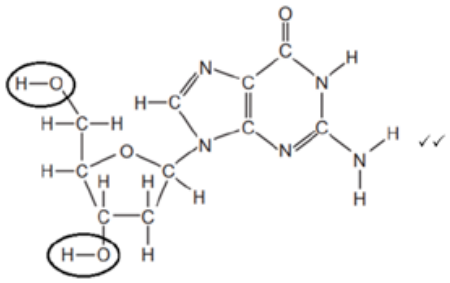
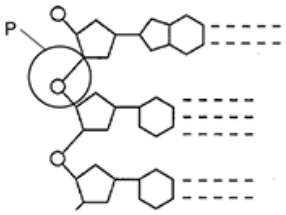
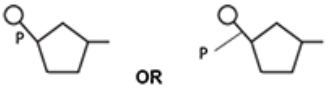
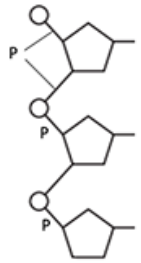
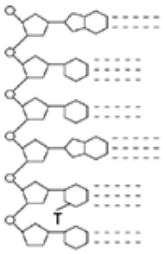
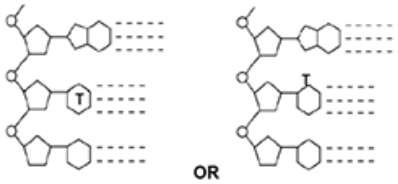
Mark scheme

Question			Answer/Indicative content	Marks	Guidance
1			B	1	**Examiner's Comments** Many correct responses, option **B** were seen. The idea of lipids being macromolecules but not polymers is a concept that has been tested before, and forms a good discussion point in class when revising biological molecules.
			Total	**1**	
2	a		 ✓✓	2	**one mark per correct circle** **ALLOW** circles around OH or H alone **ALLOW** clear, unambiguous mark other than a circle **DO NOT ALLOW** if circle encloses other parts of molecule e.g. CH_2 or O alone **If more than 2 circles drawn, -1 mark for each incorrect circle** **Examiner's Comments** A number of candidates scored 2 on this question for circling the O-H groups or the H atoms on the sugar molecule. Some candidates were unable to be credited marks for including the C atom in their circles, while other candidates circled parts of the guanine molecule.
	b		(produces) ATP to provide (chemical) energy / AW ✓ (DNA replication) requires ATP /AW ✓	1	**DO NOT ALLOW** 'produces energy' **ALLOW** requires ATP as it is an active process **ALLOW** 'because ATP is needed' e.g. need for ATP (in, DNA replication / to break bonds between bases / form phosphodiester bonds) **Examiner's Comments**

					This was well answered by most candidates. Even if they did not give a clear answer as to what the ATP was used for, they could gain the available mark for saying that ATP provides energy or DNA replication requires ATP. Some candidates did not score the mark for this question as they mentioned the use of ATP in protein synthesis, transcription or translation.
			Total	**3**	
3	a		(more than two) nucleotides joined by <u>phosphodiester</u> bonds **OR** (more than two) nucleotides joined in a condensation (reaction)✓	1	**<u>Examiner's Comments</u>** This question discriminated well and some candidates were given the mark. The main common error seen was no mention of nucleotides – candidates often just used monomers from the stem of the question, but bonds between bases and amino acids were also seen. Hydrogen bonds, peptide bonds, glycosidic and ester bonds were also seen in responses where candidates were not given marks, suggesting they were mixing up the different biological molecules.
	b	i	unzips, (DNA) double helix / strands / molecule ✓ breaks hydrogen bonds between the , two strands /(nitrogenous/complementary/named) bases / base pairs ✓	2	**ALLOW** unwinds **ALLOW** described for MP1 e.g. 'creates 2 separate strands of DNA' **<u>Examiner's Comments</u>** Some candidates were given 2 marks and some were given 1, suggesting the action of helicase is well known. Unzipping/unwinding was nearly always seen, but the most common mistake was not making it clear that there were two strands being separated and/or linking this to the DNA double helix. Many candidates missed out the breaking of Hydrogen bonds for the second mark.
		ii	mutation / described ✓ change in DNA (base) sequence / order of bases changed ✓ description of types of mutation (e.g. substitution / addition / deletion /	2 max	e.g. spontaneous / random change **ALLOW** wrong nucleotide / base inserted e.g A pairs with G not T **DO NOT ALLOW** direct ref to transcription / RNA bases / A pairing with U

			frameshift / idea of wrong complimentary base pairs being matched up (during DNA replication) etc.) ✓ e.g. exposure to (named) mutagen ✓		e.g. radiation, (named) carcinogens, (toxic) chemicals, sunlight, UV **Examiner's Comments** Most candidates were given 1 mark for correctly identifying mutations as a key term. Many candidates focused on incorrect complimentary base pairing but did not link this to the resulting DNA base sequence being different (i.e. suggesting that the base pairing was wrong but then not explaining that this leads to a different sequence of bases). A few candidates lost a mark by referring to transcription and RNA, possible due to not recognising the need to refer to DNA replication stated in the stem of the question.
	c		*Yes because*… 1. crushing, breaks down / opens, cell walls ✓ 2. salt, breaks hydrogen bonds between the DNA and water (molecules) / makes DNA less soluble in water ✓ 3. ethanol added to cause precipitation of DNA ✓ 4. ethanol would break down/disrupt the, plasma / cell surface / nuclear, membrane ✓ *No because*… 5. detergent not added to break down, plasma / cell surface / nuclear, membrane ✓ 6. enzyme not specified as a protease / enzyme must be a protease, to digest, (histone) proteins ✓ 7. ethanol is not (ice) cold so enzyme activity not reduced ✓	4 max	**DO NOT ALLOW** cell membrane **and** cell wall **IGNORE** ref to precipitation/clumping **ALLOW** DNA won't stay dissolved in ethanol / will clump the DNA together / DNA becomes visible **DO NOT ALLOW** ref to denaturing enzymes **Examiner's Comments** This question discriminated well, with only able responses gaining 3 or 4 marks. Candidates mostly knew the reason for crushing, adding ethanol, enzyme and pointed out the need for detergent. However, marks were lost for imprecise use of terms such as cell membrane or phospholipid bilayer for marking point (MP) 4 and 5. Very little reference was made to the purpose of adding salt, suggesting that candidates were unfamiliar with the reason for this stage in the procedure. Responses from candidates that gained marks reflected that they had had experience with this practical in some form, but possibly had not delved in to the detail of the purpose

					of each stage. Very few got MP2, and salt was often linked to every other process, or it was stated that it was not required, or to the breaking of Hydrogen bonds in DNA rather than between DNA and water to reduce solubility. MP3 was often seen, although quite a few thought that the ethanol would only work if ice cold. A number of candidates spend valuable time discussing the viability of the practical although this was not part of the question so were not given anymarks. Some students rightly stated that a protease would break down the histone proteins, but this wasjust a statement and it was not linked to the evaluation that the method did not state which enzyme should be added. **Misconception** Many candidates thought that crushing the strawberry broke open the plasma membrane. This stage was to break down the cell walls and would not have affected the cell membranes.
			Total	**9**	
4		i	P labelling a, bond / link, between two nucleotides in the sugar-phosphate backbone ✓	1	e.g.  **ALLOW** P labelling a bond between a deoxyribose and a phosphate e.g. 

					ALLOW If more than one bond labelled, e.g.  **Examiner's Comments** The majority of candidates gained the mark here either labelling a bond between a phosphate group and the sugar or by circling the whole phosphodiester bond. Some candidates labelled the phosphate group.
		ii	T labelling the 5th (2nd from bottom) base ✓	1	**e.g.**  **ALLOW** T written inside or next to cytosine without a label line, e.g.  **ALLOW** correct base labelled as C (for cytosine) **DO NOT ALLOW** if a second T has been included elsewhere on the diagram **Examiner's Comments**

					Few candidates were able to work out the correct part of the molecule to label. The range of responses given suggested that for many it was a guess.
			Total	**2**	
5			D ✓	1	**Examiner's Comments** Many candidates selected the correct response, D. A common error was to select answer C which suggests that although candidates were able to identify the molecule as RNA, they found it challenging to distinguish between purines and pyrimidines **Assessment for learning** Centres could help candidates recall by encouraging the use of mnemonics or aide memoires to recall certain details. For example, 'Cut the py' can be used to recall that pyramidines have been cut or have a single ring, leaving the purines with a two-ring structure.
			Total	**1**	
6			C ✓	1	
			Total	**1**	
7			(DNA polymerase) (catalyses) formation of phosphodiester bonds (between nucleotides / in DNA strand) ✓ (helicase) unwinds / separates / unzips, (DNA) double helix / (DNA) strands ✓	2 (AO1.1)	**ALLOW** proofreading of new DNA strand **ALLOW** adds nucleotides to new DNA strand **ALLOW** construction of new sugar phosphate backbone (between nucleotides / in DNA strand) **ALLOW** breaks the H bonds between, base pairs / (DNA) strands / nucleotides **Examiner's Comments** Generally, many candidates were able to access both marks for this question and gave good, detailed responses. A number of candidates mixed up the role of helicase and DNA polymerase

