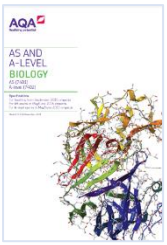
St. Ambrose College

A Level Biology (Year 12)

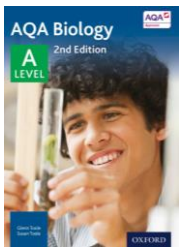
Knowledge Organiser: Unit 1 Biomolecules (1.1-1.4)

1.1 Monomers and polymers
1.2 Carbohydrates
1.3 Lipids
1.4 Proteins

For every 1 hour A Level Biology lesson you are expected to spend at least 1 hour independently reviewing the subject content. The following resources should be referred to regularly to support your independent work.



You have been provided with a printed copy of the full subject specification (also available on the AQA website https://www.aqa.org.uk/subjects/science/as-and-a-level/biology-7401-7402/specification-at-a-glance). Use this to follow the learning in lessons…track your progress and be aware of what is still to come.



Use the textbook on www.kerboodle.com after every lesson to develop your understanding. Read the relevant pages, add detail to your class notes and complete the summary tasks. Create your own summary notes/flashcards for future use in the run up to exams.

Unit 1 Biomolecules pg4-55 Monomers and polymers **(pg4-7)** Carbohydrates **(pg8-15)** Lipids **(pg16-18)** Proteins (structure **pg19-22**, enzymes **pg23-33**)

SENECA
www.senecalearning.com

Use regularly between lessons to review basic content and to become more familiar with key terminology. https://senecalearning.com/en-GB/

PMT
resources · tuition · courses

Access detailed revision notes, key definitions, flash cards, past paper questions and mark schemes.
https://www.physicsandmathstutor.com/biology-revision/a-level-aqa/

As an A Level student you are expected to take a proactive approach to your studies; arrive to lessons fully equipped and prepared for what you will be learning about (read ahead in the specification/textbook), focus and participate in lessons, ask for help/clarification when you are unsure and spend time after the lesson consolidating/embedding new learning.

1.1 Monomers and polymers

Monomers and polymers

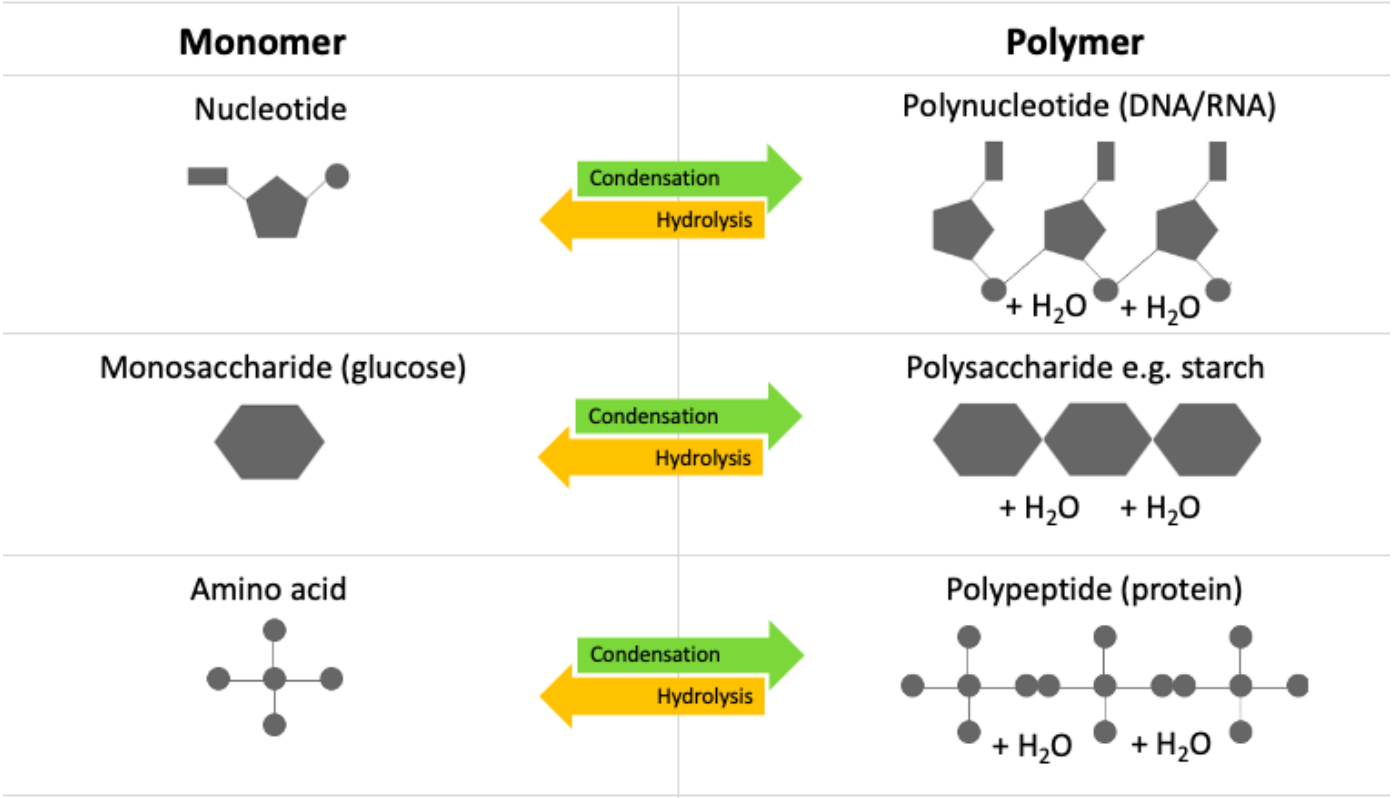
- **Monomer**: small, single molecule, many of which can be joined together to form a polymer
- **Polymer**: large molecule made up of many similar / identical monomers joined together

