

### Chapters 5-6 Enzymes

**Catalyst:** A substance that speeds up the rate of a chemical reaction but is not itself consumed.

Most biological catalysts are **proteins** but some **RNA** are catalysts too.

*e.g.* Peptide bonds are made by the catalytic activity of the RNA in ribosomes.

Some enzymes require organic coenzymes and / or metal ions.

**Apoenzyme / Apoprotein** = Protein

**Holoenzyme** = Protein + Coenzyme

**Classification of Enzymes** Add “*ase*” to the activity to obtain the name.

1. **Oxidoreductases:** transfer  $e^{-1}$  as H or  $H^{-}$ .
2. **Transferases:** group transfer.
3. **Hydrolases:** bond breakage through addition of water.
4. **Lyases:** addition to or formation of double bonds.
5. **Isomerases:** group transfer yielding isomers.
6. **Ligases:** formation of C-C, C-S, C-O, C-N coupled to ATP cleavage.

Why are enzymes necessary?

1. Most biological molecules are **stable** at pH 7, 37°C in H<sub>2</sub>O.

Enzymes accelerate bond formation and breakage by 10<sup>2</sup> – 10<sup>17</sup>.

2. Enzymes are **specific**; usually there are no side-reactions.

3. Enzymes can be **regulated**.

But, enzymes can be easily **denatured**.

Enzymes function *via* **changes in conformation**. They are dynamic, not static. Their atoms are constantly in motion.

### How do Enzymes work?

1. **Specificity**: Specific reacting molecules called **substrates (S)** bind to the enzyme (**E**) **active site** and are converted into a **product (P)**. The active site fits the substrate like a hand in a glove (but see below).

*e.g.* *Phosphofructokinase* transfers a phosphate group from ATP to Fructose-6 phosphate forming **Fructose-1,6 biphosphate** and **ADP**. The reaction is controlled by the binding of **ADP** in the **allosteric** binding site. (a)

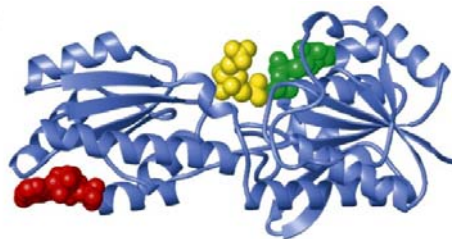
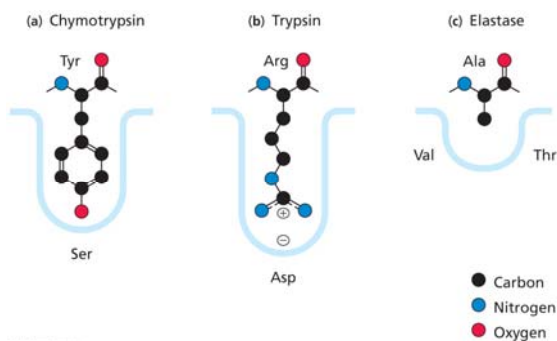
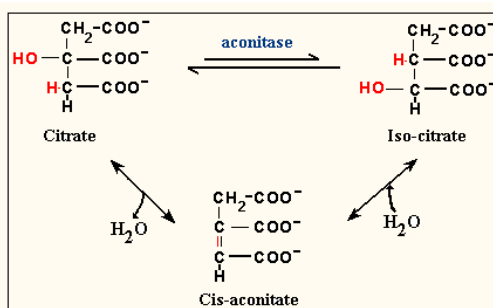


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*e.g. Trypsin, chymotrypsin,*  
and *elastase* recognize different  
classes of AA *via* the size and  
shape of their binding sites:



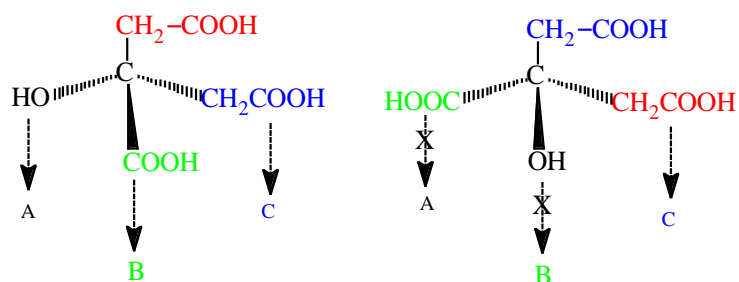
*e.g. Aconitase* can distinguish between the two ends of citrate  
even though there is no chiral C.



