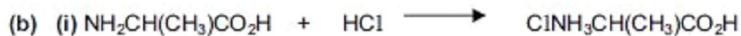


## Q1.



[1]



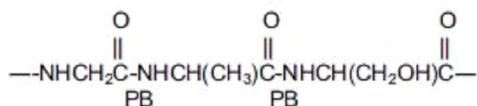
[1]



[1]

N.B. charges not needed, and deduct only [1] for incorrect side chains  
Allow ionic equations

(c)



Correct CO-NH bonding (at least one C=O shown) [1]  
At least one PB (peptide bond) labeled [1]  
3 residues [1]

(the 3 residues don't all have to be different, but must all be either gly, ala or ser)

(d) condensation or polyamide

[1]

(e) deducting 18 from each  $M_r$  value

[1]

( $M_r$  value of 3-residue fragment = 215 if this has been done; otherwise  $M_r$  = 269)

dividing 600,000 by the  $M_r$  value

[1]

(this would give 2791 if 18 had been deducted from each  $M_r$ , or 2230 if not)

multiplying the answer by 3 (since there are 3 amino acids per residue)

[1]

(correct answer is 8732. If no 18 had been deducted, answer is 6691)

Possible likely answers:

8732 ( $\pm 10$ ) → [3]

6691 ( $\pm 10$ ) → [2]

2791 ( $\pm 10$ ) → [2]

2230 ( $\pm 10$ ) → [1]

[if the answer is none of these, you can award part marks, as above.]

Total = [10]

## Q2.

- 7 (a) (i)
- addition requires an unsaturated/double bond or alkene/C=C
  - condensation **produces a small molecule or** water as well as the polymer or loss of mass occurs on polymerisation
  - the empirical formula of an addition polymer is the same as that of the monomer  
*any two [1] + [1]*
- (ii) minimum is:
- $$\begin{array}{c} \text{O} \\ \parallel \\ \text{NH}_2\text{CH}(\text{CH}_3)\text{C}-\text{N}\cdot\text{CH}_2\text{CO}_2\text{H} \\ | \\ \text{H} \end{array}$$
- peptide link shown [1]  
ala-gly NOT gly-ala [1] [4]
- (b) X = deoxyribose [1]  
Y = phosphate [1]  
Z = thymine [1] [3]
- (c) (i) (met)- ser-arg-asp- gly (ignore leading met) [2]  
whole sequence  
*three in correct order = [1]. Deduct [1] mark if "start" or "stop" is included in the amino acid sequence*
- (ii) The amino acid **gly** (or the last amino acid) would be replaced by **trp** [1] [3]
- (d) (i) e.g. Huntington's, cystic fibrosis, haemophilia, sickle cell anaemia, thalassemia, muscular dystrophy, Down's syndrome, phenylketonuria [1]
- (ii) Suitable explanation e.g. wrong amino acid coded or different aminoacid sequence or incorrect protein produced or extra chromosome (for Down's) ...results in/change in 3D structure/change in active site/loss of enzyme activity (or a specific description pertinent to the mentioned disease) [1] [3]
- [Total: 13]

Q3.

4 (a) ester

[1] [1]

(b) reaction I: acid/H<sup>+</sup>/HCl/H<sub>2</sub>SO<sub>4</sub> or alkali/OH<sup>-</sup>/NaOH (followed by H<sup>+</sup>) [1]  
heat/reflux and aqueous (allow H<sub>3</sub>O<sup>+</sup> to equal H<sup>+</sup> + aq, also assume "conc" or  
"dil" means aq (but NOT H<sub>2</sub>SO<sub>4</sub>) also allow aqueous ethanol) [1]  
(for heat: allow T ≥ 80°C; not "warm")

reaction II: methanol/CH<sub>3</sub>OH [1]  
heat with conc. H<sub>2</sub>SO<sub>4</sub>/H<sub>3</sub>PO<sub>4</sub> or HCl(g) [NOT conc HCl] [1] [4]

(c) (i) BrCH<sub>2</sub>-CHBr-CH<sub>2</sub>Br [1]

(ii) HO<sub>2</sub>C-CO-CO<sub>2</sub>H [1] [2]

(d) 890g of triglyceride produces 3 × 298 = 894g of biodiesel [1]  
∴ 500kg produces 500 × 894/890 = 502kg biodiesel  
(correct ans [2])  
(1004/1005kg or 167kg is worth [1]: 333kg is worth [0]) [2]

(e) (i) C<sub>17</sub>H<sub>35</sub>CO<sub>2</sub>CH<sub>3</sub> + 27.5 O<sub>2</sub> → 19CO<sub>2</sub> + 19H<sub>2</sub>O [1]  
(or C<sub>19</sub>H<sub>38</sub>O<sub>2</sub>)

(ii) 10 × 44 × 19/298 = 28.(05)/28.1kg ecf from equ [2]  
(-1 for each error)

some ecf values: n = 18 ⇒ 26.6kg  
n = 17 ⇒ 25.1kg (allow [2] for each)  
n = 16 ⇒ 23.6kg [3]

(f) any one of the following.  
• (saving) diminishing resources  
• economic argument (NOT just "cheaper") – e.g. oil will become increasingly more expensive as it runs out  
• ref to CO<sub>2</sub> cycle (e.g. no net increase in CO<sub>2</sub>, i.e. "carbon neutral") or less global warming (due to a smaller carbon "footprint")  
• renewable/sustainable  
• the effect of biofuel cultivation on world food prices [1] [1]

[Total: 13]

Q4.

7

polymer	addition/condensation?	formulae of monomers
1	condensation	$\text{HO}_2\text{C}-\text{CO}_2\text{H}$ or $\text{ClCO}-\text{COCl}$ $\text{NH}_2\text{-CH}_2\text{-CH}_2\text{-NH}_2$
2	condensation	$\text{HO}-\text{CH}_2\text{-CH}(\text{C}_2\text{H}_5)\text{-CO}_2\text{H}$ $\text{HO}-\text{CH}_2\text{-CH}(\text{CH}_3)\text{-CO}_2\text{H}$
3	addition	$\text{CH}_2=\text{CH-CH}_3$ $\text{CH}_2=\text{CH-CONH}_2$ $\text{CH}_2=\text{CH-C}_6\text{H}_5$

↑  
[2]  
(2 correct: [1])

↑  
[6]  
(6 correct: [5])  
etc

(2 correct: [1])

(C=C bonds not needed, but penalise -[1] if C-C drawn instead of C=C)

(if more than 7 formulae drawn, then penalise -[1] for each formula in excess of 7)

[8]

[Total: 8]

## Q5.

8	(a) primary:	covalent (ignore amide, peptide etc) diagram showing peptide bond: (-CHR-)CONH(-CHR-)	[1] [1]
	secondary:	hydrogen bonds (NOT "...between side chains") diagram showing N-H···O = C	[1] [1]
	tertiary:	two of the following: <ul style="list-style-type: none"> <li>• hydrogen bonds (diag. must show H-bonds <i>other than</i> those in <math>\alpha</math>-helix or <math>\beta</math>-pleated sheet – e.g. ser-ser)</li> <li>• electrostatic/ionic attraction,</li> <li>• van der Waals'/hydrophobic forces/bonds,</li> <li>• (covalent) disulphide (links/bridges)</li> </ul>	[1] + [1]
		suitable diagram of <b>one</b> of the above (for disulphide: S-S <b>not</b> S=S or SH-SH)	[1] [7]
	(b)	met-ala-gly-ala-gly-arg-val-lys any <b>possible</b> sequence with more than 8 residues, that "uses" all 6 tripeptides (overlapping or not), and that starts with <i>met</i> and ends with <i>lys</i> is worth [1] mark any sequence that does <b>not</b> start with <i>met</i> or end with <i>lys</i> gets zero.	[2] [2]
	(c)	CARE – this is not about DNA! candidates should describe <b>TWO</b> potential effects on tertiary or quaternary structures caused by amino acid sidechains... these include: <ul style="list-style-type: none"> <li>disruption of H-bonding</li> <li>disruption of disulphide bridges</li> <li>disruption of electrostatic/ionic attraction</li> <li>disruption of van der Waals' forces</li> </ul> (only allow effects on the secondary structure if proline is specifically mentioned)	2 x [1]
		then award [1] mark each for <b>two</b> of the following bullet points:	
		<ul style="list-style-type: none"> <li>• a description of the amino acids involved in the above, (or a labelled diagram) (award [1] mark for each example)</li> <li>• a description of an effect of interchanging amino acids, such as the..</li> <li>• unfolding of tertiary structure/different folding/different shape (NOT denatured)</li> <li>• inactivity of an enzyme or changing the active site</li> <li>• causing of a protein to become less soluble/coagulate (e.g. sickle cells)</li> </ul>	2 x [1] [4]
			[Total: 13 max 12]

## Q6.

- 9 (a) (i) correct diagram showing at least one monomer unit, and at least one N-H and C=O.  
 i.e.  $-\text{NH-C}_6\text{H}_4\text{-NH-CO-}$  or  $-\text{CO-C}_6\text{H}_4\text{-CO-NH-}$   
*(no mark for this, but apply a penalty of -[1] if candidate's diagram does NOT show these points correctly)*  
 one H-bond between N-H of original chain and C=O group of new chain [1]  
 one H-bond between C=O of original chain and N-H group of new chain [1]

- (ii) hydrogen bonds or H-bonds (in words; can be written on diagram)  
 (ignore ref to v d W) [1]

(iii)



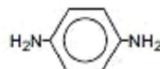
or



[1]

allow  $\text{HO}_2\text{C-}$   
 $\text{HOOC-}$   
 $\text{HOCO-}$

allow  $\text{ClICO-}$



allow  $\text{NH}_2-$

[1]

[5]

- (b) (i) Water-hating/fearing/repelling/resistant or can't form bonds with water (molecules) [1]

[NOT insoluble or does not dissolve in water, also NOT "non-polar"]

- (ii) Fluorine-containing groups form van der Waals bonds (with the oil molecules)... [1]  
 ...but cannot form hydrogen bonds (with the water molecules) [1]

- (iii) Teflon/PTFE

[1]

[4]

[Total: 9]

Q7.

8 (a)

Block letter	Identity of compound
J	Deoxyribose (NOT "sugar" or "pentose")
K	Guanine
L	Phosphate
M	Thymine

All 4 correct score 3 marks, 3 score 2, 2 score 1

[3]

(b) hydrogen bonds (1) between the bases (1)

[2]

- (c) 1 RNA is a single strand; DNA is double strand  
 2 RNA contains ribose; DNA contains deoxyribose  
 3 RNA contains uracil; DNA contains thymine  
 4 RNA is shorter than DNA

(1)  
 (1)  
 (1)  
 (1)  
 (4 max 3) [3]

- (d) mRNA – copies the DNA gene sequence  
 or forms a template for a particular polypeptide / in protein synthesis

(1)

tRNA – carries amino acids to the ribosome

(1) [2]

**[Total: 10]****Q8.**

- 6 (a) (i) Primary – the **amino acid** sequence / order / chain  
 or diag. e.g. NH-C-CO-NH-C-CO  
 or amino acids bonded by covalent / amide / peptide bonds

(1)

- (ii) Tertiary – the coiling / folding of the protein / polypeptide chain due to interactions between side-chains on the amino acids or the structure which gives the protein its 3-D / globular shape

(1) [2]

- (b) (i) Diagram:  
 Minimum is  $\text{CH}_2\text{S}-\text{SCH}_2$

(1)

- (ii) Oxidation / dehydrogenation / redox

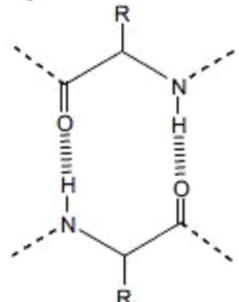
(1)

- (iii) Hydrogen / H bonds; ionic interactions / bonds or ion-dipole or salt bridges;  
 van der Waals' or id-id or induced / instantaneous dipole forces  
 (ignore hydrophobic interactions)

(2) [4]

(c) (i) Hydrogen bonds (1)

- (ii) Correct new strand present (see below) needed  
Diagram showing C=O bonding to N-H in new strand... ✓  
...and N-H bonding to C=O in new strand ✓  
e.g.



New strand must contain a minimum of two amino acid residues in a single chain. Deduct a penalty of -(1) for any wrong H-bond **only** if (2) marks have already been scored. (2) [3]

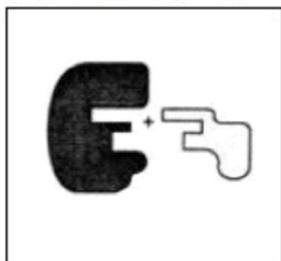
(d) There are bonds or S-S bridges / linkages **between the layers / sheets** (in  $\beta$ -keratin) (but only van der Waals interactions between the layers in silk) (1) [1]

[Total: 10]

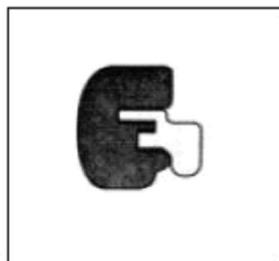
Q9.

- 7 (a) The tertiary/3-dimensional structure/shape is held together by hydrogen/ionic/van der Waals bonds  
 These break (relatively) easily/are weak/break at/above 45 °C [1] [1]

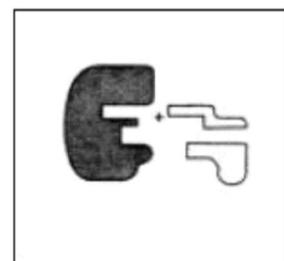
(b) (or similar diagrams)



Enzyme + substrate



Enzyme-substrate complex



Enzyme + products

$3 \times [1]$

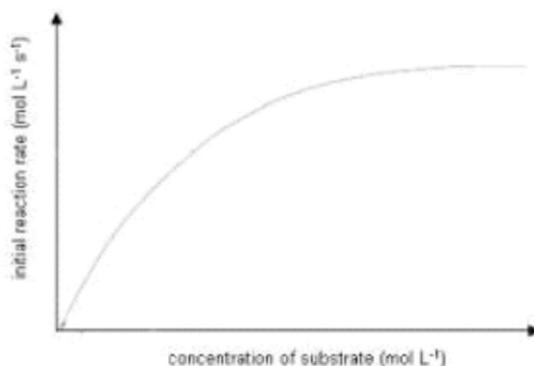
- (c) a competitive inhibitor combines with the enzyme's active site (so preventing the substrate from binding) [1]

non-competitive inhibitor bonds with the enzyme away from the active site/at an allosteric site [1]

this changes the shape of the active site [1]

*Also allow* competitive inhibition can be overcome by increasing [substrate] or non-competitive inhibition cannot be removed by increasing [substrate] for the 3rd mark

(d) (i)



Line must be of similar shape to original but level out below original line [1]

(ii) Inhibitor reduces the number of enzymes with 'working' active sites (owtte) [1]

[Total: 10]

Q10.

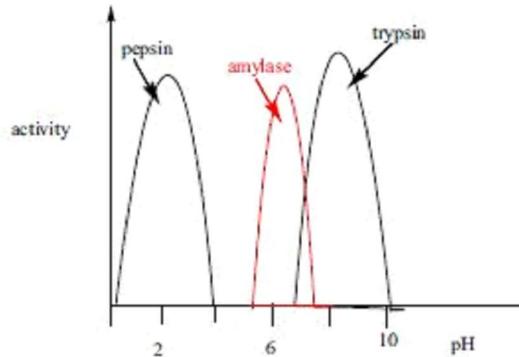
- 9 (a) (i) One [1]
- (ii) Any alkene (**or** allow a cyclic amide, as in caprolactam) [1]
- (b) Any TWO from: addition needs unsaturated/double bonds/alkene  
 condensation eliminates a small molecule  
 condensation needs a molecule other than a hydrocarbon  
 empirical formula of addition polymer is the same as that of its monomer  
 condensation needs two different functional groups  
**(NOT – “condensation needs two different monomers”)**  $2 \times [1]$
- (c) (i) Water [1]
- (ii)
- 
- Correct 'ester' bond [1]  
'sticks' to rest of molecule [1]  
Note : candidates need only show 'brackets' if more than one repeat unit shown
- (iii) Polyesters [1]
- (d) Monomers in *Terylene* have to alternate in order to condense out water (owtfe) [1]  
Alkenes can link in any order (and still form a polyalkene) (**or** diagram showing this) [1]
- [Total: 10]**

**Q11.**

- 6 (a) They are polar/ionic or can hydrogen-bond or are hydrophilic. [1]  
 (NOT 'contain the -OH group', on its own) [1]

- (b) (i) Primary structure is the sequence/order of amino acids [1]  
 Secondary structure is the H-bonding between C=O & N-H or peptide group/bonds [1]  
 Tertiary structure gives the (overall) 3D structure/shape/folding/globularity  
 (not 'coiling' on its own)  
 or mention of at least one method of forming the 3° structure, e.g.; hydrogen bonding  
**between R-groups/side chains**; -S-S- bridges; van der Waals forces; ionic interactions [1]
- (ii) The 3° structure provides a complementary shape to that of the substrate  
 or it provides the right/specifically shaped cavity for the substrate. (NOT just 'a cleft')  
 or provides nearby groups to aid the reactions of the substrate (owtfe) [1]
- (iii) Two conditions out of the following:  
 (a) Increased temperature  
 (b) Decreased temperature  
 (c) Change in pH  
 (d) Addition of heavy metals (or specified, e.g. Hg/Ag)  
 (e) Addition of inhibitors (competitive or non-competitive)  
 Suitable reasons:  
 (i) 3D structure changes shape/is deformed/is broken or R-R interactions (or a specific example, e.g. H-bonding) are broken  
 (ii) inhibitor occupies active site.  
 (iii) either fewer substrate molecules with  $E > E_a$  or fewer successful collisions [2]
- [6]

(c) (i)



- left hand peak labelled as pepsin [1]  
 right hand peak labelled as trypsin [1]  
 (Correct enzymes, but wrong way round, scores [1] only)

- (ii) Peak between pH 6 and pH 8, **and** correct name (amylase) [1]  
[3]

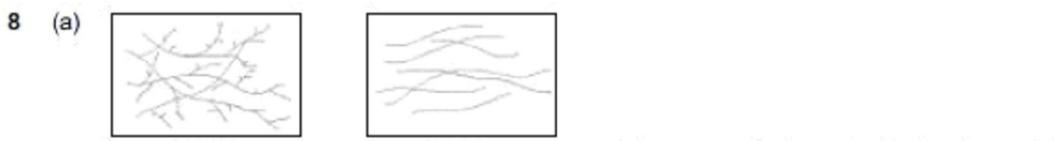
**[Total: 10]**

**Q12.**

- 6 (a) (i) Condensation [1]
- (ii) ala-ala, gly-gly, ala-gly [2]  
[3]
- (b) (i) Correct sugar-phosphate backbones  
(with **two sugars and one phosphate attached**) [1]
- C – G pair correct **or** A – T pair correct [1]
- deoxyribose label **and** all bases coming from sugars [1]
- (ii) Replication would be slower/difficult  
because the DNA/strands could not be separated [1]  
[4]
- (c) (i) Some amino acids have more than one (triplet) code [1]
- (ii) loss/disruption of ionic bonding/hydrogen bonding [1]
- (iii) There would be a potential loss of all tertiary structure  
*or*  
frameshift – deletion of a base changes protein structure [1]  
[3]

[Total: 10]

Q13.



LDPE                    HDPE                    minimum of 2 chains suitable sketches [1]  
 (The close packing of unbranched side chains means)

LDPE **more space** between the chains/polymers or HDPE less empty space between the chains  
 [1]  
 [2]

- (b) van der Waals' (VDW) forces  
 are weaker [1]  
 [1]  
 [2]

(c)

Addition OR	condensation
requires C=C/double bond	does not need C=C/double bond
uses the same functional group	needs two different functional groups
same general (empirical) formula as monomer	different formula
no loss of small molecule/H <sub>2</sub> O/HCl	small molecule /H <sub>2</sub> O/HCl is formed

Any two differences [1]  
 [2]

- (d) (i) (through its long chain of) delocalised electrons/mobile electrons  
*free electrons is not sufficient* [1]

(ii) planar  
 the  $\pi$  bonds/p-orbitals overlap (with each other) [1]

(iii) C<sub>8</sub>H<sub>6</sub>  
 C<sub>4</sub>H<sub>3</sub> [2]

[5 max 4]

**Total: 101**

**Q14.**

6 (a)

amino acid	structure	type of interaction
alanine	$\text{H}_2\text{NCH}(\text{CH}_3)\text{CO}_2\text{H}$	van der Waals' (NOT hydrophobic)
cysteine	$\text{H}_2\text{NCH}(\text{CH}_2\text{SH})\text{CO}_2\text{H}$	disulfide bonds or S-S
lysine	$\text{H}_2\text{NCH}((\text{CH}_2)_4\text{NH}_2)\text{CO}_2\text{H}$	ionic/electrovalent hydrogen/H bonds
serine	$\text{H}_2\text{NCH}(\text{CH}_2\text{OH})\text{CO}_2\text{H}$	hydrogen/H bonds

[3]

[3]

- (b) Iron – in haemoglobin or red blood cells; transport of oxygen/ $\text{CO}_2$   
or in myoglobin; transport of oxygen (in muscle)  
or in cytochromes; cell respiration

[1]

Potassium – in cell membranes/enzymes; controlling the flow of ions/water into or out of cells  
or – in nerves; controlling nerve impulses  
or –  $\text{Na}^+ - \text{K}^+$  pump; nerve impulses/control of cell volume/active transport

[1]

Zinc acting as a cofactor in enzymes (or a named one, e.g. carbonic anhydrase);  
or in making of insulin

[1]

[3]

- (c) (i)  $\text{ATP} + \text{H}_2\text{O} \rightarrow \text{ADP} + \text{Pi}$

[1]

(ii) Hydrolysis or nucleophilic substitution

[1]

[2]

- (d) (i) Sodium or chloride (sweat is salty) and Potassium (water retention in cells)

[1]

(ii) Hydrogen bonding and reference to water or bonding in mucous molecules

[1]

[2]

[Total: 10]

Q15.

6 (a)

substance	protein synthesis	formation of DNA
adenine		✓
alanine	✓	
aspartate	✓	
phosphate		✓

[3]

[3]

(b) protein : hydrogen bonds [1]

between  $-\text{NH}$  and  $\text{C=O}$  groups on different (peptide) groups

[1]

DNA : hydrogen bonds

[1]

between bases / A & T / C & G on different chains

[1]

[4]

(c) primary: covalent bonds between (successive) amino acids [1]

tertiary :

hydrogen bonds	between $-\text{COOH}$ / $-\text{OH}$ and $-\text{NH}_2$ (in side chains)
ionic bonds	between $-\text{NH}_3^+$ and $-\text{CO}_3^{2-}$ (in side chains)
disulfide bonds	between cysteine molecules / residues / $-\text{SH}$ groups (in side chains)
van der Waals/VDW forces	between alkyl groups / non-polar residues (in side chains)

any two rows

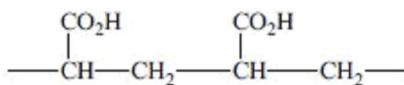
[2]

[3]

[Total: 10]

Q16.

8 (a) (i)



[1]

(ii) Addition

[1]

(iii) Hydrogen bonding

[1]

[3]

(b) (i) more / increase water absorbing properties (allow attracts water more)

[1]

more polar(ity)/more hydrophilic / has ionic side-chains (as well as hydrophilic ones)

[1]

(ii) It should be biodegradable/decompose

[1]

[3]

(c) idea of ion exchange / replacement of  $\text{Na}^+$  for  $\text{Cd}^{2+}/\text{Pb}^{2+}$

[1]

(the metal ions) will be attracted to the carboxylate ions

[1]

[2]

(d) (i) condensation

[1]

(ii) OH/alcohol groups

so highly soluble / able to form hydrogen bonds

[1]

[2]

[Total: 10]

Q17.

6 (a)

substance	protein synthesis	formation of DNA
cysteine	✓	
cytosine		✓
glutamine	✓	
guanine		✓

[3]

[3]

(b) (i) Hydrogen bonding

[1]

Between bases or between A,T, C and G (all four needed)

[1]

(ii) Bonds are (relatively) weak or easily broken

[1]

This enables strands to separate or DNA to unzip/unwind/unravel.

[1]

[4]

(c) changes / mutations in DNA

- by the addition / insertion /deletion / substitution / replacement of a base
- adds / deletes / replaces an amino acid or changes the amino acid sequence
- this causes a loss of function or changes the shape / tertiary structure of the protein

any three points [3]

[3]

**[Total: 10]**

**Q18.**

- 8 (a) (i)  $\text{CH}_2 = \text{CH}-\text{CO}_2\text{H}$  or  $\text{CH}_2 = \text{CH}-\text{CO}_2\text{R}$  or  $\text{CH}_2 = \text{CH}-\text{COCl}$  [2]
- (ii) addition (polymerisation) [1]
- (iii)  $\text{C}(\text{CH}_2\text{OH})_4$  [1]
- (iv) water [1]  
[5]
- (b) (water is bonded to the polymer by) hydrogen bonding [1]  
hydrogen bonds are weak or easily broken [1]  
[2]
- (c) (i) cross-linking causes no reduction in the number of  $-\text{OH}$  groups  
or cross-linking molecules also have  $-\text{OH}$  groups [1]
- (ii) property e.g. becomes harder / more rigid / less flexible / stronger / higher melting point.  
because the chains are more strongly / tightly held [1]  
[1]  
[3]

[Total: 10]

