Mark scheme

Question			Answer/Indicative content	Marks	Guidance
1		i	amine ✓ carboxyl ✓	2	**IGNORE** structural / molecular, formulae **ALLOW** amino for 'amine' **ALLOW** carboxylic acid (group) for 'carboxyl' **Examiner's Comments** Well answered with most candidates achieving 2 marks. Some answers referred to the carboxylic acid as a hydroxyl group. Candidates should realise that the functional group relates to all the atoms coming from the terminal carbon.
		ii	circle drawn completely around bond between C=O **AND** the N-H	1	**ALLOW** circle to encompass C=O **AND** the N-H **IGNORE** circle line **on part of** the bonds immediately before and after C=O **AND** the N-H **Examiner's Comments** Many candidates correctly identified the peptide bond and often restricted their circle to just one bond. A lot of candidates omitted this question part.
		iii	hydrolysis ✓	1	**Examiner's Comments** The majority of candidates achieved this mark. Some answers confused it with condensation. **Assessment for learning** Splitting the word and discussing lysis as breaking will cement any reference to breaking with lysis to help eliminate

<table>
<tr><td></td><td></td><td></td><td></td><td></td><td>confusion with these two opposing terms.</td></tr>
<tr><td></td><td></td><td></td><td>Total</td><td>4</td><td></td></tr>
<tr><td>2</td><td></td><td></td><td><table>
<tr><th>Biological molecule</th><th>Is a monomer</th><th>Is a polymer</th><th>Contains glycosidic bond(s)</th></tr>
<tr><td>Amino acid</td><td>✓</td><td></td><td></td></tr>
<tr><td>Amylopectin</td><td></td><td>✓</td><td>✓</td></tr>
<tr><td>Glucose</td><td>✓</td><td></td><td></td></tr>
<tr><td>Sucrose</td><td></td><td></td><td>✓</td></tr>
</table>
1 mark per correct row ✓✓✓</td><td>3</td><td>IGNORE crosses and hybrid ticks
<u>Examiner’s Comments</u>
Many candidates were able to recall the correct features of amylopectin and glucose. Fewer were able to correctly complete the row for sucrose. A common error was to include sucrose as a polymer. Most candidates followed the instructions in the question to place a tick (rather than a cross), and there were very few “hybrid” ticks, with candidates who changed their minds crossing out and rewriting.</td></tr>
<tr><td></td><td></td><td></td><td>Total</td><td>3</td><td></td></tr>
<tr><td>3</td><td></td><td></td><td>Quaternary / 4°
Primary / 1°
tertiary / 3°
secondary /2°</td><td>2</td><td>1 correct = 0 marks
2 or 3 correct = 1 mark
4 correct = 2 marks
ALLOW numbers 1,2,3,4 or 1ry, 2ry, 3ry, 4ry or terms first, second, third, fourth
<u>Examiner’s Comments</u>
This was generally well answered. Candidates commonly found the primary structure easiest to identify and tertiary and quaternary the most difficult to distinguish between.</td></tr>
<tr><td></td><td></td><td></td><td>Total</td><td>2</td><td></td></tr>
<tr><td>4</td><td></td><td>i</td><td><table>
<tr><th>Statement</th><th>Level of Protein Structure</th></tr>
<tr><td>Disulfide bonds are formed when two cysteine amino acids in an a-globin chain come together after the alpha helix folds</td><td>tertiary</td></tr>
</table></td><td>3</td><td>4 correct answers = 3 marks ✓ ✓ ✓
3 correct answers = 2 marks ✓ ✓
2 or 1 correct answer(s) = 1 mark ✓
ALLOW phonetic spelling e.g. quarternary
<u>Examiner’s Comments</u>
Most candidates were given 1 or 2 marks here. Some candidates lost all marks as they misunderstood the question and wrote ‘once’, ‘more than</td></tr>
</table>

