



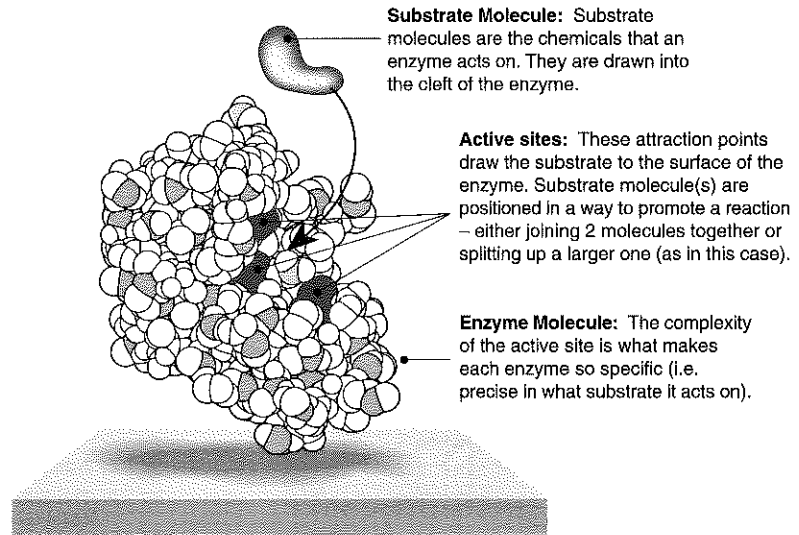
Enzymes

Most enzymes are proteins. They are capable of catalysing (speeding up) biochemical reactions and are therefore called **biological catalysts**. Enzymes act on one or more compounds (or **substrates**). They may break a single substrate molecule down into simpler substances, or join two or more substrate molecules chemically together. The enzyme itself is unchanged in the reaction – its presence merely allows the reaction to take place more rapidly. When the substrate attains the required **activation energy** to enable it to change into the product, there is a 50% chance that it will proceed forward to form the product, otherwise it reverts back to a stable form of the reactant again.

The part of the enzyme's surface into which the substrate is bound and undergoes reaction is known as the **active site**. This is made of different parts of polypeptide chain folded in a specific shape so they are closer together. The substrate fits into the cleft and locks into position. For some enzymes, the complexity of the binding sites can be very precise, allowing only a single kind of substrate to bind to it. Some other enzymes have low **specificity** and will accept a wide range of substrates of the same general type (e.g. lipases break up any fatty acid chain length of lipid). This is because the enzyme is specific for the type of chemical bond involved and not an exact substrate.

Enzyme Structure

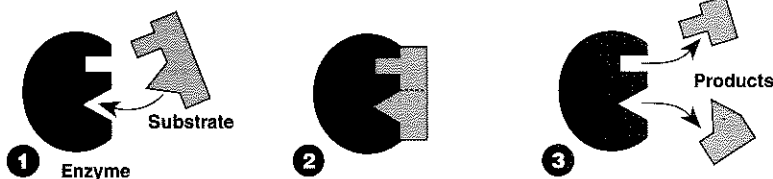
The model on the right is of an enzyme called *Ribonuclease S*, that breaks up RNA molecules. It is a typical enzyme, being a globular protein and composed of up to several hundred atoms. The darkly shaded areas are called **active sites** and make up the **cleft** – where the substrate molecule(s) are drawn to. The correct positioning of these sites is critical for the catalytic reaction to occur. The substrate (RNA in this case) is drawn into the cleft by the active sites. By doing so, it puts the substrate molecule under stress, causing the reaction to proceed more readily.



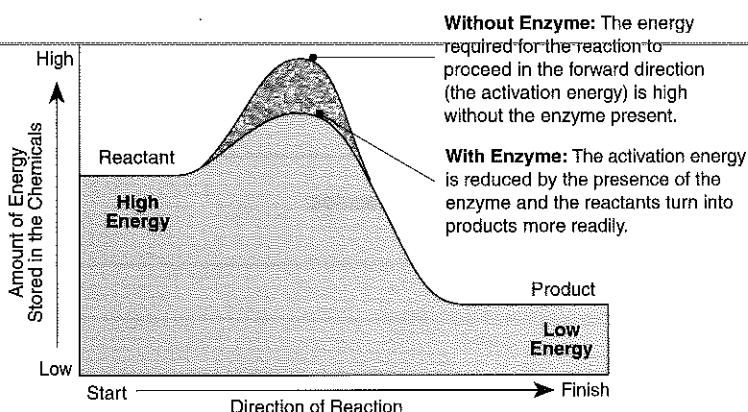
Source: *Biochemistry*, (1981) by Lubert Stryer

How Enzymes Work

The **lock and key** model proposed earlier this century suggested that the substrate was simply drawn into a closely matching cleft on the enzyme molecule. More recent studies have revealed that the process more likely involves an **induced fit** (see diagram on the right), where the enzyme and/or the reactants change their shape slightly. The reactants become bound to enzymes by weak chemical bonds. This binding can weaken bonds within the reactants themselves, allowing the reaction to proceed more readily.

