PROTEIN STRUCTURE

Enzymes are proteins. How does their structure help them function to speed up chemical reactions?

Analogy: car engine—have to understand structure to understand function.

What is a protein molecule? A long chain of amino acids. (Like a necklace with the amino acids represented by beads). These chains are approx. 1000 amino acids long.

Whiteboard questions:

1. What makes amino acids the same and different? They all have:

SAME: H2N= an amino group
A central Carbon with a Hydrogen
A carboxylic acid group

DIFFERENT: The R group (there are twenty different ones) This is what makes the amino acid different from another amino acid.

The R groups have unique chemical properties like: polar, non polar, positively charged or negatively charged.

2. Diagram an amino acid chain. Tell how it can fold into a protein.

Remember the rules of polar/nonpolar and positive and negative:

1. Dipole-dipole= **Polar attracts to Polar.** Because polar molecules have unbalanced charges (a little positive and a little negative), they are attracted to other polar molecules.
2. Nonpolar-Nonpolar= they **associate**. They hang out with each other. Oil is an example of a nonpolar molecule.
3. Positive-Negative= They **attract.**
4. Positive-positive, Negative- Negative= **Repel**
5. Polar- charged= **attract**. Like salt in water.

These R groups in the chain will respond to the forces above. This will cause the chain to fold and twist and tangle up into a shape. The **shape** is very important to how it works. The shape of every protein is very unique. It will only attract a specific substrate to its active site.

3. Show the active site of the protein and say why a substrate would tend to enter. Use the ***Lock and Key model*** to explain the relationship between enzyme, substrate, and active site.

Lock= Enzyme
Key= Substrate
Keyhole= Active Site, a groove that is specific and specially designed to fit the key (substrate).

The **active site** is the binding site of enzymes and their substrates.

Enzyme notes: 09/04/08

!!!!Enzymes cause stable molecules to react by lowering activation energy. But HOW?

In exothermic reactions, there is more energy at the beginning, and less at end. That bit of energy required at the beginning is the activation energy. Once this is put in, the reaction begins and continues until the end.

Unstable molecules have low activation energy.

But living things have stable molecules—that have high activation energy. To get these reactions to begin, we need enzymes.

Enzymes are proteins—long chains of amino acids. This long chain tangles and folds into a specific functional shape. In that shape, there is a groove or nook on the surface (the active site). This is where the enzyme reacts with the substrate.

The **Lock and Key Model** is a way of thinking about how this works.

Lock= enzyme; Key= substrate; keyhole= active site

This model doesn't really explain how enzymes cause stable molecules to react by lowering activation energy. We need another model to explain this---

Induced Fit Model: induce= cause something to happen; it picks up where lock and key leaves off.

It explains how when the substrate is in the active site, a small amount of activation energy will be applied to cause the substrate to breakdown.

The enzyme's active site will only grab a specific molecule of substrate.

********When the substrate is in the active site, the amino acids lining the active site will exert forces on the substrate molecules and induce the bonds to break and the substrate to break down.*

Additional info:

Denaturing—additional heat adds forces that disrupts the forces holding the protein together. This causes it to unravel and it no longer has the same shape to attract the substrate.