Citrate is converted into iso-citrate by firstly a dehydration (cleavage of water) so that cis-aconitate is formed. Then cis-aconitate is hydrated (water added) and iso-citrate is formed. This reaction is catalysed by aconitase.

[http://www.natuurlijkerwijs.com/english/Citrate\\_cycle.htm](http://www.natuurlijkerwijs.com/english/Citrate_cycle.htm)

It can, because the enzyme is a 3-dimensional molecule with 3 sites of interaction:



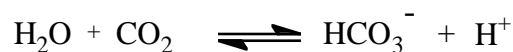
On the other hand, enzymes are less specific and can sometimes bind several different substrates.

*e.g. Hexokinase phosphorylates glucose, fructose, and mannose.*

So the enzymes provide a binding site that is **complementary** to the **steric** and **electronic** features of the substrate: “*hand-in-glove*”.

## How do Enzymes work?

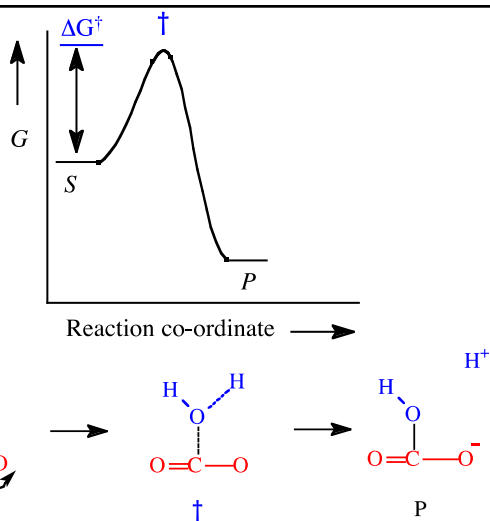
2. Enzymes provide a *special environment* in which bond formation / breakage is easier.



is slow because energy is required to break the O-H bond of water and stretch one of the C=O bonds of CO<sub>2</sub>.

We can keep track of the G changes by a “**Reaction co-ordinate diagram**”.

The Reaction co-ordinate indicates the free energy changes as the reaction progresses from substrate, *S*, to product, *P*.



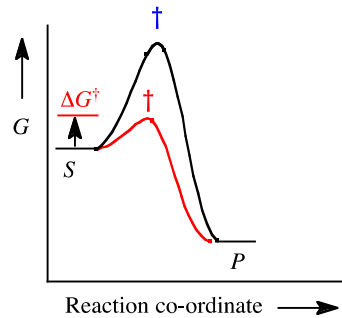
*G* must be added to **stretch the bonds** to the point of breaking.

The **Transition State** † is the point at which there is an equal probability of the O-H and C=O bonds re-forming and new HCO<sub>3</sub><sup>-</sup> bonds forming.  $\Delta G^\ddagger =$  **Activation Energy**.

$$\Delta G^\ddagger_{S \rightarrow P} = G^\ddagger - G_S$$

Enzyme catalysts work by lowering  $\Delta G^\ddagger$ , so that in the presence of an enzyme

$$\Delta G^\ddagger_{cat} \ll \Delta G^\ddagger_{uncat}$$



And the reaction catalyzed by *Carbonic anhydrase*:



is  $10^7$  times faster than by itself in water.

Notice that  $K_{eq}$  is **not** affected by a catalyst. If the enzyme increases the forward rate, then the backward rate will also be increased because  $\Delta G^\ddagger_{P \rightarrow S} = G^\ddagger - G_P$  is lowered.

$K_{eq}$  depends on the difference in  $G$  between product and substrate:  $\Delta G^o = G^o_P - G^o_S$  as follows:

$$\Delta G^o = -RT \cdot \ln_e(K_{eq}) \quad \text{and is path independent.}$$

$R$  = Gas Constant =  $8.31 \text{ J/mol} \cdot \text{K}$ ;

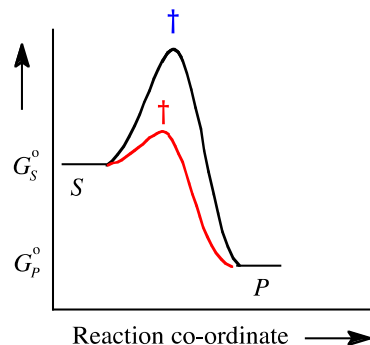
$T$  = Temp in Kelvin

$\ln$  is the natural logarithm to base  $e$ ;

$e$  is 2.71828....