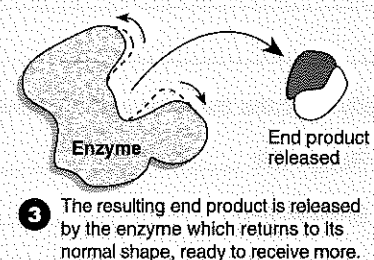
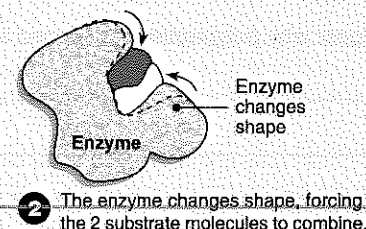
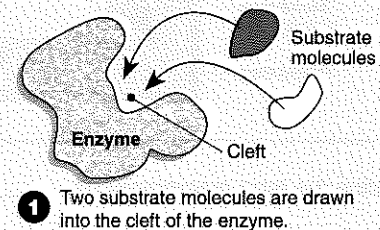


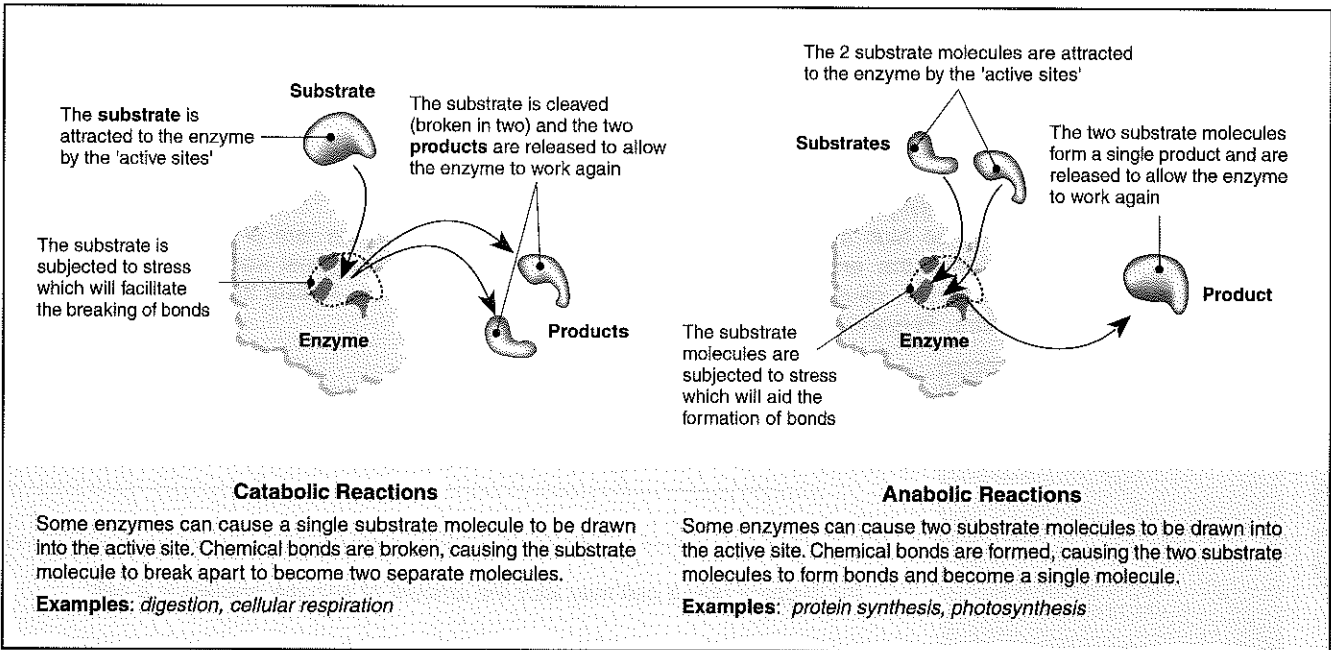
The presence of an enzyme simply makes it easier for a reaction to take place. All **catalysts** speed up reactions by influencing the stability of bonds in the reactants. They may also provide an alternative reaction pathway, thus lowering the activation energy needed for a reaction to take place (see the graph below).



Induced Fit Model

An enzyme and its substrate act like a lock and key. The shape of the enzyme changes when the substrate fits into the cleft:





1. Explain why an enzyme is called a **biological catalyst**: _____

2. Explain what the **substrate** is when considering enzyme action: _____

3. Describe the role that **active sites** have in enzyme function: _____

4. Define the following terms (see the page on "Control of Metabolism" if you need extra help):
 - (a) **Catabolism**: _____

 - (b) **Anabolism**: _____

5. (a) Name an example of an **anabolic** reaction: _____
 (b) Name an example of a **catabolic** reaction: _____
6. (a) Describe the basic features of the **induced fit** model of enzyme action: _____

 (b) Contrast this model with the older lock and key model: _____

7. Explain what might happen to the functioning of an enzyme if the gene that codes for it was altered by a mutation: _____

