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 <u>complementary</u> 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;;

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

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 (÷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 NH_2/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 <u>complementary</u> **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 / NH_2 and carboxyl / COOH;

Accept between amino (group) and carboxylic / acid (group)

2

(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;

2

(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

[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) 1.93×10^{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 ($1.926^{\bullet} \times 10^{11}$). 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) <u>active site</u> 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'

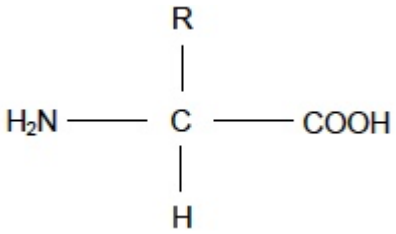
Accept description for E-S complexes.

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 <u>active site</u>
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

[9]