The rate constants depend on  $\Delta G^\ddagger$ .

$$\Delta G^\ddagger = -RT \cdot \ln_e\left(\frac{k \cdot h}{k_B \cdot T}\right)$$



$k_B$  = Boltzmann constant =  $1.38 \times 10^{-23} \text{ J/K}$

$h$  = Planck's constant =  $6.6 \times 10^{-34} \text{ J} \cdot \text{s}$

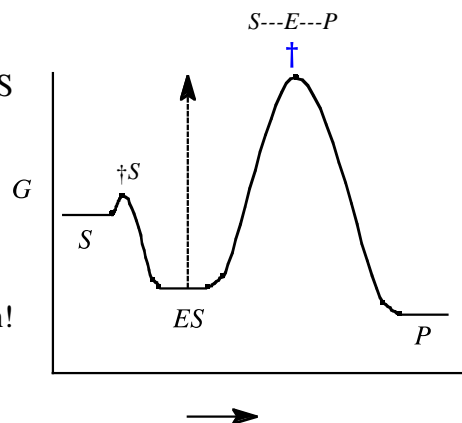
The smaller is  $\Delta G^\ddagger$  the bigger is  $k$ .

$$+6.9 = \ln(0.001) \quad 0 = \ln(1) \quad -6.9 = \ln(1000)$$

### How do enzymes lower $\Delta G^\ddagger$ ?

Strong binding between E and S would lower the  $G$  of ES (ES would be more stable) and increases  $\Delta G^\ddagger$ .

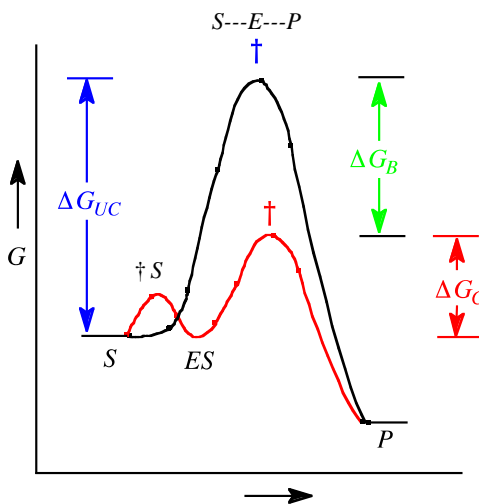
So this would slow the reaction!