Condensation and hydrolysis reactions

A **condensation reaction:**
- Joins 2 molecules together
- Eliminates a water molecule
- Forms a chemical bond e.g. glycosidic bond

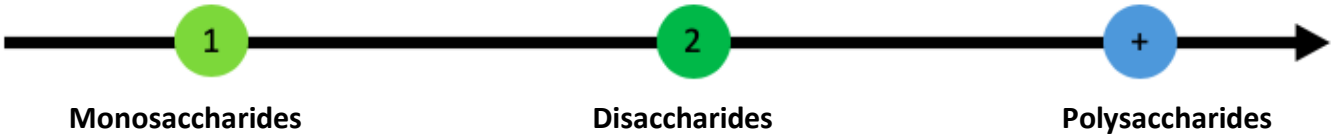
A **hydrolysis reaction:**
- Separates 2 molecules
- Requires addition of a water molecule
- Breaks a chemical bond

Exam tip: to get full marks for a diagram of a condensation or hydrolysis reaction, you need to include the H_2O molecule that is added or removed



1.2 Carbohydrates

Carbohydrates can be classified into 3 groups based on how many units they are made of (1, 2 or many)



Monosaccharides	Disaccharides	Polysaccharides
The monomers from which larger carbohydrates are made	Formed by the condensation of 2 monosaccharides	Formed by the condensation of many monosaccharides

Monosaccharides and disaccharides

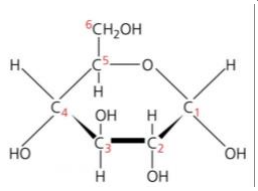
Monosaccharides and disaccharides are simple carbohydrates (sugars)

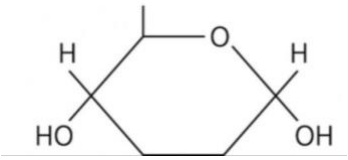
Monosaccharides

- Monosaccharides are the monomers from which larger carbohydrates are made
- E.g. glucose, fructose and galactose

Structure of glucose

- 6 carbon atoms, labelled in red on diagram **(a)**
- Learn how to draw glucose in as much detail as diagram **(b)**

