Mark schemes

Q1.

(a) 1. Amylase;

2. Glycosidic;

3. Peptide;

Reject dipeptide/ polypeptide bond

4. Amino acid(s);

Biological molecule	**Enzyme**	**Name of bond hydrolysed**	**Product of digestion**
	Amylase	Glycosidic	
		Peptide	Amino acid(s)

4

(b) 1. Add biuret (solution);

Reject burette or Beirut

Reject heat

Accept a description of the biuret test: eg copper sulfate and sodium hydroxide or $CuSO_4$ + NaOH or alkaline copper sulfate

Purple (colour produced);

Accept lilac/violet/mauve for purple

2

(c) 1. (Positive because) enzymes are protein;

2. (Because) enzymes not used up (in reactions)

OR

(Because) enzymes still present;

Accept correct answer in any order

Accept enzymes reused for enzymes not used up

Presence of enzyme after reaction must be implied

2

(d) Correct answer of 1.30 = **2 marks**;;

Evidence of correct rearranged equation, for example

Maximum rate of reaction = k_{cat} × Enzyme concentration = **1 mark**

OR

Evidence of 1 or 1.298 or 1.29 or 1.3 (correct answer but incorrect significant figures) = **1 mark;**

2

[10]

Q2.

(a) 1. (Inhibitor) binds (to enzyme) away from active site

OR

(Inhibitor) does not bind to active site;

Ignore inhibitor not similar or not same shape as substrate

Accept binds to allosteric (binding) site for does not bind to active site

2. Changing (enzyme) tertiary structure

OR

Changing active site (shape);

3. No/fewer enzyme-substrate complexes (form)

OR

Enzyme-substrate not complementary;

Accept a description of enzyme-substrate complex, eg so no/fewer substrate molecules fit/bind/enter (the active site)

Accept no/fewer ES complexes

3

(b) 1. (Independent) Time (of measurement/test /sample taken);

2. (Dependent) Casein concentration;

2

(c) 1. and 2. Correct answer of 20–30 = **2 marks**;;

Tangent drawn touching (2, 35) with incorrect calculation = **1 mark**

OR

17.5 (for incorrect method with correct reading at 2 minutes (35) and division by correct time, (2)) = **1 mark**;

2

(d) 1. Curve drawn entirely to the left of the curve given;

2. Similar shaped curve from (0, 180) to intersect x axis between (0, 0) and (6, 0);

2

[9]

Q3.

(a) 1. Variety **and** D **and** E in left column;

Accept if no table lines are shown, figures clearly written in rows and columns

Accept tables where mean is given in middle column and time is given in right column

Accept type ***OR*** *apple for variety*

Accept D and E in either order

2. Time **and** '/ min' **and** Mean (time) '/ min' in column heading only;

Accept mean values shown in rows rather than in columns

Accept brackets ***OR*** *"in" for solidus*

Ignore average for mean

Accept min ***OR*** *mins for minutes*

Accept seconds ***OR*** *secs* ***OR*** *sec for seconds*

Reject mixed units eg "/ minutes and seconds"

3. Correctly calculated times **and** means calculated to one decimal place;

Accept correct times and correct means however presented

Examples achieving 3 marks

Variety	Time / minutes	Mean / minutes
D	15.8/15.83/16	16.1 **OR** 16.2 **OR** 16.3
	18	
	14.5/15	
E	6.5/7	7.2 **OR** 7.3
	8	
	7	

Apple	Time / s	Mean / s
D	950	
	1080	966.7
	870	
E	390	
	480	430.0
	420	

3

(b) 1. More phenol/substrate in E

OR

More PPO/enzyme in E

OR

Higher PPO/enzyme activity in E;

Ignore oxygen

2. (So) more enzyme-substrate/E-S complexes (form);

Accept the converse for D

Ignore ESC

2

(c) 1. Use (enzyme's) higher/optimum temperature;

2. More kinetic energy

OR

(So) more active enzyme;

3. (Causing) increased rate of reaction

OR

(Causing) more enzyme-substrate complexes/collisions;

OR

4. Use (enzyme's) lower/optimum temperature

OR

Use (enzyme's) optimum pH;

1 and 4 Accept change in temperature

5. Less denaturation;

OR

(So) more active enzyme;