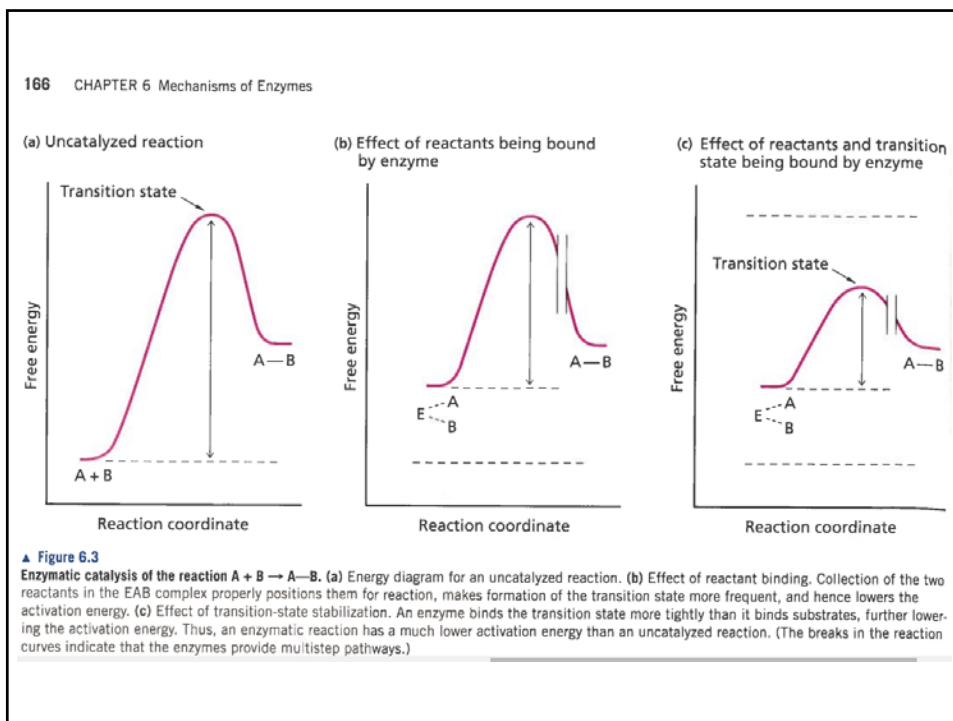


Instead, the E binds the **transition state of the substrate** tightly.

Formation of bonds between E and  $\ddagger$  releases **Binding Energy**,  $\Delta G_B = G^\ddagger_{\text{uncat}} - G^\ddagger_{\text{cat}}$ , which can be used to reduce  $G^\ddagger$ .

$$\Delta G^\ddagger_{\text{cat}} = \Delta G^\ddagger_{\text{uncat}} - \Delta G_B$$



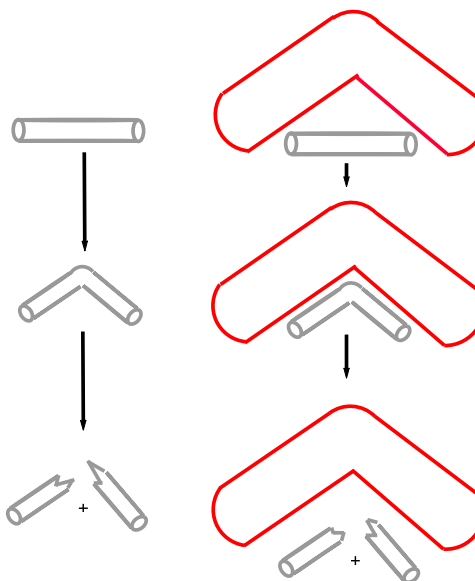


Here is a mechanical analogy: The enzyme is a magnet.

The substrate is an iron rod.

$\ddagger$  = bent rod

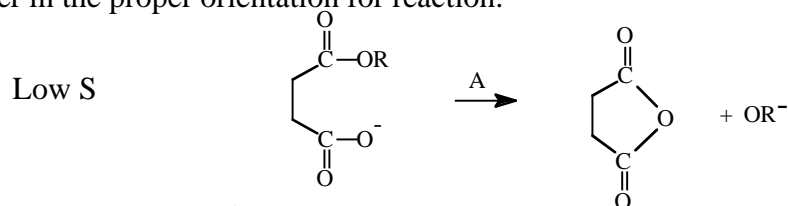
Products are the rod fragments.



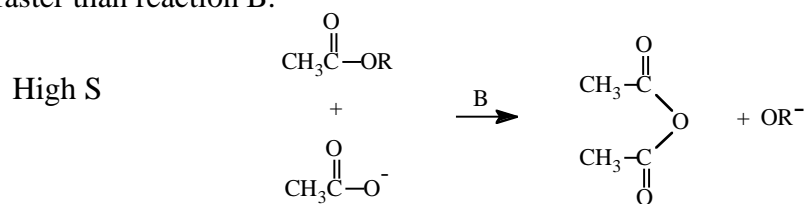


Binding Energy is also used for:

1. **Entropy Reduction:** enzymes hold the substrates close together in the proper orientation for reaction.



For *e.g.* reaction A is  $10^5$  times faster than reaction B.



2. **Desolvation:** Substrate molecules are surrounded by a water hydration shell that usually must be removed for reactions to occur.

3. **Strain Reduction:** Substrate steric and/or electronic strain must be overcome.

4. **Induced Fit:** Change the conformation of the enzyme to obtain the proper orientation of the active site AA.

*e.g.* glucose changes the conformation of *hexokinase*.

