

Mark schemes

Q1.

- (b) Endo(peptidase);
Correct spelling 1
- (c) 3; 1
- (d) 1. (6 amino acids in length) 1;
2. (20 amino acids in length) 2;
Accept for 1 mark, 55 (2 5 + 3 15) if no other mark awarded. 2

Q2.

- (a) 1. Substrate binds to the active site/enzyme
OR
Enzyme-substrate complex forms;
Accept for 'binds', fits
2. Active site changes shape (slightly) so it is complementary to substrate
OR
Active site changes shape (slightly) so distorting/breaking/forming bonds in the substrate;
3. Reduces activation energy; 3
- (b) 1. Adenosine diphosphate; 1
- (c) Mark in pairs, 1 **and** 2 OR 3 **and** 4 OR 5 **and** 6
1. Boil
OR
Add (strong) acid/alkali;
Accept heat at > 50°C OR at very high temperatures
2. Denatures the enzyme/ATP synthase;
OR

Accept for 'denatures', a description of denaturation

3. Put in ice/fridge/freezer;
4. Lower kinetic energy so no enzyme-substrate complexes form;

OR

Accept ES for enzyme substrate complex

5. Add high concentration of inhibitor;
6. Enzyme-substrate complexes do not form;

2

- (d) 1. (With) increasing Pi concentration, more enzyme-substrate complexes are formed;
2. At or above 40 (mmol dm⁻³) all active sites occupied

OR

At or above 40 (mmol dm⁻³) enzyme concentration is a limiting factor;

2

[8]

Q3.

- (a) 1. Starch (solution) in first column;
Ignore columns with replicates/ mean
Ignore lines
2. Headings for starch concentration/solution **and** time for (starch) hydrolysis/digestion with mg dm⁻³ **and** minutes/mins/min/m/seconds/s;
Accept brackets for solidus
Ignore reference to enzyme
Reject graph

2

- (b) As starch concentration increases, time to hydrolyse/digest starch increases;

Accept converse

1

- (c) 1. Inhibitor similar shape to substrate;
Reject same shape
Accept 'complementary to active site'

2. Fits/binds to active site;
3. Prevents/reduces enzyme-substrate complex forming;

3

- (d) 1. Less hydrolysis of starch;

Accept no hydrolysis

2. (To) maltose;
3. (So) less absorption (of glucose)

OR

(So) more egested (starch/carbohydrate);
Accept description of egestion, eg lost in faeces

3

[9]

Q4.

- (b) 1. Structure is determined by (relative) position of amino acid/R group/interactions;
Accept for 'interactions', hydrogen bonds / disulfide bridges / ionic bonds / hydrophobichydrophilic interactions
2. Primary structure is sequence/order of amino acids;
3. Secondary structure formed by hydrogen bonding (between amino acids);
Accept alpha helix/ β -pleated sheet for 'secondary structure'
4. Tertiary structure formed by interactions (between R groups);
Accept for 'interactions', hydrogen bonds / disulfide bridges / ionic bonds / hydrophobichydrophilic interactions
5. Creates active site in enzymes

OR

Creates complementary/specific shapes in antibodies/carrier proteins/receptor (molecules);

6. Quaternary structure contains >1 polypeptide chain

OR

Quaternary structure formed by interactions/bonds between polypeptides;

Accept for 'intereactions', hydrogen bonds/ disulfide bridges/ionic bonds/hydrophobichydrophilic interactions

Accept prosthetic (group)

5 max

Q5.

- (e) 1. One amine/ NH_2 group joins to a carboxyl/ COOH group to form a peptide bond;

Accept on diagram, for example (at least) two amino acids joining by a correctly drawn peptide bond (MP1) with NH_2 at one end and COOH at the other (MP2).

Ignore incorrect names of NH_2 and COOH groups.

2. (So in chain) there is a free amine/ NH_2 group at one end **and** a free carboxyl/ COOH group at the other

OR

Each amino acid is orientated in the same direction in the chain;

Allow ECF for incorrect naming of groups.

2

Q6.