					gaining no credit. Common errors included: • not being able to state the specific bond that is made by DNA polymerase. Some candidates stated it to be a hydrogen bond, while some stated it to be sugar bond • mixing up translation and transcription with DNA replication and referring to mRNA formation • not making it clear that the two strands of DNA were being separated by helicase, e.g., "unwinds DNA" rather than "unwinds DNA double helix/strands".
•			**Total**	**2**	
8		i	1 movement of cells ✓ 2 strengthening / supporting , cells ✓ 3 movement of (named) organelles ✓ 4 holds organelles in place ✓ 5 form (mitotic / meiotic) spindle ✓ 6 movement of , chromatids / chromosomes ✓ 7 cleavage in (some) cells / cytokinesis ✓	max 3 (AO1.2)	**Mark as continuous prose** **IGNORE** cilia / flagella **MP1 ALLOW** change in cell shape e.g phagocytosis **MP2 ALLOW** maintains cell shape **IGNORE** structure **MP3 ALLOW** form tracks for motor proteins **MP4 ALLOW** attachment of (named) organelle(s) **MP7 IGNORE** cleavage / cytokinesis , in plant cells **<u>Examiner's Comments</u>** This question was generally well answered with most candidates gaining at least 1 mark. Some candidates gave two answers that were the same marking point. For example, vesicles are considered organelles, and therefore 2 marks would not be gained for stating movement of vesicles, and movement of organelles, as this is still MP3.

		ii	1 change in , structure / function , of (cytoskeleton) protein ✓ 2 less / no , movement of vesicles / exocytosis / release of neurotransmitter ✓ 3 less / no , synaptic transmission / AW ✓ 4 could change diameter of axon ✓ 5 affects speed of nerve impulses ✓ 6 *idea that* it could affect Schwann cell integrity / AW ✓	max 2 (AO2.1)	**MP1 ALLOW** non-functional protein is producde **MP2 DO NOT ALLOW** 'no vesicles released' **MP3 ALLOW** impulse cannot cross synapse / action potentials do not continue from one neurone to the next **MP3 DO NOT ALLOW** action potential cannot cross the synapse **Examiner's Comments** This question was challenging for some candidates. Good responses included suggestions that this could result in lack of movement of vesicles or affect the release of neurotransmitters and went on to suggest that this could result in loss of transmission at the synapse. Some candidates did not make the connection between mutation and change in protein structure or function and others described the effects resulting from a mutation to protein channels which, although relevant to protein structure, did not form part of the response about cytoskeleton proteins.
			Total	**5**	
9			A ✓	1 (AO1.1)	
			Total	**1**	
10			(cell / nuclear / mitochondrial / chloroplast) membrane(s) ✓ protease ✓ alcohol / ethanol ✓	3(AO1.2)	**Mark the first answer in each space** **ALLOW** nuclear envelope **ALLOW** named protease e.g. pepsin / trypsin **Examiner's Comments** Candidates generally scored 2 or 3 marks. Most knew that detergent is used to break down membranes (often nuclear membranes mentioned). Relatively few knew that protease was required and often offered water as a suitable way to hydrolyse the histones. More knew

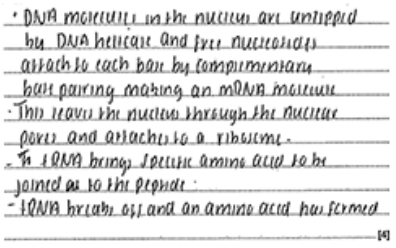
					that (ice cold) ethanol is used although many suggested salt was used to precipitate the DNA.
			Total	**3**	
11			D ✓	1(AO1.1)	**Examiner's Comments** Only a minority got the right answer here. The most common incorrect answer was B, perhaps suggesting that candidates were aware that adenine is a purine but unaware that the sugar in ATP is ribose.
			Total	**1**	
12		i	1 = threonine ✓ 2 = proline ✓	2(AO2.1)	**Examiner's Comments** Almost all candidates got both marks here.
		ii	joins / adds , (RNA) nucleotides ✓ forms phosphodiester bonds (between nucleotides) ✓	2(AO1.2)	**IGNORE** bases **ALLOW** forms sugar–phosphate backbone **IGNORE** covalent bonds **Examiner's Comments** This question differentiated well between candidates of differing abilities but only a minority of candidates gained both marks. Many candidates thought RNA polymerase formed hydrogen bonds between the mRNA and the template strand and a few confused it with DNA polymerase or even helicase.
		iii	CAC ✓	1(AO2.1)	**ALLOW** cytosine adenine cytosine **IGNORE** CAU **Examiner's Comments** Not many candidates gave the correct answer to this stretch and challenge question. Some used Fig. 16.3 to identify an anticodon for valine but did not appreciate that GUG was the only substitution mutation of GAG that would result in valine. Many

					candidates suggested codons, rather than anticodons.
		iv	**Level 3 (5–6 marks)** Explains in detail why mutations may leave the function of a protein unchanged using Fig 16.3 **and** referring to more than one level of protein structure. *There is a well-developed line of reasoning which is clear and logically structured. The information presented is relevant and substantiated*. **Level 2 (3–4 marks)** Explains why mutations may leave the function of a protein unchanged using Fig 16.3 **and** referring to protein structure. *There is a line of reasoning presented with some structure. The information presented is relevant and supported by some evidence*. **Level 1 (1–2 marks)** Suggests why mutations may leave the function of a protein unchanged using Fig 16.3 **or** referring to protein structure. *There is an attempt at a logical structure with a line of reasoning. The information is in the most part relevant*. **0 marks** *No response or no response worthy of credit*.	6(AO2.1)	**Indicative points may include** *Mutations* • genetic code is degenerate • point mutation might code for the same amino acid • use of example from Fig 16.3 to support *Protein structure and function* • haemoglobin function is dependent on tertiary structure • silent mutation would leave primary structure unchanged • unchanged primary structure would leave tertiary structure unchanged • substitution of amino acid with similar properties to the original amino acid might leave tertiary or secondary structure unchanged • mutation might change part of the tertiary structure away from the functional part of the protein, e.g. away from the active site of an enzyme **<u>Examiner's Comments</u>** The question asked candidates to refer to three things in their answers: Figure 16.3, mutations and levels of protein structure. Responses that did not do all three were limited to Level 1. However, the question provided a good spread of marks and differentiated well between candidates. Most candidates appreciated the degenerate nature of the genetic code and most illustrated this with reference to Fig. 16.3. Many could also explain the implications of this degeneracy in terms of silent mutations. Some of these candidates could also clearly explain why a silent mutation would have little impact on protein structure.

					Some even discussed the effect of substituting an amino acid for another with an R-group with similar properties. Many responses showed poor understanding within both sections, which was often illustrated by inaccurate use of technical terms. Confusion between bases and amino acids was evident, as were frequent references to amino acids, bases or DNA being degenerate. Candidates seemed more confident discussing mutations than they were protein structure, but a few candidates appeared to think that the amino acids were *produced*, as opposed to *selected*, on the basis of the generic code. Some responses were not given the communication mark because of confusing use of technical terms. Many other responses were presented as either an explanation of the three types of mutation and their effects or as a description of protein structure which did not answer the question that had been asked. **Exemplar 1**  Level 3 was achieved in the first 13 lines of this response. The rest of the response was irrelevant to the question that was asked and so was a waste of the candidate's time.
			Total	**11**	
13	a		insulin is made from <u>two</u>, polypeptide chains / amino acid chains / primary	2	**IGNORE** 'multiple chains' or 'more than one'

			structures ✓ chains joined by disulfide bonds (between, cysteine / CYS) ✓		**ALLOW** disulfide bridges **Examiner's Comments** The figure clearly shows two polypeptide chains, and the chains are joined by bonds between cysteine residues. Many candidates simply described what is meant by a quaternary structure as having 'more than one' or 'many' polypeptide chains. Many candidates also correctly stated that there were disulfide bonds between cysteine residues but did not point out that these were on separate chains and therefore joined the chains together. Only a minority of candidates were able to appreciate the detail provided in figure 21.1 and state correctly the two required features. **Assessment for learning** Candidates should read the question carefully. They should appreciate that the question refers to the insulin molecule in the figure rather than to a generalised protein with a quaternary structure. A reference to the figure is essential to gain marks.
	b	i	change in primary structure changes, tertiary structure / 3D shape ✓ (tertiary structure / 3D shape) no longer complementary (to shape of enzyme) ✓ less likely to be broken down by enzymes / enzyme-substrate complexes less likely to form ✓ change in solubility ✓	Max 1	**ALLOW** change in complementary shape **IGNORE** takes longer to be broken **ALLOW** can't be broken down easily / harder to break down **DO NOT ALLOW** can't be broken down by enzyme / ESC can't be formed **ALLOW** more or less **DO NOT ALLOW** ref to insulin glargine being insoluble