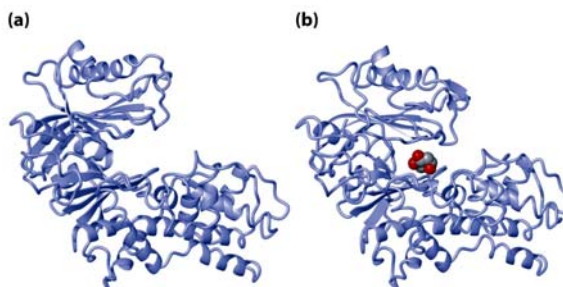


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Enzymes usually also **participate** in the chemical transformation by their AA side-chains. Here is a classic example:

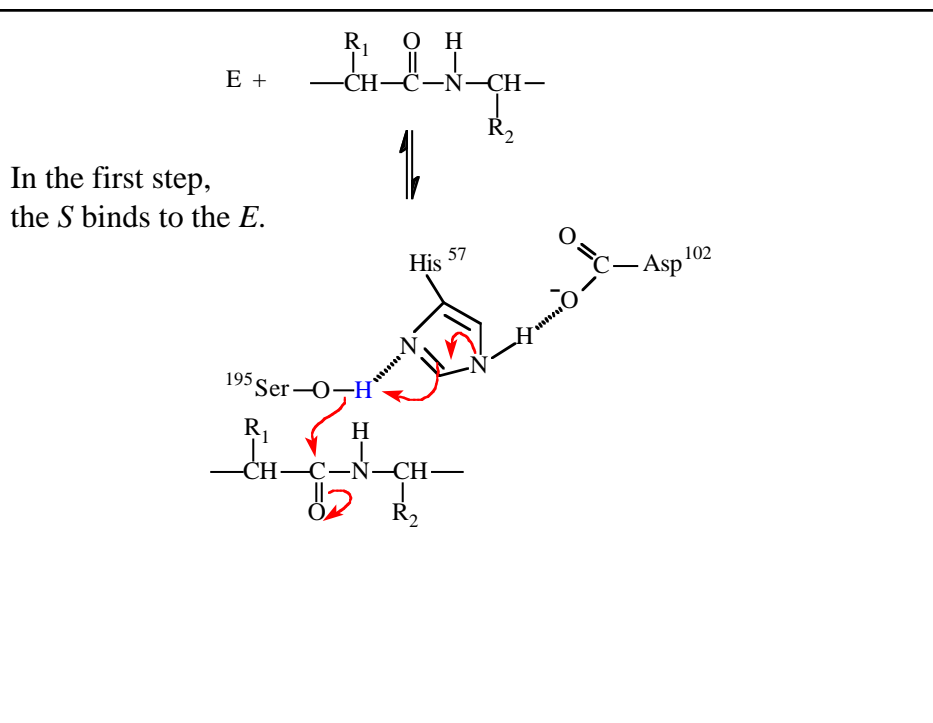
### Chymotrypsin: General Acid-Base Catalysis

**Acids:** donate  $H^+$  & accept electron pairs (Lewis).

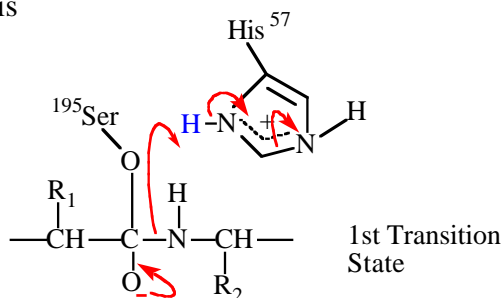
**Bases:** accept  $H^+$  & donate electron pairs (Lewis).

Recall that *chymotrypsin* is a proteolytic enzyme that severs peptide bonds at Trp, Tyr, Phe.

The side chains of His, Asp, Ser in the chymotrypsin active site form a **Catalytic Triad**.



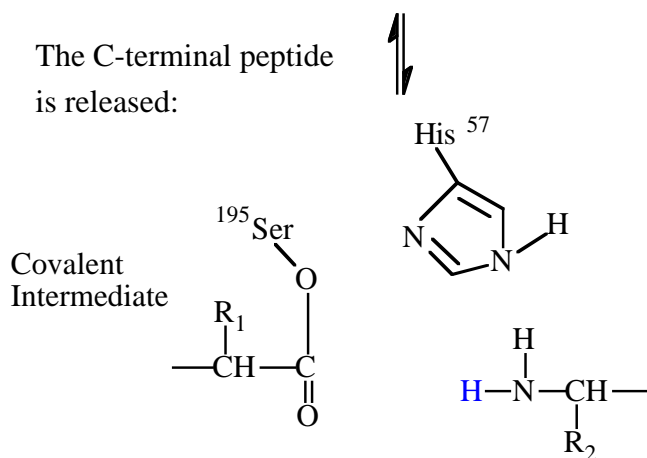
The 2<sup>nd</sup> step involves electron flow (arrows above) from the **General Base** Catalytic Triad into S. This creates the 1<sup>st</sup> transition state below:



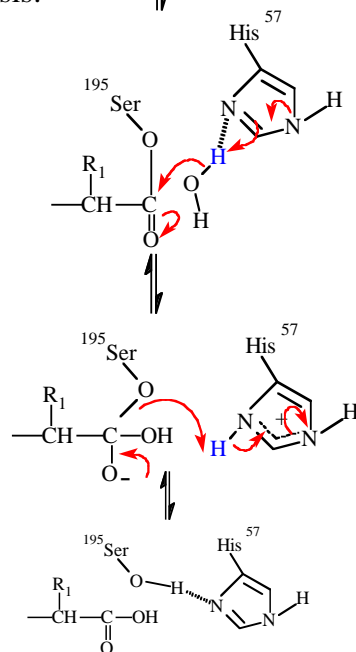
The **oxyanion** ( $O^-$ ) is stabilized by H-bonding to groups in the protein (not shown). Notice that a covalent bond has formed between the E and S.

In the next step, electrons flow from the substrate to the **General Acid** Catalytic Triad (arrows above).

The C-terminal peptide is released:



The N-terminus is released by hydrolysis:



The mechanism is the same as in the first half of the reaction – general base catalysis followed by general acid catalysis.

Go here to view an animation:

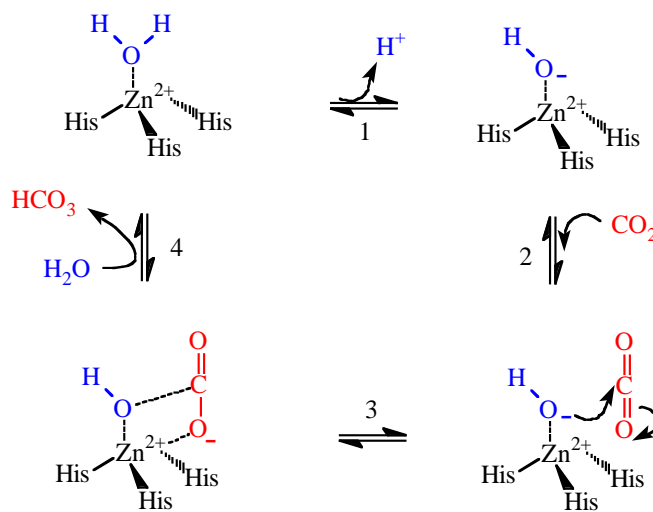
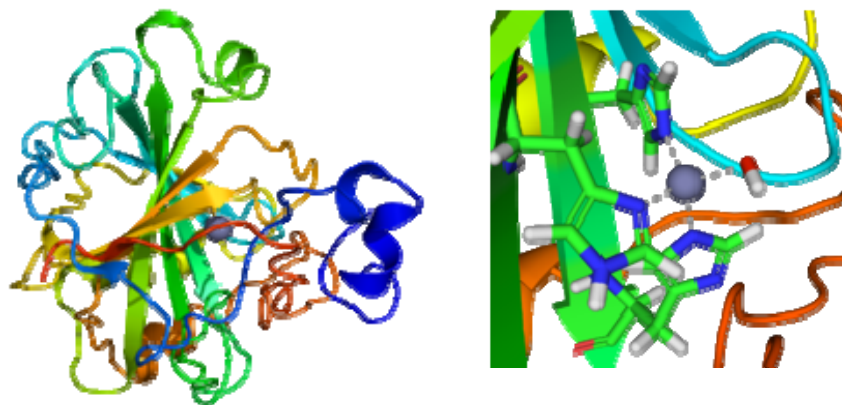
<http://www.angelo.edu/faculty/nflynn/Biochemistry/CT%20Catalytic%20Mechanism.htm>

About 1/3 of all enzymes use metal cofactors.

1. Weak interactions between metals and the substrate help stabilize the charged  $\ddagger$  and may help orient and bind the substrate.

*e.g.* zinc in carbonic anhydrase

PDB 1CA2



2. Metals accept & donate electrons in Redox reactions:

