

Source: [KBhBIO101AminoAcids](#)

1 | Enzymes

Proteins that build things up and break things down!

A macromolecular **catalyst**, it...

1. Speeds up the rate of reactions
2. Does not get consumed by the reaction
 1. Not a fundamental product
 2. Not a fundiment reactant
3. Shape determines the reactions that it can participate in
4. Enzymes are subject to **protean denaturation** => if the protein unfolds, its function will be lost.
Triggered by excess heat, acid, and other problems

(4) is unlike non-protein, inorganic catalyst — inorganic non-proteins need to unwrap or wrap.

Enzyme activity: promote a reaction without participating in it directly

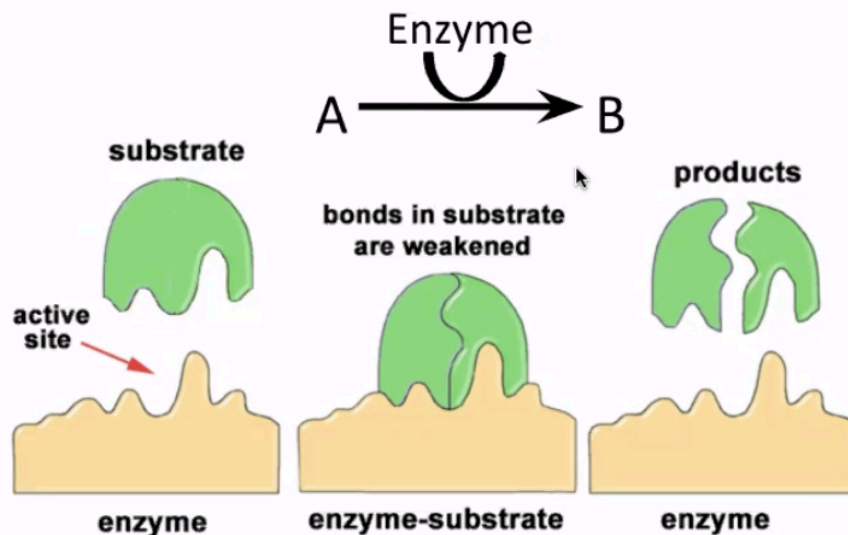


Figure 1: Screen Shot 2020-09-30 at 2.45.04 PM.png

1.1 | Enzymes doing things

1. The reactant (called “substrate”) fits into a pocket (“active site”) in the enzyme for the reaction to occur. Yes, there could be multiple active sites for multiple reactants
2. The enzyme rearrange itself slightly to hold the enzyme in place
3. A cofactor (“catalyst to the catalyst”) also bind to the active sites

Enzymes minimize the **activation energy hump**

1.2 | Why do Enzymes work?

There are three main ways that Enzymes work:

1. Stress and straining of the bonds to force towards the necessary transition state
2. Changing the substrate to favourable orientation
3. Active site amino acids rearranging electrons + creating partial charges to favor a reaction

Remember: The Fundamental Energy Difference does not change whether or not reactions are helped by the Enzyme.

For more information about the reaction hump and its related energy changes, see [\[KBhBIO101Enthalpy\]](#), and [\[KBhBIO101Entropy\]](#)