6. (Causing) increased rate of reaction

OR

(Causing) more enzyme-substrate complexes/collisions;

OR

7. Crush/grind/blend/chop the apple (tissue);

Accept cube for apple

Accept dice ***OR*** *homogenise* ***OR*** *cut up* ***OR*** *slice for crush*

8. (So) more PPO/phenol/substrate in contact with oxygen/air;

9. (Causing) increased rate of reaction

OR

(Causing) more enzyme-substrate complexes/collisions;

Mark in groups, 1, 2 and 3. ***OR*** *4, 5 and 6* ***OR*** *7, 8 and 9*

3. 6. and 9. Accept ES complexes for enzyme-substrate complexes

3. 6. and 9. Accept a description of increased rate, eg 'speeds up reaction'

If oxygen is suggested, no mark for oxygen but MP8 and MP9 are available

3 max

(d) Measure the intensity of brown colour by comparing apple tissue with a colour chart showing a range of apple tissues of known pigment concentration.

1

[9]

Q4.

(a) 1. Sequence/order of amino acids;

2. (Joined by) peptide bonds;

2

(b) 1. (Universal) The same codon/triplet always codes for the same amino acid;

2. (Non-overlapping) Each base is only part of one triplet/codon

OR

(Adjacent) codons/triplets do not overlap;

Accept ‘3 bases’ for triplet

Accept ‘base/triplets/codons only read once’

3. (Degenerate) More than one codon/triplet codes for each amino acid;

3

[5]

Q5.

(a) Quaternary

Condensation/phosphorylation/redox

Release/loss/formation

(Aerobic) respiration;;

All correct = **2 marks**,

2–3 correct = **1 mark**,

0–1 correct = **0 marks**

Accept ‘elimination’, ‘production’ for release

2

(b) (Catalyses the synthesis of ATP)

1. Active site <u>complementary</u> to ADP + Pi;
2. Enzyme-substrate complex forms;

   ‘E-S’ alone is insufficient

(Allows the movement of H^+ ions)

3. Channel (in membrane/protein/enzyme);

   Accept ‘pore’

4. Allows <u>facilitated</u> diffusion of H^+

OR

(Channel) has tertiary structure specific for (only) H^+;

4

[6]

Q6.

(a) 1. Amino acids joined by peptide bond(s);

2. (By) condensation reaction(s);

3. Secondary structure is formed by hydrogen bonding;

Accept alpha helix OR β-pleated sheet for ‘secondary structure’

4. Tertiary structure formed by interactions (between R groups);

Accept 3^o for tertiary

5. Quaternary structure contains >1 polypeptide

OR

Quaternary structure formed by interactions/bonds between polypeptides;

4 and 5 Accept for ‘interactions’, hydrogen bonds OR disulfide bridges OR ionic bonds OR hydrophobic OR hydrophilic interactions

Ignore peptide

5

(b) 1. Polymer of nucleotides;

Accept ‘polynucleotide’

2. (Nucleotide) consists of deoxyribose, phosphate and an organic/nitrogenous base;

Accept ‘phosphoric acid’ for phosphate

3. Phosphodiester bonds (between nucleotides);

4. DNA double helix held by H bonds

OR

2 strands held by H bonds;

5. (Hydrogen bonds/pairing) between adenine, thymine **and** cytosine, guanine;

Ignore bases identified with letters (A, T, G, C)

Reject adenosine and cysteine

6. DNA is associated with histones/proteins;

7. (During mitosis/when visible) chromosome consists of two chromatids joined at a centromere;

Accept correctly annotated diagram(s) for equivalent marking points

6 max

(c) 1. Independent segregation of homologous chromosomes/pairs;

If no marks awarded accept one principle mark ‘Meiosis producing cells that are genetically different (from one another)’

For ‘independent’ accept ‘random’

For ‘segregation’ accept ‘assortment’

2. Crossing over between homologous chromosomes/pairs;

Accept ‘within bivalent’ for ‘between homologous pair’

3. Random fertilisation of gametes;

Ignore ‘random mating’

Accept ‘random fusion’ for ‘random fertilisation’

4. (Produces) new combinations of alleles;

Accept as an additional mark point

(Produces) new combinations of maternal and paternal chromosomes

Ignore reference to epigenetics

4

[15]

Q7.