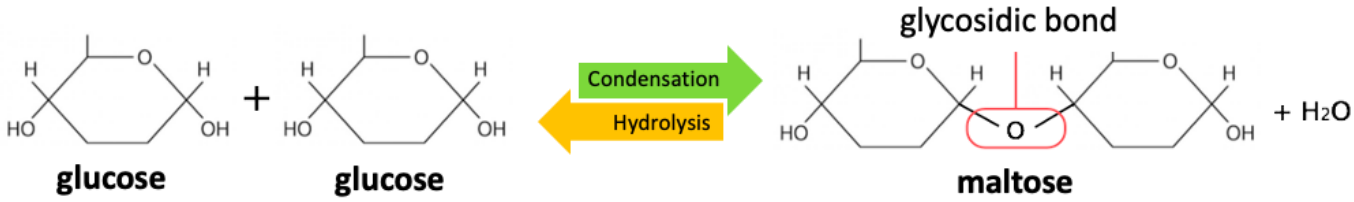




Disaccharides

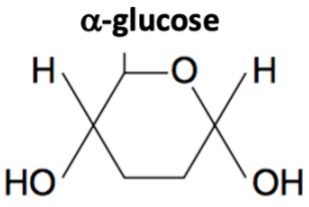
- Glucose + glucose = **maltose**
- Glucose + fructose = **sucrose**
- Glucose + galactose = **lactose**

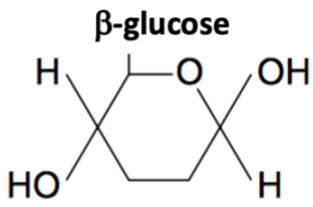
A condensation reaction between 2 monosaccharides forms a **glycosidic bond**



Isomers of glucose: α- and β-glucose

- **Isomer**: same molecular formula but differently arranged atoms
- **Difference in structures:** OH group is below C1 on α-glucose but above C1 in β-glucose

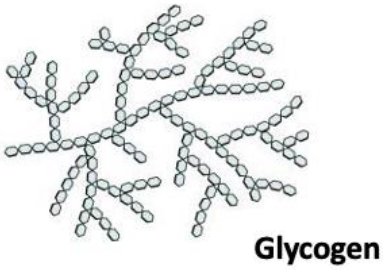




Polysaccharides

Examples: starch, glycogen and cellulose

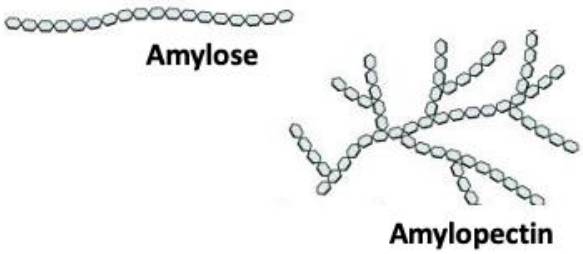
Glycogen



- **Function:** energy store in animal cells
- **Structure:** polysaccharide of α-glucose with C1-C4 and C1-C6 glycosidic bonds so branched

Structure of glycogen related to its function:
- ✓ Branched; can be rapidly hydrolysed to release glucose for respiration to provide energy
- ✓ Large polysaccharide molecule; can't leave cell
- ✓ Insoluble in water; water potential of cell not affected i.e. no osmotic effect

Starch



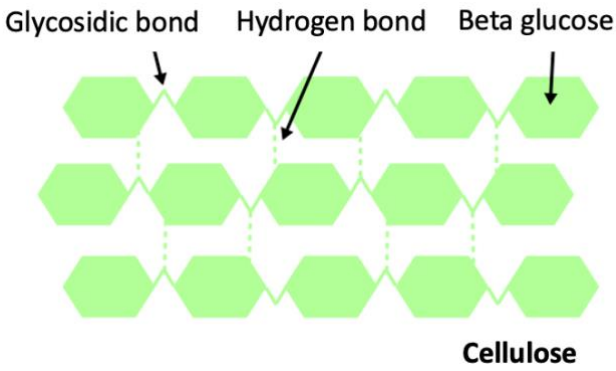
- **Function:** energy store in plant cells
- **Structure:** polysaccharide of α-glucose. Mixture of amylose and amylopectin; amylose has C1-C4 glycosidic bonds so is unbranched, while amylopectin has C1-C4 and C1-C6 glycosidic bonds so is branched

