have a negative charge and are attracted to the positive end of the gel.

ii Each individual will contain different alleles and thus different DNA sequences. This means the individuals will vary in the number and position of the restriction enzyme's recognition site and this will result in different fragment lengths for each individual.

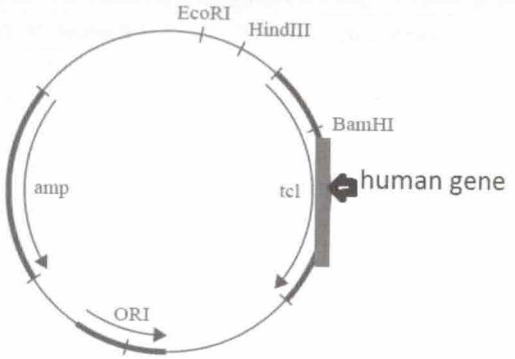
c In this example, hybridisation refers to the bonding by complementary base pairing, of a single strand of DNA with a single strand of RNA. This is necessary, as the radioactive RNA will allow the bands to be seen by autoradiography enabling the patterns of the two individuals to be compared.
(Note hybridisation should refer to this particular experiment.)

2-149 [VCAA 2017 SB Q9]

a Vector refers to the use of a plasmid to introduce recombinant DNA into another cell or organism.

b i BamHI is a restriction enzyme that cuts DNA at a specific recognition site. The resulting cut is uneven leaving sticky ends. If the same restriction enzyme is used to cut a plasmid and the gene to be inserted, the plasmid and the gene will have complementary sticky ends that can then be joined using ligase.

ii



c Plasmids that have taken up the human gene contain the gene for ampicillin resistance but not for tetracycline resistance as the gene for tetracycline resistance has been disrupted by the insertion of the human gene. The disruption has occurred because the recognition site for BamHI is found within the gene for tetracycline resistance. This means that bacteria that are able to grow on ampicillin but not on tetracycline must contain the recombinant DNA.

2-150 [VCAA 2006 SB Q4]

a Circular. (Note: a circular fragment of DNA is not acceptable.)

b Transformation

c i No growth of bacteria.

ii Bacterial cells on plate B have not been exposed to the plasmid; therefore, they do not contain the gene for the enzyme, which provides resistance to tetracycline; therefore, they will die when exposed to tetracycline.

d On plate A, there is no tetracycline therefore all bacteria can grow and continuous growth occurs. On plate C where tetracycline is present, only bacteria that have taken up the modified plasmid will survive. Not all bacteria will have taken up the plasmid so the colonies are the descendants of those bacteria that did take up the plasmid.

2-151 [VCAA 2018 SB Q10]

a Transgenic organisms have genes from a different species in their cells. Bt cotton cells have genes from a bacterium (*Bacillus thuringiensis*) and Golden rice has genes from a bacteria (*Erwinia uredovora*) and a daffodil (*Narcissus pseudonarcissus)* therefore they are both transgenic.

b Bt cotton produces a protein that stops insects eating the cotton plants therefore more plants will survive and the yield will be greater.

c

	Social implication	Biological implication
Bt cotton	Any one of - expensive as new seed must be bought each year - increased yield therefore more money is available for an increased standard of living	Any one of - increased skin disease in farmers - less pesticides are used - insects may develop resistance therefore more genetic modification maybe required - crops are less resistant to *Helicoverpa*
Golden Rice	Any one of - profits are increased as rice can be kept from one year's crop until the next - population is healthier therefore increased standard of living - proven safe	Any one of - less vitamin A deficiency - improved nutrition - risk of cross pollination with wild rice

2-152

Transgenic species contain a gene from another species. An example of a transgenic species is bacteria that been genetically engineered to produce human insulin.

In this transgenic bacterium, the human insulin gene has been inserted in a plasmid and then the plasmid has been transformed into the bacteria. This has enabled the production of contamination-free insulin for diabetics and has resulted in improved health and life expectancy for diabetics.

Many people think that bacteria should not be used to produce insulin. The use of antibiotic resistant genes in plasmids to select transformed bacteria could be dangerous. If these plasmids were transferred to disease-causing bacteria, it could lead to a strain of bacteria that could not be treated with antibiotics.

Others say that this is very unlikely and that the supply of contamination-free insulin will improve the quality of life for so many diabetics that it is worth the risk.

Chapter 3: How are biochemical pathways regulated?

3-1 Energy is never used. In doing work, energy is converted from one form to another and at the end of the process may be unusable. Most organisms store energy in chemicals such as fat or starch. The energy is made available to do cellular work during cellular respiration.

3-2 Cells need energy to do cellular work. Processes that require energy are cell division, synthesis of new parts and materials, muscular contraction, active transport and nervous conduction.

3-3 Anabolic reactions are those involving the building or synthesis of molecules whereas catabolic reactions are breakdown reactions.

3-4 **Exergonic reactions** (breaking things) release energy, e.g. respiration.
Endergonic reactions (making or doing things) require an input of energy for them to proceed, e.g. any synthesis reaction such as protein synthesis.

3-5 An enzyme is an organic catalyst. They are proteins that alter the rate of reactions – usually to speed them up to a biologically useful rate. Many reactions occur naturally but at extremely slow rates. Enzymes only alter the rate (amount produced in a given time) of reaction. They do not alter the final amount of product produced.

3-6 Specific enzymes catalyse (alter the rate) of specific reactions. Enzymes bind with the substrates (reactants or ingredients) to form a temporary enzyme substrate complex. The enzymes have areas called active sites. The shape of a specific substrate molecule will match the active sites on a specific enzyme. Only the correct enzyme with the correct molecular shape will bind to the substrate molecule, in the same way that a particular key will open a particular lock. The induced fit model states that there can be some change in the active site. The flexibility allows for closer fit between the substrate and the enzyme.

3-7 Substrates are the materials that are to be processed. The processing could be a breakdown reaction (e.g. digestion) or a synthesis reaction (e.g. making proteins). The materials present at the end of the reaction are the products. Enzymes allow the formation of product from substrate in a time that allows the efficient operation of an organism. Many of the reactions catalysed by the enzyme would otherwise occur too slowly.

3-8 Enzymes do not increase the amount of product produced. They reduce the time it takes to produce the product.

3-9 The rate of reaction refers to the amount of product produced in a given time. For example, the rate of reaction could be measured in micrograms of product produced per minute.

3-10 Enzymes are proteins. The folding of the protein into its tertiary structure provides a site that matches with specific substrates. This site is called the active site.

3-11 Enzymes are proteins so they can be denatured by:
- high temperatures (break H bonds and van der Waals forces destroying the quaternary and tertiary structure)
- extremes of pH (break ionic bonds, destroying the quaternary and tertiary structure).

3-12 Competitive inhibitors have a similar shape to the specific substrate on which an enzyme acts. They compete with the enzyme for the active site reducing the amount of enzyme available to catalyse the reaction.
Non-competitive inhibitors do not bind to the active site. Instead, they bind to another area of the enzyme (allosteric site). This results in a change in the shape of the active site which decreases the amount of enzyme available to catalyse the reaction.

3-13 Coenzymes are small, non-protein molecules that temporarily bind to enzymes increasing the enzyme's ability to bind to the substrate. Coenzymes are also carrier molecules – they may carry electrons, protons, specific atoms or groups of atoms such as phosphate and energy.