## Q19.

5	(a) (i) addition (polymerisation)	[1]
	(ii) condensation (polymerisation)	[1]
		2
	(b) hydrogen bonding	[1]
		1
	(c) (i) HO <sub>2</sub> CCH <sub>2</sub> CH <sub>2</sub> CO <sub>2</sub> H	[1]
	(ii) ester (accept "covalent")	[1]
		2
	(d) (i) heat with H <sub>3</sub> O <sup>+</sup> or heat with OH <sup>-</sup> (aq)	[1]
	(ii) H <sub>2</sub> N-CH <sub>2</sub> -CH(OH)-CH <sub>2</sub> -NH <sub>2</sub> or H <sub>3</sub> N <sup>+</sup> -CH <sub>2</sub> -CH(OH)-CH <sub>2</sub> -NH <sub>3</sub> <sup>+</sup>	[1]
	HO <sub>2</sub> C-CH(OH)-CH(OH)-CO <sub>2</sub> H or O <sub>2</sub> C-CH(OH)-CH(OH)-CO <sub>2</sub> <sup>-</sup>	[1]
	(allow bonus mark if the acid/base forms are consistent with the reagent used for the hydrolysis)	[1]
		4 max 3
	(e) (i) NC-CH <sub>2</sub> -CO <sub>2</sub> <sup>-</sup> K <sup>+</sup>	[1]
	(ii) II: H <sub>2</sub> + Ni or Na in ethanol [allow LiAlH <sub>4</sub> ]	[1]
	III: dilute HCl or H <sub>2</sub> SO <sub>4</sub> or H <sup>+</sup> (aq)	[1]
		3
		total: 11

Q20.

8	(a) (i) Two interlinked spirals or chains or strands woven round each other	[1]
	(ii) By hydrogen bonds between bases	[1]
		[2]
(b)	Transcription – (1)DNA/RNA/nucleic acid unravels – (2)strand is used as a template – (3)mRNA reads the sequence on this strand/ produces complementary strand	[1] [1] [1]
	Translation – (4)mRNA binds to the ribosome – (5)tRNA translates the codon from mRNA – (6)tRNA carries amino acids to ribosome/adds a.a. to chain	[1] [1] [1]
		[max 4]
(c) (i)	Disruption of the secondary/tertiary/quaternary/3D structure of the protein (could be answered in terms of bonds e.g. hydrogen bonds break)	[1]
	(ii) The covalent/peptide bonds in the (protein) chain are too strong	[1] [2]
(d)	Energy is provided by the breakdown/hydrolysis of adenosine triphosphate (ATP) ATP (+ H <sub>2</sub> O) → ADP + P <sub>i</sub> (+ energy) or in words ATP is produced during respiration/Krebs cycle/oxidation of glucose, fats or proteins/ in mitochondria/ADP is recycled	[1] [1] [1] [3]

[Total: 11]

## Q21.

4	(a) (i) CH <sub>2</sub> =CH-CH <sub>2</sub> CH <sub>2</sub> CH <sub>3</sub> accept C <sub>3</sub> H <sub>7</sub> on RHS	[1]
	(ii) 8	[1]
(b) (i)	e.g. C <sub>40</sub> H <sub>82</sub> → C <sub>16</sub> H <sub>34</sub> + 2 C <sub>12</sub> H <sub>24</sub> OR C <sub>24</sub> H <sub>48</sub>	[1]
	(ii) heat + catalysts/SiO <sub>2</sub> /Al <sub>2</sub> O <sub>3</sub> /Pt/ceramic/pumice/zeolite etc if temp given >500 °C	[1]
	(iii) bonds broken: 4(C-C) = 4 × 350 = 1400 kJ mol <sup>-1</sup> bond formed: 2 (C=C) = 2 × 610 = 1220 kJ mol <sup>-1</sup> ∴ ΔH = +180 kJ mol <sup>-1</sup> from eqn in (i) : +90 kJ mol <sup>-1</sup> for each C=C formed (could be multiples of 90)	[1]
	(iv) endothermic reactions ΔH > 0	[1]

[Total: 6]

## Q22.

- 10** (a) (i) silkworm – hydrogen bonds  
spider – van der Waals' OR hydrogen bonds [1]  
[1]
- (ii) spider silk is more elastic/flexible/less rigid than silkworm silk/has a lower density  
silkworm silk absorbs water more easily [1]  
[1]
- (iii) this increases the elasticity/hydrophobic nature of the silk [1]
- (b) (i) a polymer formed with the elimination/formation of a small molecule  
(or example) [1]
- (ii) any addition polymer e.g. poly(ethene), PVC, etc. [1]
- (iii) 3 from:  
addition polymers have a limited range of bonds/monomers [1]  
addition polymers are non-polar/have fewer/no H-bonds [1]  
condensation polymers/proteins have a range of combinations of amino acids which give  
a wide range of properties [1]  
condensation polymers/proteins have more functional groups/sidechains [1]  
different sequences of amino acids result in different 2°/3° structure [1]

[Total: 12 max 10]

### Q23.

- 6** (a) All three amino acids correctly paired (2)  
Two amino acids correctly paired (1)
- One labelled H-bond between strands (1) [3]
- (b) (i) tRNA – each amino acid has its own specific / appropriate tRNA (1)  
– carry amino acids to ribosomes / mRNA (1)  
– contains a triplet code / anticodon (1)
- (ii) ribosome – attaches / moves along / binds to mRNA (1)  
– assemble amino acids in correct sequence for / synthesises protein (1) [5]
- (c) (i) Base miscopied / deleted (1)
- (ii) Sequence of bases is changed (1)  
This may result in different amino acid sequence – different protein (1)  
Can affect shape / tertiary structure of protein (1) [Max 3]

[Total: 12 max 11]

### Q24.

7	(a) Primary:	Covalent bond (ignore amide, peptide etc.) Diagram showing peptide bond: (-CHR-)CONH(-CHR-)	[1] [1]
	Secondary:	Hydrogen bonds (NOT between side chains") Diagram showing N-H···O=C	[1] [1]
	Tertiary:	<b>Two of the following:</b> <ul style="list-style-type: none"> <li>• hydrogen bonds (diagram <b>must</b> show H-bonds <i>other</i> than those in <math>\alpha</math>-helix or <math>\beta</math>-pleated sheet – e.g. ser-ser)</li> <li>• electrostatic/ionic attraction,</li> <li>• Van der Waals'/hydrophobic forces/bonds,</li> <li>• (covalent) disulphide (links/bridges)</li> </ul>	[1] + [1]
		Suitable diagram of <b>one</b> of the above (for disulphide: S-S <b>not</b> S=S or SH-SH)	[1] <b>[max 6]</b>

## Q25.

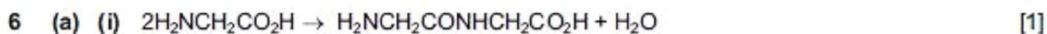
- 7 (a) (i) Disulfide bond / group / bridge (1)  
 (ii) The tertiary structure (1)  
 (iii) The substrate will no longer bond to / fit into the active site (1)  
 or shape of active site is changed [3]
- (b) (i) Acid-base / proton donor / neutralisation / salt formation (1)  
 (ii) The ability of the  $-\text{CO}_2\text{H}$  group to form hydrogen bonds (1) and ionic interactions (1)  
 The  $-\text{CO}_2\text{H}/-\text{CO}_2^-$  group is no longer able to interact with  $-\text{NH}_2/-\text{NH}_3^+$  (1)  
 The  $\text{Ag}^+$  forms a strong bond with  $-\text{COO}^-$  (1) [5] max [4]
- (c) (i) 8 but allow 4 $\text{O}_2$  if specified as molecules (1)  
 (ii) Dative / co-ordinate (1)  
 (iii) Octahedral / 6 co-ordinate (1) [3]
- [Total: 10]**

## Q26.

- 9 (a) Sugar/deoxyribose, phosphate, base (or better)(not ribose) (1) [1]
- (b) Diagram showing sugar-phosphate backbone (chain) (1)
- Bases on side-chain (1)  
Base paired – A-T or G-C (1)
- H-bonds shown and labelled (1) [4]
- (c) mRNA, ribosome, tRNA all three correct (2)  
(mRNA first allow 1 mark) [2]
- (d) (i)  $(4 \times 4 \times 4) = 64$  (1)
- (ii) START (or Met) – ser – arg – leu – asp – val (2)  
(5 correct order score (1))
- (iii) Amino acid leu is changed to pro (1) [4]

[Total: 11]

Q27.



(ii) Skeletal formula required [1]  
[2]

(b) (i)  $\alpha$  helix [1]  
 $\beta$  pleated sheet [1]

(ii) Students should choose one of the structures below  
For  $\alpha$  helix:  
Need to show a helix with  $\text{C=O} - \cdots \text{H-N}$  between turns  
For  $\beta$  pleated sheet:  
Need to show two parallel 'zig-zag' strands with  $\text{C=O} - \cdots \text{H-N}$  between them

Whichever is chosen, overall structure [1] position of H bonds [1]

[4]

(c)

amino acid residue 1	amino acid residue 2	type of bonding
$-\text{HNCH}(\text{CH}_2\text{CH}_2\text{CH}_2\text{CH}_2\text{NH}_2)\text{CO}-$	$\text{HNCH}(\text{CH}_2\text{CH}_2\text{CO}_2\text{H})\text{CO}-$	Ionic bonds or hydrogen bonds
$-\text{HNCH}(\text{CH}_3)\text{CO}-$	$-\text{HNCH}(\text{CH}_3)\text{CO}-$	van der Waals'
$-\text{HNCH}(\text{CH}_2\text{SH})\text{CO}-$	$-\text{HNCH}(\text{CH}_2\text{SH})\text{CO}-$	Disulfide bonds
$-\text{HNCH}(\text{CH}_2\text{OH})\text{CO}-$	$-\text{HNCH}(\text{CH}_2\text{CO}_2\text{H})\text{CO}-$	Hydrogen bonds

[4]

[Total: 10]

Q28.

8 (a)

traditional material	modern polymer used
Paper/cardboard/wood/leaves hessian/hemp/jute steel/aluminium	PVC in packaging
Cotton/wool/linen	Terylene in fabrics
Glass/china/porcelain/earthenware metal/leather	Polycarbonate bottle

3 → 2 marks, 2 → 1 mark

[2]

- (b) Reasons: Plastics/polymers pollute the environment for a long time do not decompose/  
biodegrade quickly [1]

They are mainly produced from oil [1]

Produce toxic gases on burning [1]

max two

Strategy 1: Recycle polymer waste / use renewable resources [1]

Strategy 2: Develop biodegradable polymers [1]

[max 3]

- (c) PVC [1]

Combustion would produce HCl / dioxins as a pollutant [1]

or [1]

nylon/acrylic [1]

Combustion would produce HCN [1]

[2]

- (d) (i) Polythene (or other addition polymer) [1]

(ii) Addition polymerisation [1]

The polymer chains don't have strong bonds between them – easy to melt [1]

Could be answered with a suitable diagram [3]

[Total: 10]

Q29.

- 6 (a) (i) K, because it is the (only) one to contain nitrogen or it's an amino acid  
 or because it contains CO<sub>2</sub>H or NH groups [1]
- (ii) molecule: J, polymer: RNA (**not** DNA)  
 or molecule: L, polymer: starch, cellulose, glycogen or polysaccharide  
 (**not** carbohydrate) [2]
- (b) (i) Covalent bonding [1]  
 (ii) Hydrogen bonding [1]  
 (iii) Ionic/electrovalent bonding or disulphide/-S–S– bonding or van der Waals' forces [1]  
 [3]
- (c) (i) Enzymes [1]  
 (ii) • change in pH  
 • increase in T (NOT decrease; T > 40 °C or "too high" are OK)  
 • addition of heavy metal ions or specific, e.g. Hg<sup>2+</sup>, Ag<sup>+</sup>, Pb<sup>2+</sup> etc.  
 any two bullet points [1] + [1]
- change in pH disrupts ionic bonds  
 or metal ions disrupt ionic bonds  
 or metal ions disrupt –S–S– bonds  
 or heating disrupts hydrogen bonds  
 any one [1]
- This changes: the 3D structure or shape of the enzyme or the active site [1]  
 [max 4]
- [Total: 9]

**Q30.**

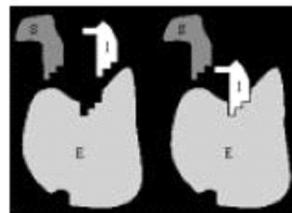
6 (a)

bonding	structure involved
disulfide bonds between parts of the chain	tertiary
hydrogen bonds in a $\beta$ -pleated sheet	secondary
ionic bonds between parts of the chain	tertiary
peptide links between amino acids	primary

zero/one correct only → [0], two correct only → [1], three correct only → [2] all four correct [3]

[3]

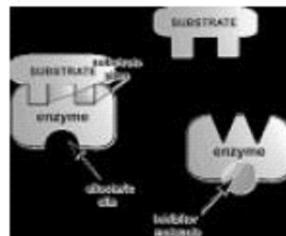
(b) labelled diagrams such as:



Competitive *any two from:*

- complementary shape to substrate / able to bind to active site of enzyme
- so preventing the substrate from binding / able to compete with substrate
- can be overcome by increasing [substrate]

2 × [1]



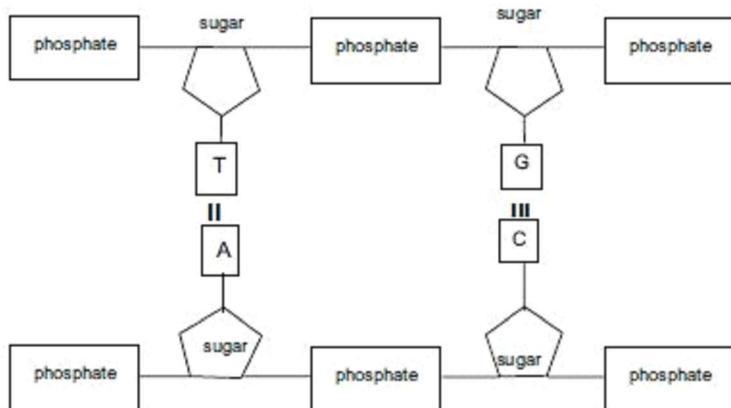
Non-competitive: *any two from:*

- binds elsewhere in the enzyme than active site / at an allosteric site
- this changes the shape of the active site
- cannot be removed by increasing [substrate]

2 × [1]

[4]

(c)

A and C **and** other strand correct [1]

H-bonds labelled [1]

adenine **AND** cytosine [1]

[3]

[1]

[1]

**[Total: 10]****Q31.**

- 8 (a) (i) It could denature the enzyme **or**  
alter the 3D structure/tertiary structure/shape of active site.

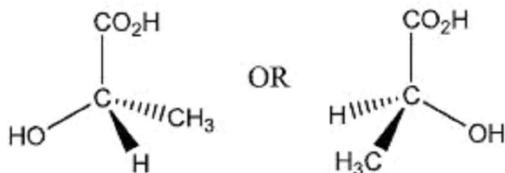
[1]

- (ii) condensation

[1]

[2]

(b)



or correct diagram of the S isomer

[1]

[1]

- (c) (i) (Acid present would) hydrolyse the ester (linkage)

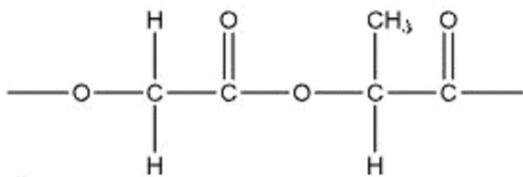
[1]

- (ii) (Hot water would) **soften** (the container)

[1]

[2]

(d) (i)



ester linkage shown  
rest of repeat unit correct (ONE)

[1]  
[1]

- (ii) van der Waals' from CH<sub>3</sub>/methyl group [1]  
**permanent** dipole-dipole from ester group [1]

- (iii) Accept any sensible physical property suggestion e.g. different melting point or different density or different solubility. [1]

[5]

[Total: 10]

Q32.

6 (a) It has no chiral centre/asymmetric carbon/optical isomers or is not optically active [1]

[Total: 1]

(b) (i) structure –  $\alpha$ -helix or  $\beta$ -(pleated) sheet [1]

hydrogen (bonding) (for either) [1]

(ii) any two pairs from the following:

bonding	possible amino acid
van der Waals'	ala, gly, leu, ile, val, pro, phe, try, met
ionic	asp, arg, glu, his, lys
disulfide bond	cysteine
hydrogen bond	asn, asp, arg, gln, glu, his, lys, ser, thr, try, tyr

[1] + [1]

[1] + [1]

(candidates can identify amino acids by name, three-letter abbreviation, formula of sidechain or formula of whole amino acid)

[Total: 6]

(c) (globular proteins/enzymes need) polar/H-bonding/ionic (side chains) so as to....  
...enhance their solubility or as part of their active site or to help their catalytic activity [1]

[Total: 1]

(d) (i) A – T [1]  
C – G [1]

(ii) (start or met) – gly – ser – leu – ala – ser – (stop)  
If an amino acid is shown before gly, then it must be met.  
correct sequence of the 5 in bold [2]

(iii) leu would be replaced by val [1]

[Total: 5]

[TOTAL: 13]

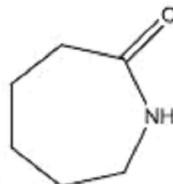
Q33.

8 (a) A monomers:  $\text{H}_2\text{N}-(\text{CH}_2)_6-\text{NH}_2$  and  $\text{HO}_2\text{C}-(\text{CH}_2)_4-\text{CO}_2\text{H}$  or  $\text{ClCO}(\text{CH}_2)_4\text{COCl}$  [1]

Condensation or nucleophilic substitution or addition-elimination [1]

B monomer:  $\text{H}_2\text{C}=\text{CHCH}_3$  [1]

Addition (NOT additional) [1]



C monomer:  $\text{H}_2\text{N}-(\text{CH}_2)_5-\text{CO}_2\text{H}$  or  $\text{H}_2\text{N}-(\text{CH}_2)_5-\text{COCl}$  or [1]

Condensation [1]

[max 5]

(b) (i) Need a statement from both columns for [1] mark.

(a)	(b)
more compact packing in A chains closer in A chains further apart in B	stronger (inter-chain) forces in A hydrogen bonding in A weaker (inter-chain) or van der Waals' forces in B B contains side-chain/branched chains

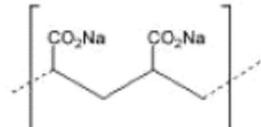
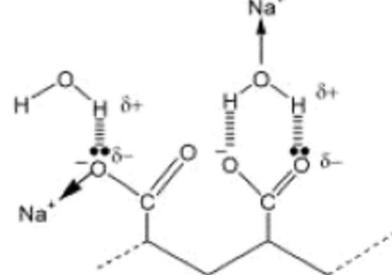
[1]

(ii) Polymer B – van der Waals'/London (dispersion) forces/induced-instantaneous/induced dipoles  
NOT just 'dipole' [1]

[Total: 2]

[TOTAL: 7]

Q34.

- 5 (a) (i) many monomers form a polymer [1]
- (ii) addition [1]
- (iii) C=C/double/ $\pi$  bond is broken **and** new C-C single bonds **s** are formed or double bond breaks and forms single bonds with other monomers [1]
- [3]
- (b) propenoic acid [1]
- [1]
- (c) (i) 
- carbon chain **and** CO<sub>2</sub>H  
at least one sodium salt [1]  
[1]
- (ii) 120° to 109(.5)°  
due to the change from a trigonal/sp<sup>2</sup> carbon to a tetrahedral/sp<sup>3</sup> carbon [1]  
[1]
- [4]
- (d) (i) 
- Any four:*
- hydrogen bond **labelled**  
water H-bonded to O through H atom  
 $\delta+$ / $\delta-$  shown on each end of a H-bond  
lone pair shown on O<sup>-</sup> or C=O or H<sub>2</sub>O on a **correct H-bond**  
Na<sup>+</sup> shown as coordinated to a water molecule [3]
- (ii) Solution became paler **and** Cu<sup>2+</sup> swapped with Na<sup>+</sup>  
or darker in colour **and** polymer absorbs water [1]
- [4]

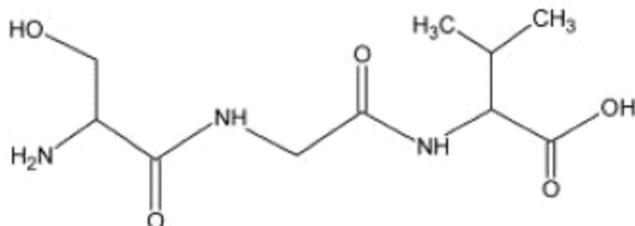
(e) (i) alkene(1), amide(1)	[2]
(ii) NH <sub>3</sub>	[1]
(iii) H <sub>2</sub> O	[1]
(iv) HCl (aq)/H <sub>3</sub> O <sup>+</sup> <b>and</b> heat/reflux ( <b>not</b> warm) or OH <sup>-</sup> (aq), heat and acidify	[1]
	[5]

[Total: 17]

### Q35.

6 (a) (i) six/6 (gsv, sgv, gvs, vgs, svg, vsg) [1]

(ii)



two **displayed** peptide bonds  
correct formula of peptide

[1]

[1]

(iii) valine (allow glycine) [1]

(iv) *any two of:*

hydrogen bonds **and** CO<sub>2</sub>H or OH or NH<sub>2</sub> or CONH or CO or NH or CO<sub>2</sub><sup>-</sup>  
ionic bonds **and** NH<sub>3</sub><sup>+</sup> or CO<sub>2</sub><sup>-</sup>

van der Waals' **and** -CH<sub>3</sub> or -H

2 × [1]

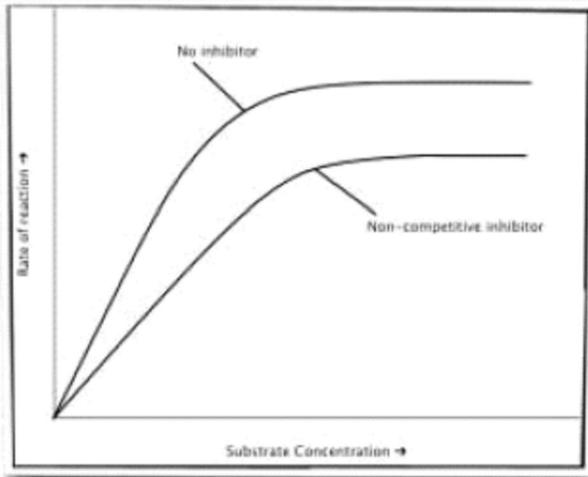
[6]

(b) (i) same shape/structure as substrate [1]

(inhibitor) competes/blocks/binds/bonds to **active site**  
or substrate cannot bind to **active site** [1]

(ii) binds with enzyme **and** changes shape/3D structure (of enzyme/active site) [1]

(iii)



[1]

[4]

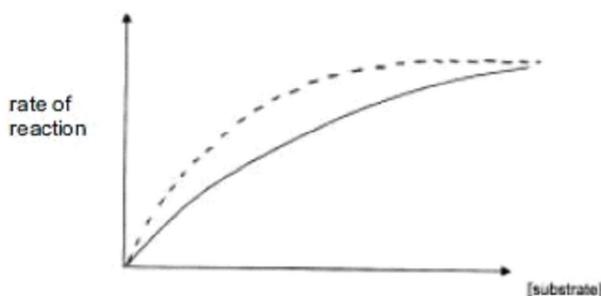
[Total: 10]

Q36.

- 7 (a) (i) Metals such as Hg, Ag, Cd, Pb, Cu (identified – NOT just "heavy metals")  
 (allow names, atomic symbols or ions, names or formulae of salts – e.g.  $\text{Pb}(\text{NO}_3)_2$ )  
 or penicillin or organophosphorus insecticide etc. [1]

- (ii) The ion/inhibitor binds to a part of the enzyme molecule away from the active site  
 onto an allosteric site [1]  
 This changes the shape of the active site or denatures the enzyme [1]  
**OR**  
 the inhibitor forms a **covalent/permanent** bond with the active site [1]  
 blocking entry of the substrate [1]

(iii)



[1]  
 [4]

- (b) (i) (DNA)  $\longrightarrow$  mRNA  $\longrightarrow$  ribosome  $\longrightarrow$  tRNA  $\longrightarrow$  (Protein) [2]

- (ii) stop codon/it is used to stop the growth of a protein chain  
 (allow: used at the start of protein synthesis) [1]  
 [3]

- (c) (i) Adenosine diphosphate (ADP) or AMP **and** (inorganic) phosphate/ $\text{P}_i/\text{PO}_4^{3-}/\text{H}_3\text{PO}_4$  [1]

- (ii) Any two of –  
 muscle contraction  
 transport of ions/molecules or active transport or exocytosis or Na/K pump  
 synthesis of new compounds/proteins etc.  
 movement of electric charge in nerve cells  
 bioluminescence  
 non-shivering thermogenesis  
 DNA synthesis/reproduction

2 x [1]  
 [3]

[Total: 10]

Q37.

9 (a) (i) diamond and graphite [1]

(ii) any three from

	graphite	diamond
colour	black	transparent/colourless
electrical conductivity	good conductor	non-conductor
hardness	soft/slippery	hard/non slippery
density	less dense than diamond	more dense than graphite
melting point	lower	higher

3 × [1]  
[4]

(b) Because each carbon is only bonded to 3 others or is unsaturated/doubly-bonded/ $sp^2$  or has 3 bonding locations  
(NOT forms only 3 bonds) [1]



[1]  
[2]

(c) (i) Number of atoms carbon present =  $0.001 \times 6.02 \times 10^{23} / 12 = 5.02 \times 10^{19}$  [1]

(ii) Number of hexagons present =  $5.02 \times 10^{19} / 2 = 2.51 \times 10^{19}$

$$\text{Area of sheet} = 690 \times 2.51 \times 10^{19} = 1.73 \times 10^{22} \text{ nm}^2$$

[1]

(iii) Graphene: Yes, since it has free/delocalised/mobile electrons

[1]

Buckminsterfullerene: No, (although there is delocalisation within each sphere)  
it consists of separate/simple/discrete molecules/spheres/particles,  
(so no delocalisation from one sphere to the next)  
or electrons are trapped within each molecule/sphere

[1]  
[4]

[Total: 10]