Structure of starch related to its function (amylose):
- ✓ Helical; compact for storage in cell
- ✓ Large polysaccharide molecule; can't leave cell
- ✓ Insoluble in water; water potential of cell not affected i.e. no osmotic effect

Cellulose

- **Function:** provides **strength** and structural support to **plant cell walls**
- **Structure:** polysaccharide of b-glucose. Alternate 180 degree rotation. C1-C4 glycosidic bonds so is unbranched. Chains of glucose molecules are arranged in a linear pattern

Structure related to function:
- ✓ Every other beta-glucose molecule is inverted in a long, straight, unbranched chain
- ✓ Many hydrogen bonds link parallel strands (crosslinks) to form micro fibrils (strong fibres)
- ✓ H bonds are strong in high numbers
- ✓ Provides strength and structural support to plant cell walls



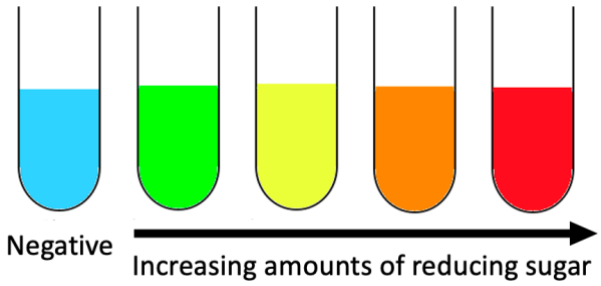
Biochemical tests for carbohydrates

Benedict's test for sugars

Reducing sugar	Non-reducing sugars
• All monosaccharides e.g. glucose	• No monosaccharides
• Most disaccharides e.g. maltose / lactose	• Some disaccharides e.g. sucrose

Benedict's test for reducing sugars

1. Add benedict's reagent (blue) to sample
2. Heat in a boiling water bath
3. Positive = green / yellow / orange / red precipitate (reducing sugar present)



Benedict's test can also be used to test for non-reducing sugars, indirectly:

Benedict's test for non-reducing sugars

1. Add a few drops of dilute hydrochloric acid (hydrolyse sugar into its constituent reducing sugars)
2. Heat in a boiling water bath
3. Neutralise with sodium bicarbonate
4. Add Benedict's reagent and heat again
5. Non-reducing sugar present = green / yellow / orange / red precipitate

Determining glucose concentration

1. Produce a **dilution series** of glucose solutions of known concentrations
2. Perform a **Benedict's test** on each sample
   - Heat with Benedict's solution
   - Use same amount of solution for each test
   - Use excess Benedict's
   - Remove precipitate by filtering
3. Using a **colorimeter**, measure the **absorbance** of each sample and plot a **calibration curve**
   - Calibrate colorimeter using unreacted Benedict's
   - Use a red filter
   - Less absorbance of filtrate = more sugar present (as removed precipitate)
   - Plot absorbance against glucose concentration
4. Repeat with unknown sample (find absorbance) and use graph to **determine glucose concentration**

Iodine test for starch

1. Add **iodine dissolved in potassium iodide** to solution and **shake/stir**
2. **Blue-black** colour = starch present

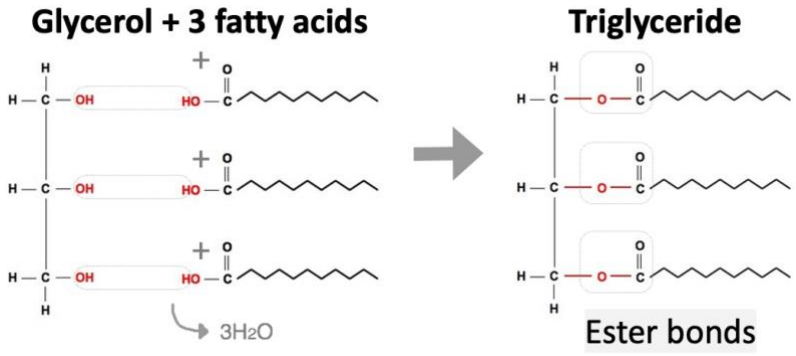
1.3 Lipids

Triglycerides and phospholipids are 2 groups of lipids

Triglycerides

Triglycerides are formed by the condensation of **1 molecule of glycerol and 3 fatty acids**