(a) 1. Condensation reaction between amino acids;

Accept descriptions of condensation reaction: eg loss of water

2. (Forming) peptide bonds;

3. Creating (specific) sequence/order of amino acids;

3

(b) (Similarity)

1. Substrate fits/binds to active site

OR

Enzyme-substrate complex (formed);

(Difference)

2. Active site changes shape, but does not change in lock and key

OR

(Initially) active site not complementary to substrate with induced-fit, but is complementary in lock and key;

Reject 'substrate changes shape'

Accept 'flexible' for changes shape and 'rigid' for does not change

2

(c) Lower/reduce activation energy (needed to start a reaction);

1

(d) Correct answer for 2 marks = 300;;

Accept for 1 mark,

2 000 000 or 2×10^6 (correct calculation of maltase rate per second)

OR

$6 \times 10^8 \div 4 \times 10^7$

OR

× 15 (correct division but not multiplied by 20)

2

(e) Increased maltase concentration;

1

[9]

Q8.

(a) More than one polypeptide;

Ignore prosthetic group OR named interactions between chains, eg disulfide bridge

1

(b) 1. (Both) active sites have similar/identical tertiary structures

OR

(Both) active sites have identical amino acid sequences;

Ignore shape for tertiary structure

Accept (both) have active sites that are complementary to different parts of the substrate;

Accept attach/bind for complementary

2. (So) form enzyme-substrate complexes (with the same substrate);

Accept E-S for enzyme-substrate

2

(c) 1. Same volume of (each) buffer/pH solution;

2. Same concentration/mass of substrate (at start);

3. Same concentration/mass of **denatured** enzyme;

Accept description of denatured, eg boiled

If no marks gained, accept for 1 mark,

Buffer **and** substrate **and** denatured enzyme

OR

Buffer **and** substrate **and** no enzyme

OR

Buffer **and** substrate **and** water;

3

Ignore temperature

Ignore amount for volume, concentration OR mass

Accept pH solution for buffer

(d) 1. Both/**P** and **Q** (are) active at pH 8.4;

2. **P** is (equally/most) active at both pHs
OR
Q is less active than **P** at both pHs
OR
P not affected by pH (change)
OR
Q is affected by pH (change);

3. **Q** is denatured/not active at pH 7.5
OR
Q is less active than the control at pH 7.5;
Accept description of denatured

4. Reaction occurs without enzyme(s)
OR
Reaction occurs in the control;

5. All (reactions) reach same end (point)
OR
Substrate is not used up;
Accept broken down OR catalysed OR digested OR hydrolysed for used (up)
Accept does not reach zero for not used up

3 max

Do not mark across all three conclusions
Accept catalyse OR breakdown (substrate) OR hydrolyse (substrate) OR digest (substrate) OR cause reaction for active/reaction
Ignore works better for active/reaction
Ignore reference to optimum

[9]

Q9.

(a) **Two** marks for three correct answers, **one** mark for two correct answers;;

(Left amino acid) Serine

(Middle amino acid) Alanine

(Right amino acid) Aspartic (acid)

Accept phonetic spellings

2

(b) One mark for each correct row

DNA	ATP	Reverse transcriptase	Phospholipid	
		✓		;
✓	✓	✓	✓	;
✓		✓		;

3

(c) Correct answer of 574 (amino acids) = **2 marks;**;

573.99936 = **1 mark**

OR

146/145.99986 = **1 mark**

OR

287 = **1 mark**

OR

292 = **1 mark**;

2

(d) Accept curve drawn to the right, following the same pattern **and** starting at Y = 0 and finishing at the same percentage saturation as original curve;

1

(e) 1. During exercise

OR

At low pO_2 (in the tissues);

Accept 'high altitude' or 'lack of red blood cells' for 'exercise'

Accept when there is a high pCO_2 (in the tissues)

Accept at low concentration of O_2 (in the tissues)

2. (Allowing) more oxygen for respiration

OR

(Allowing) **more** aerobic respiration

OR

To delay anaerobic respiration;

Accept descriptions of aerobic respiration, eg more oxygen to act as a terminal electron acceptor

*Accept oxygen can unload/dissociate eas**ier/more** readily for respiration*

2

[10]