<table>
<tr><td></td><td></td><td></td><td><table><tr><td>Haemoglobin is made up of two α-globin chains and two β-globin chains</td><td>quaternary</td></tr><tr><td>Each α-globin and β-globin chain undergoes folding into a spherical shape</td><td>tertiary</td></tr><tr><td>β-globin is an amino acid sequence, 147 amino acids in length</td><td>primary</td></tr></table></td><td></td><td>once' or 'not at all' in the boxes, taking these from the question stem. Some thought that all the structures needed to be used, and so mistakenly identified secondary for one of the statements. Both of these points indicate that some candidates need more practice with this style of question and/or need to take more time to understand the task outlined and should be advised not to rush into this style of question.</td></tr>
<tr><td></td><td></td><td>ii</td><td>carbonic anhydrase ✓</td><td>1</td><td>ALLOW phonetic spelling
ALLOW 'carbonate hydrolase'
<u>Examiner's Comments</u>
When attempted, this was well answered and many candidates were given the mark. When attempted correctly, spelling was generally good with only a small number not spelling the enzyme correctly, although clear phonetic spelling was given the mark. Those who were not given the mark either gave other enzymes or did not give a response.</td></tr>
<tr><td></td><td></td><td></td><td>Total</td><td>4</td><td></td></tr>
<tr><td>5</td><td></td><td></td><td>hydrolysis and (water added and) peptide bonds broken ✓</td><td>1</td><td>ALLOW hydrolysis of peptide bonds
<u>Examiner's Comments</u>
Many candidates knew that the reaction was called 'hydrolysis'. A few candidates, however, did not describe the breaking of 'peptide bonds'. Common errors were to call the reaction 'condensation' or to call the bond broken a 'polypeptide bond' or a 'glycosidic bond'.</td></tr>
<tr><td></td><td></td><td></td><td>Total</td><td>1</td><td></td></tr>
<tr><td>6</td><td></td><td></td><td>D ✓</td><td>1</td><td></td></tr>
<tr><td></td><td></td><td></td><td>Total</td><td>1</td><td></td></tr>
<tr><td>7</td><td></td><td></td><td>B ✓</td><td>1</td><td></td></tr>
<tr><td></td><td></td><td></td><td>Total</td><td>1</td><td></td></tr>
</table>

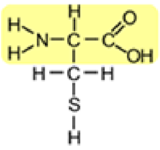
8		i	(named part of) Immune system attacks, cells/tissues, as it recognises them as, foreign/non self. ✓	1 (AO1.2)	**IGNORE** body attacks itself for 'immune system attacks' **ALLOW** have an abnormal immune response as body cells treated as foreign **<u>Examiner's Comments</u>** Few candidates gave the correct meaning as they did not refer to why the immune system was attacking body cells. Some answers referred to the body attacking its own cells without specifying the immune system. Some candidates confused this with a disease that attacks the immune system itself.
		ii	Any two from fibrous ✓ insoluble ✓ (high) tensile strength ✓ resistant to stretching ✓	Max 2 (Ao2.1)	**ALLOW** (high) mechanical strength **<u>Examiner's Comments</u>** Most candidates recognised that collagen was a fibrous protein and some answers referred to it being insoluble. Many candidates gave statements about it needing to be strong for its role but not being precise with the type of strength it exhibits. Some answers referred to collagen as having elastic properties, confusing collagen with elastin.
		iii	bone marrow ✓	1 (AO1.1)	**IGNORE** embryos
		iv	Error 1: perforins Correction: interleukins / cytokines ✓ Error 2: antigen-toxin Correction: antigen-antibodies (complex) ✓	2 (Ao2.5)	**<u>Examiner's Comments</u>** Most candidates identified the errors in the statement, but some struggled to correct those errors. Perforins to interleukins was recalled the most but very few candidates were able to correct antigen-toxin to antigen-antibody. Some candidates did not state the error and only stated the correction.
			Total	**6**	
9			A ✓	1 (AO1.1)	

			Total	**1**	
10			B ✓	1 (AO1.1)	**<u>Examiner's Comments</u>** This is an example of a multiple choice question that asks candidates to identify the option that is **not** correct/true. Most candidates were able to identify **B** as the statement that is **not** true about protein structure. Option **C** was the most common incorrect response with candidates possibly scanning for a 'correct' statement about protein structure. Candidates are advised to read all options carefully before deciding on their response.
			Total	**1**	
11			C ✓	1 (AO1.1)	
			Total	**1**	
12			B ✓	1(AO1.1)	**<u>Examiner's Comments</u>** Around half of responses were correct but many answered C or D.
			Total	**1**	
13	a	i	<u>peptide</u> ✓	1(AO1.1)	**<u>Examiner's Comments</u>** Most candidates got the correct answer, the most common incorrect answers being 'hydrogen', 'glycosidic' and 'disulfide'.
		ii	<u>haem</u> ✓	1(AO1.1)	**IGNORE** prosthetic group / iron / C atom **<u>Examiner's Comments</u>** Around half of candidates correctly identified 'haem'. Some candidates gave a less specific answer such as 'prosthetic group'. Candidates should be guided to give specific answers to questions with the command word 'Name', especially when they have