A condensation reaction between glycerol and a fatty acid (RCOOH) forms an **ester bond**



Zig zags represent a simplified hydrocarbon tail, also sometimes represented as 'R'

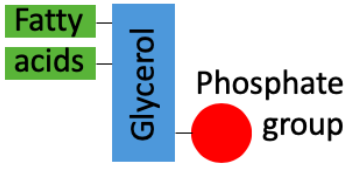
Properties related to structure

Triglycerides: energy storage molecules

- High ratio of C-H bonds to C atoms in hydrocarbon tail
  so release more energy than the same mass of carbohydrates
- Insoluble in water (clump together as droplets)
  so no effect on water potential of cell

Phospholipids

In phospholipids, one of the fatty acids of a triglyceride is substituted by a phosphate-containing group



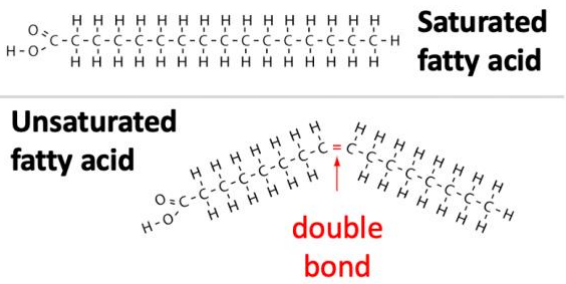
Properties related to structure

Phospholipids: form bilayer in cell membrane, allowing diffusion of non-polar / small molecules

- Phosphate heads are polar / hydrophilic
  so are attracted to water → orient to aqueous environment either side of membrane
- Fatty acid tails are non-polar / hydrophobic
  so are repelled by water → orient to interior of membrane → repels polar / charged molecules

Saturated & unsaturated fatty acids

- **Saturated:** no C=C double bonds in hydrocarbon chain; all carbons fully saturated with hydrogen
- **Unsaturated:** one or more C=C double bonds in hydrocarbon chain



Emulsion test for lipids

1. Add ethanol and shake (dissolves lipids)
2. **Then** add water
3. Positive: milky/cloudy white emulsion

To get the marks in the exam, you must state steps 1 and 2 in the correct order

4.1 General properties of proteins

Amino acids, dipeptides and polypeptides

Amino acids are the monomers from which proteins are made

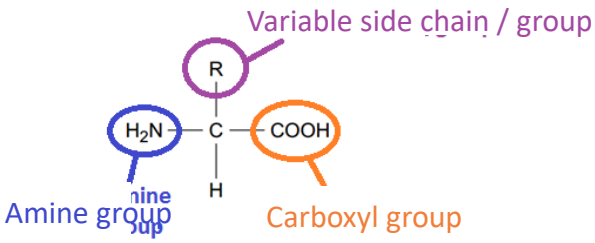
20 amino acids are common in all organisms – differ only in their side group

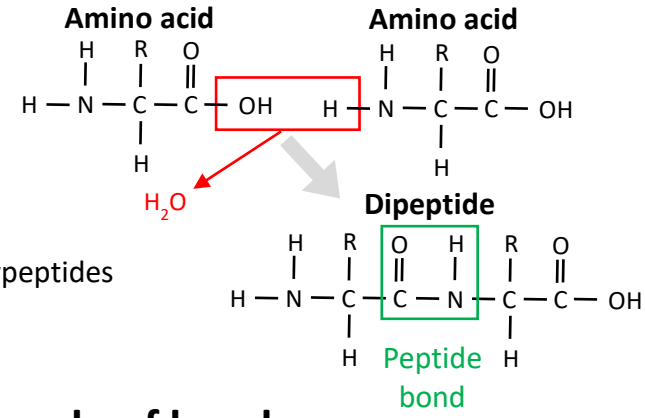
A condensation reaction between 2 amino acids forms a **peptide bond**