- (a) 1. Lowers activation energy;
2. Induced fit **causes** active site (of enzyme) to change shape;
3. (So) enzyme-substrate complex **causes** bonds to form/break;
- Accept: description, of induced fit*
- Accept: enzyme-substrate complex causes stress/strain on bonds.*

3

- (b) Size/dimensions /mass/variety of potato

OR

Temperature (of solution/flask)

OR

pH (of solution);

Accept : weight of potato

Ignore : amount of potato

Ignore concentration/ volume of catalase

1

- (c) 0.33, 0.60, 0.86, 1.0, 1.0 = 2 marks;;

$\frac{6}{\text{time}}$

2 significant figures

If answer incorrect accept for 1 mark,

Correct values but incorrect number of significant figures

OR

1.0 written on row for hydrogen peroxide 2.0/2.5 in the table

OR

Answers showing correct division, eg 0.3, 0.6, 0.9

OR

Answers showing correct significant figures using incorrect calculation ($\div 18$) 1.0, 0.56, 0.39, 0.33, 0.33

2

- (d) 1. Hydrogen peroxide concentration on x axis **and** rate of reaction on Y axis, linear number sequence **and** appropriate scale;
Graph should cover half or more of the grid; eg reject if Y axis covers only three big squares
2. Correct units /mol dm⁻³ **and** /arbitrary units/au;
Accept brackets instead of solidus
3. All co-ordinates plotted accurately **with** point-to-point or smooth curve;
Accept accurate plotting of co-ordinates given in part (c)
Reject : bar chart
Reject : if ruled straight line of best fit
Accept: if x axis starts at 0.5
Accept: if line is extended to (0,0)

Plot coordinates must be processed data, hydrogen peroxide vs time = 0

3

- (e) Cut up/use discs/homogenise/increase surface area (of potato chips)
OR
Use bigger chips
OR
Increase temperature
OR
Change pH;
Reject answer if the temperature is above 40°C
Ignore: more/increase heat

1

[10]

Q7.

- (a) 1. Add biuret (reagent);
Accept sodium hydroxide (solution) and copper sulphate (solution)
Reject addition of other incorrect chemicals
2. (Positive result) purple/lilac/violet /mauve;
Reject other colours
Ignore references to heating

2

(b) Similarities

*2 max for similarities**Accept for three marks, a labelled diagram of a dipeptide showing $\text{NH}_2/\text{NH}_3^+$, COOH/COO^- and different R groups.*

1. Amine/ NH_2 (group at end);
Accept amino/ NH_3^+
2. Carboxyl/ COOH (group at end);
Accept carboxylic / COO^-
3. Two R groups;
4. All contain C **and** H **and** N **and** O;
Accept examples of different R groups

Difference

5. Variable/different R group(s);

3

- (c) 1. Moved to negative (electrode) **because** positive(ly charged);
2. (Spots move) different distances/rates **because** (amino acids) different charge/mass;
Accept size for mass.
3. Two spots (not three) **because** (amino acids) same charge/mass
OR
One spot has 2 amino acids **because** (amino acids) same charge/mass;
Accept size for mass.

3

[8]**Q8.**

- (a) 1. Attaches to the enzyme at a site other than the active site;
Accept 'attaches to allosteric/inhibitor site'
2. Changes (shape of) the active site
OR
Changes tertiary structure (of enzyme);
3. (So active site and substrate) no longer complementary **so** less/no substrate can fit/bind;
Accept 'no longer complementary so less/no enzyme-substrate complexes form'
Accept abbreviations of enzyme-substrate complex.

3

- (b) (With inhibitor) increase substrate/lipid (concentration) does not increase/affect/change rate of reaction

OR

(With inhibitor) increase substrate/lipid (concentration) does not increase/affect/change lipase activity

OR

High substrate (concentration) does not overcome inhibition

OR

High substrate (concentration) does not meet maximum rate of reaction/lipase activity;

Ignore references to competitive inhibitors.

1

Q9.

- (a) 1. Condensation (reaction) / loss of water;
Accept each marking point if shown clearly in diagram.
2. Between amine / NH₂ and carboxyl / COOH;
Accept between amino (group) and carboxylic / acid (group)
- (b) 1. Hydrogen bonds;
Accept as a diagram
Reject N - - - C / ionic / disulfide bridge / peptide bond
2. Between NH (group of one amino acid) and C=O (group);
OR
Forming β pleated sheets / α helix;
- (c) 1. Different sequence of amino acids
OR
Different primary structure;
If candidate assumes proteins are the same, accept effect of different pH/ temperature
2. Forms ionic / hydrogen / disulfide bonds in different places;

2

2

2

[6]**Q10.**

- (a) 1. Reduces activation energy;
Accept 'reduces E_a'.
2. Due to bending bonds
OR
Without enzyme, very few substrates have sufficient energy for reaction;
Accept 'Due to stress/pressure/tension on bonds'
OR 'Due to weakening bonds'.

Ignore references to 'breaking bonds'.

2

(b) $1.93 \times 10^{11};;$

Allow 1 max for

$578/3.0 \times 10^{-9}$

1.93×10^x when $x \neq 11$

Correct answer with incorrect standard form e.g. 19.3×10^{10}

Accept any number of significant figures ≥ 2 , if rounding correct (1.926×10^{11}). Same principle applies to one max answers.

2

(c) 31.4;;

Allow 1 max for

0.44 and 1.4

32.8

33.1

30

29.3

Accept any number of significant figures ≥ 2 , if rounding correct (31.4284714).

Same principle applies to 1 max answers.

32.8 = Both readings at 2.5 mmol dm^{-3} (0.44/1.34)

33.1 = Both readings at 2.5 mmol dm^{-3} (0.44/1.33)

30 = Incorrect reading for C (0.42/1.4)

29.3 = Incorrect reading for C (0.41/1.4)

2

- (d) 1. (Binding) alters the tertiary structure of the enzyme ;

Max 1

if lyxose acting as an inhibitor

OR if answer linked to lower rate of reaction

OR if lyxose used an energy source/respiratory substrate

2. (This causes) active site to change (shape);

3. (So) More (successful) E-S complexes form (per minute)

OR

E-S complexes form more quickly

OR

Further lowers activation energy;

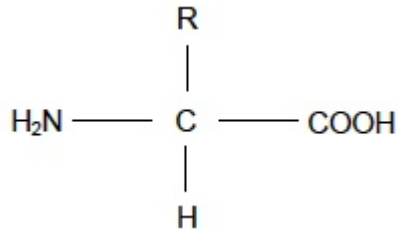
*Accept 'acts as a co-enzyme'**Accept description for E-S complexes.*

3

[9]

Q11.

(a)

*Accept other correct representations.*

1

- (b) 1. More than one codon codes for a single amino acid;
Accept 'triplet' or 'sequence of 3 bases/nucleotides' for 'codon'.
Reject 'production/produces' for 'codes for'.
Do not infer mp1 from mp2.

2. Suitable example selected from Table 1;

2

(c) 1395;

*Accept 1398 and 1401 (for those that include start and/or stop codons)**Allow 2796 or 2802 or 2790**Ignore 'bases/base pairs/bp/bps' written after the numerical answer.*

1

(d) ✓CAA → CGA

1

- (e) 1. (Both) negatively charged to positively charged change in amino acid;
2. Change at amino acid 300 does not change the shape of the active site
OR
 Change at amino acid 300 does not change the tertiary structure OR
 Change at amino acid 300 results in a similar tertiary structure;
Reference to 'shape' of active site only needed once.
3. Amino acid 279 may have been involved in a (ionic, disulfide or

hydrogen) bond **and** so the shape of the active site changes

OR

Amino acid 279 may have been involved in a (ionic, disulfide or hydrogen) bond **and** so the tertiary structure changed;

OR

Amino acid 279 may be in the active site **and** be required for binding the substrate;

Reference to 'shape' of active site only needed once.

Both parts are required for each mark option.

For 'a bond' reject peptide bond.

3

[8]

Q12.

- (a)
1. IV on x axis and DV on y axis **and** both axes on linear scales;
 2. Axes labelled clearly and with correct units separated from variable by solidus or in brackets;
 3. All rates calculated correctly;
 4. Points plotted correctly **and** joined by ruled lines and no extrapolation;

4

(b) Yes:

1. Expect optimum temperature of enzyme to be same

OR

Similar to temperature where bacterium lives;

2. Optimum temperature for enzyme (appears to be around) 15 °C;

No:

3. Need data from more temperatures (between 10 °C and 20 °C);
4. Data for only isolated enzyme

OR

Isolation may affect activity;

4

- (c)
1. Initial / starting substrate concentration
 2. Enzyme concentration
 3. pH.

Any 2 for 1 mark

1 max