					been given some detail in the question – they knew it was haemoglobin so ought to have been able to name the prosthetic group. Common incorrect responses were 'iron', 'alpha helix' or 'beta sheet'.
		iii	spherical (shape) / no fibres / (contains) prosthetic groups ✓	1(AO2.1)	**ALLOW** round / ball-shaped **IGNORE** coiled / compact / tertiary structure **Examiner's Comments** Over half of candidates achieved this mark, usually for a description of the shape. The most common uncreditworthy response was 'coiled'.
	b	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

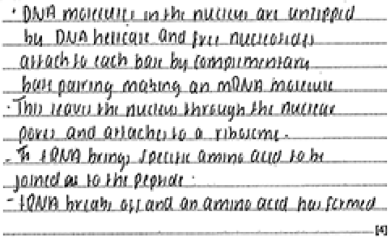
					candidates suggested codons, rather than anticodons.
		iv	**Level 3 (5–6 marks)** Explains in detail why mutations may leave the function of a protein unchanged using Fig 16.3 **and** referring to more than one level of protein structure. *There is a well-developed line of reasoning which is clear and 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**  Some gene mutations such a a silent substitution mutation may ~~[illegible]~~ form a different codon, however codons are degenerate, so more than one codon codes for the same amino acid, so although base sequence is different, the primary protein structure, which is the basic sequence of amino acids remains the same, so there's no change in tertiary protein structure, so the shape and function of the protein can remain the same. Fig 16.3 supports this because for example, for Threonine, there are 4 different codons which code for Threonine, so even if ~~[illegible]~~ ACA has a mutation and changes to ACC, Threonine is also produced. Alternatively a conservative ~~[illegible]~~ mis sense mutation can occur, which codes for a different amino acid, so this changes the primary [6] protein structure, which can change the secondary Additional answer space if required. protein structure, which is hydrogen bonding, and may even have a small impact on tertiary protein structure (disulfide bonds ionic bonds hydrogen bonds and hydrophilic/hydrophobic interactions) however [illegible] [illegible] 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	**14**	

14	a		R group attached to central carbon ✓ amine group on (one side of) central carbon ✓ carboxyl group on (the other side of) central carbon ✓	3	 **ALLOW** amine and carboxyl group either way round **ALLOW** –NH$_2$, –COOH **IGNORE** separate diagram showing the generalised structural formula **Examiner's Comments** Many candidates knew the general formula for an amino acid and drew this to the side, but they didn't gain any marks as the question specifically stated to 'complete Fig. 21.2'. Only a few candidates were able to interpret the figure provided as just the R group and clearly added the remainder of the molecule. A common error was to use the carbon atom of the R group as the central carbon atom of the amino acid and convert the hydrogen atoms into amine groups or carboxylic acid groups.
	b		insulin is made from two, polypeptide chains / amino acid chains / primary structures ✓ chains joined by disulfide bonds (between, cysteine / CYS) ✓	2	**IGNORE** 'multiple chains' or 'more than one' **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.
	c	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 **<u>Examiner's Comments</u>** 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 ✓	2	For two marks: **ALLOW** 1st A and 2nd A replaced by

			is replaced by, GGT / GGC / GGA / GGG ✓		GG. **ALLOW** A replaced by G twice **ALLOW** 2 A's replaced by 2 G's For one mark: **ALLOW** A replaced by G **<u>Examiner's Comments</u>** 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)✓ 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 ✓	Max 4	**<u>Examiner's Comments</u>** 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 molecules in the nucleus are unzipped by DNA helicase and free nucleotides attach to each base by complementary base pairing making an mRNA molecule · This leaves the nucleus through the nuclear pores and attaches to a ribosome. · The 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	**12**	