- Dipeptide – 2 amino acids joined
- Polypeptide – many amino acids joined

- A functional protein may contain one or more polypeptides

General structure of an amino acid





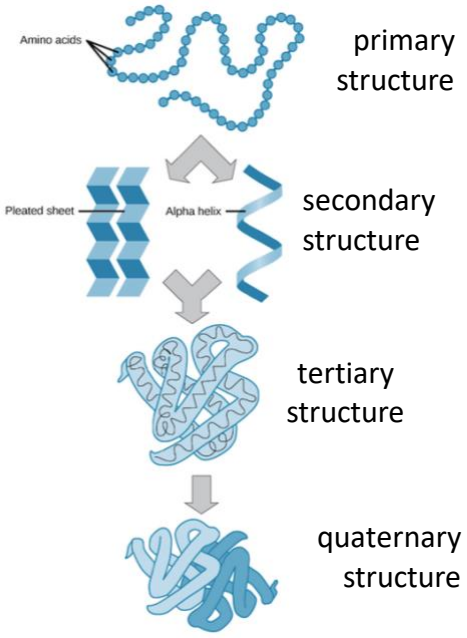
Structural levels of proteins and the role of bonds

Primary (1°) structure
- Sequence of amino acids in a polypeptide chain

Secondary (2°) structure
- Hydrogen bonding between amino acids (between carbonyl O of one and amino H of another)
- Causes polypeptide chain to fold into a repeating pattern e.g. alpha helix or beta pleated sheet

Tertiary (3°) structure
- Overall 3D structure of a polypeptide held together by interactions between amino acid side chains:
- Ionic bonds / disulfide bridges / hydrogen bonds

Quaternary (4°) structure
- Some proteins are made of 2+ polypeptide chains
- Held together by more hydrogen, ionic and disulfide bonds



Proteins have a variety of functions within all living organisms. You need to be able to relate the structure of proteins to properties of proteins named throughout the specification e.g. enzymes / antibodies

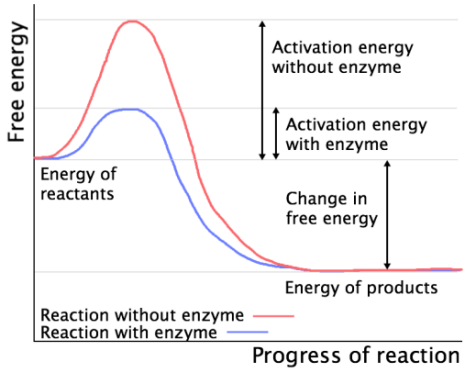
Biuret test for protein

- Add biuret solution: sodium hydroxide + copper (II) sulfate
- **Protein present: purple colour** (negative = stays blue)
- Detects presence of peptide bonds

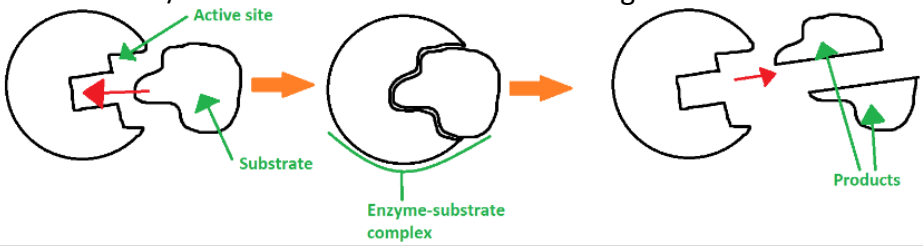
4.2 Many proteins are enzymes

Introduction to enzymes

- Each enzyme **lowers the activation energy** of the reaction it catalyses (see diagram) → speed up rate of reaction
- Enzymes are **biological catalysts**; they catalyse a wide range of intracellular (within cells) and extracellular (outside cells) reactions that determine structures and functions from cellular to whole-organism level.