					Examiner's Comments The most able candidates were able to spot that there would be a change in the tertiary structure which would mean the molecule was no longer fully complementary in shape to the active site of the enzyme. However, this was often worded simply as 'the molecule is harder to break down'. This simplified mark point was accessed by many more candidates. Very few candidates were able to make the link between the change in primary structure and the resulting change in the tertiary structure. Many suggested that simply making the polypeptide longer meant there were more bonds to break and so this would take longer.
		ii	AAT / AAC ✓ is replaced by, GGT / GGC / GGA / GGG ✓	2	For two marks: **ALLOW** 1st A and 2nd A replaced by GG. **ALLOW** A replaced by G twice **ALLOW** 2 A's replaced by 2 G's For one mark: **ALLOW** A replaced by G **Examiner's Comments** Most candidates were able to extract the correct information from the table and gain full credit. The most common error was not making it clear that both adenine bases were replaced by guanine. A small number of candidates seemed to be unfamiliar with using DNA code data tables and referred to ASN (Asparagine) or GLY (Glycine) as the code or codon being altered; they were apparently unaware that these are just the accepted abbreviations for amino acids. Other candidates misread the question and used the code for arginine rather than the code for asparagine.
		iii	1. (modified gene undergoes) transcription (in nucleus)✓	Max 4	**Examiner's Comments**

			2. production of (modified) mRNA / described ✓ 3. mRNA, leaves nucleus / goes to ribosomes ✓ 4. translation at ribosome(s) ✓ 5. tRNA with specific amino acid binds its anticodon (to codon of mRNA) ✓ 6. (formation of) peptide bonds between amino acids ✓		Those candidates that read the question correctly often did very well, gaining 3 or 4 marks. Some excellent responses were seen with well-sequenced and detailed accounts. The majority of the candidates showed good knowledge and understanding of the production of mRNA followed by leaving the nucleus or going to the ribosomes. Less well known was the fact that the tRNA has a specific anticodon and brings a specific amino acid to the ribosome. The formation of peptide bonds was often missed out. Many of the more able candidates continued beyond the requirement of the question, (e.g., to the point where the polypeptide is made) and gave details of the transformations required to produce the quaternary structure of the protein. Many candidates did not use the terms ‘transcription’ and ‘translation’. Unfortunately, a relatively large number of candidates did not read the question with sufficient care. Having seen the references to genetic engineering they then gave an account of that process to describe how the gene could be modified to produce insulin glargine. Another common error was that candidates described DNA replication rather than transcription. **Exemplar 1**  • DNA molecule in the nucleus are unzipped by DNA helicase and free nucleotides attach to each ban by complimentary ban pairing making an mRNA molecule • This leaves the nucleus through the nuclear pores and attaches to a ribosome. • Te tRNA brings specific amino acid to be joined on to the peptide. • tRNA breaks off and an amino acid has formed [4] Exemplar 1 shows a typical response that gives a clearly sequenced outline, but that could with more detail to gain full marks. This response was given 2

					marks for production of mRNA and the mRNA leaving the nucleus. More marks could have been achieved if more detail of translation had been given. For example, stating that the tRNA has a specific anticodon that is complementary to the codon on the mRNA which ensures the specific amino acid is held in the correct position. Naming the peptide bond used to join the amino acids together would also gain credit.
			Total	**9**	
14			**B** ✓	1	**Examiner's Comments** Most candidates gave the correct response (B). The most common incorrect responses appeared to be A and C.
			Total	**1**	
15			**B** ✓	1	**Examiner's Comments** Most candidates gave the correct response (B). The most common incorrect responses appeared to be A and C. Candidates who chose A as the correct option, didn't read the question carefully. Instead of calculating the probability of having a mutation in a gene that codes for a protein they calculated the probability of a non-coding DNA. In order for candidates to get the correct answer they had to first identify the proportion of coding DNA (22/25) and multiply that with the probability of having a mutation (22/25 * 1/333).
			Total	**1**	
16			**C** ✓	1	**Examiner's Comments** Most candidates gave the correct

					response (C). The most common incorrect response appeared to be B, which was the distractor in the question. Candidates who did chose B misinterpreted the question, with unzipping of DNA rather than cutting the DNA molecule.  **Misconception** Candidates seem to have a misconception with the function of restriction endonuclease enzymes and how sections of DNA can be obtained.
			Total	**1**	