Models of enzyme action

Lock and Key model	Induced Fit model
Old, outdated	Recent, accepted
• Active site is a fixed shape / doesn't change shape; it is complementary to one substrate • After a successful collision, an enzyme-substrate complex forms leading to a reaction	1. Before reaction, enzyme active site not completely complementary to substrate / doesn't fit substrate 2. Active site shape changes as substrate binds and enzyme-substrate complex forms 3. This stresses / distorts bonds in substrate leading to a reaction 

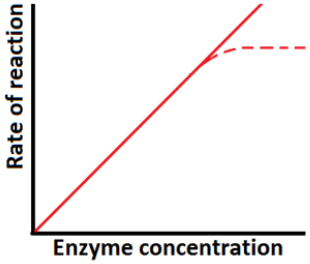
The specificity of enzymes

- Enzymes have a **specific shaped tertiary structure and active site**
  - Sequence of amino acids (primary structure) determines tertiary structure
- Active site is **complementary** to a specific substrate
- Only this substrate can **bind** to the active site, inducing fit and forming an **enzyme-substrate complex**

Factors affecting rate of enzyme-controlled reactions

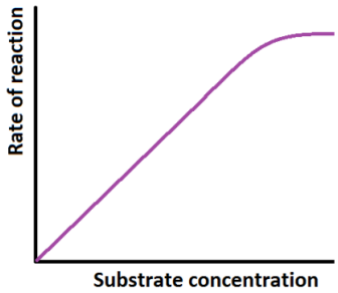
Enzyme concentration

- Increasing enzyme conc. → rate of reaction increases
  - **Enzyme conc. = limiting factor** (substrate in excess)
  - More enzymes → more available **active sites**
  - More successful **E-S collisions and E-S complexes**
- At a certain point, rate of reaction **plateaus**
  - **Substrate conc. = limiting factor** (all substrates in use)



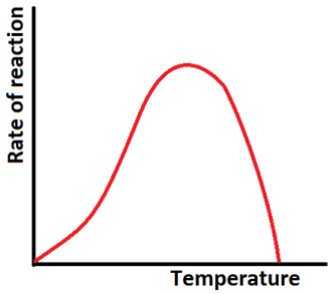
Substrate concentration

- Increasing substrate conc. → rate of reaction increases
  - **Substrate concentration = limiting factor** (too few enzyme molecules to occupy all **active sites**)
  - More successful **E-S collisions and E-S complexes**
- At a certain point, rate of reaction **plateaus**
  - **Enzyme conc. = limiting factor** (all active sites saturated; excess substrate)



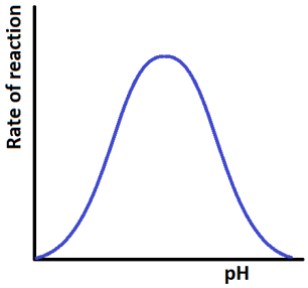
Temperature

- Increasing temp. up to optimum → rate of reaction increases
  - Increase in **kinetic energy**
  - More successful E-S collisions and **E-S complexes**
- Increasing temp. above **optimum** → rate of reaction falls
  - Enzymes **denature**; **tertiary structure** and **active site change shape** (hydrogen / ionic **bonds break**)
  - Fewer **E-S collisions and E-S complexes** (substrate no longer binds to active site)
- Rate of reaction **0** when **all** enzymes denatured



pH

- pH above / below optimum pH → rate of reaction decreases
  - Enzymes **denature; tertiary structure** and **active site change shape** (hydrogen and ionic **bonds break**)
  - Complementary substrate can no longer bind to active site
  - Fewer **E-S collisions and E-S complexes**
- pH = - $\log_{10}$ [H^+]



Concentration of competitive and non-competitive inhibitors

Competitive inhibitors decrease rate of reaction

- **Similar shape to substrate**
- Competes for / binds to / blocks **active site** so substrates can't bind
- Fewer E-S complexes
- **Increasing substrate conc. reduces effect** of inhibitor (level of inhibition dependent on relative concs. of substrate and inhibitor)

Non-competitive inhibitors decrease rate of reaction

- Binds to **site away from the active site** (allosteric site)
- Enzyme **tertiary structure / active site change shape** so substrate can't bind to active site
- Fewer E-S complexes
- **Increasing substrate concentration has no effect** on rate of reaction as causes permanent change to active site