2.2 Reversible Inhibitors

- Characterized by a <u>rapid dissociation</u> of the enzyme-inhibitor complex
- Usually these inhibitors bind through non-covalent interactions
 & inhibitor maintains a reversible equilibrium with the enzyme
- Reversible inhibitors can be divided into two classes: competitive & noncompetitive
- ➤ The double-reciprocal plots are highly useful for distinguishing among these inhibitors

2.2.A. Competitive inhibition

Substrate -**Enzyme** The inhibitor competes with substrate Competitive

> A competitive inhibitor

inhibitor

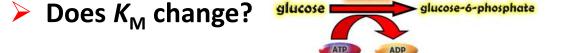
Competitive inhibitor **Enzyme** Relative rate Competitive inhibition

Substrate cannot enter 100 r No inhibitor 80 $[1] = K_i$ 60 $[1] = 5 K_i$

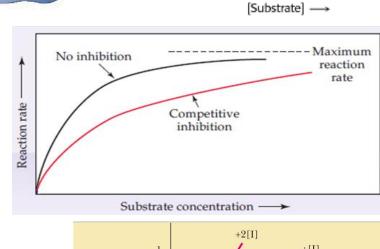
 $[I] = 10 K_i$

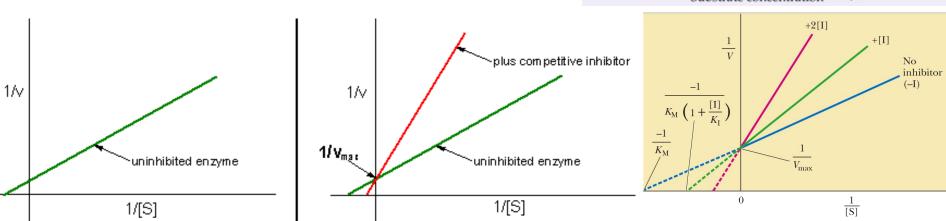
Increasing [S] can overcome the

inhibition (V_{max})



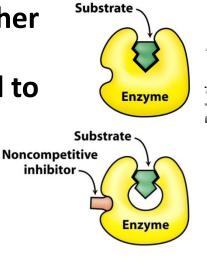
Significance (ex. Hexokinase)

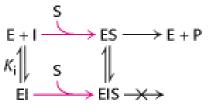


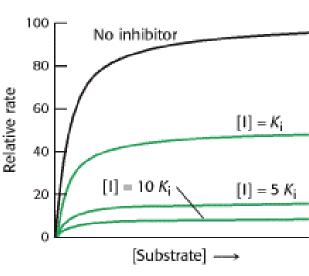


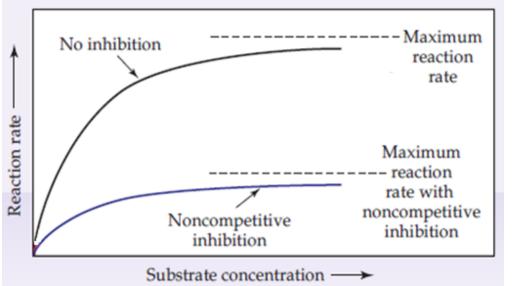
2.2.B. Noncompetitive inhibition

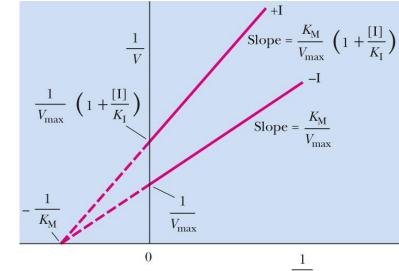
- The inhibitor binds at a site other than the active site
- ➤ The complex does not proceed to form product or has a lower efficiency
- $\triangleright V_{\text{max}} \text{ vs. } K_{\text{M}}$
- \triangleright Can we reach V_{max} ?











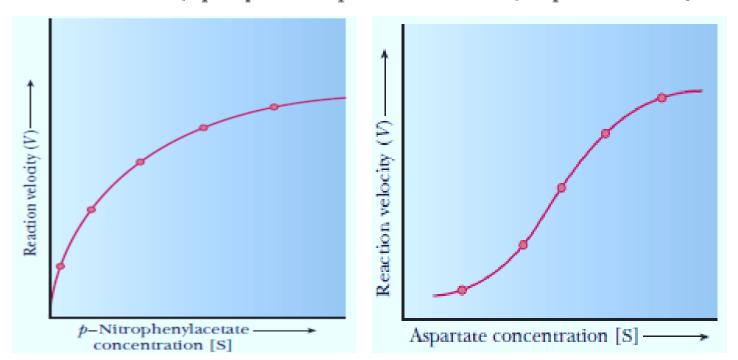
3. REGULATION THROUGH CONFORMATIONAL CHANGES

- These regulatory mechanisms include
 - A. Allosteric activation and inhibition;
 - B. Phosphorylation or other covalent modification;
 - C. Protein-protein interactions between regulatory & catalytic subunits or between two proteins;
 - D. Proteolytic cleavage
- These types of regulation can rapidly change an enzyme from an inactive form to a fully active conformation

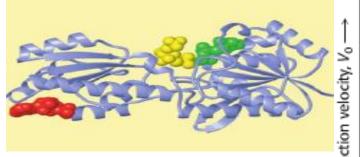
3.A. Not all enzymes follow Michaelis-Menten equation; Chymotrypsin vs. ATCase

- Chymotrypsin: Specificity for aromatic residues mainly. Also, hydrolysis of ester bonds
- ➤ Aspartate transcarbamoylase (ATCase): synthesis of CTP & UTP for RNA and DNA synthesis

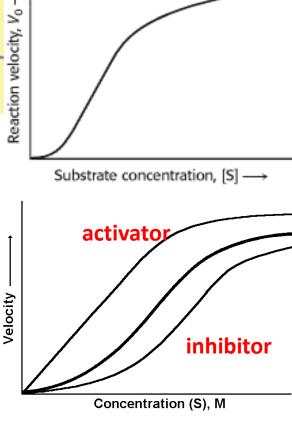
Carbamoyl phosphate + Aspartate → Carbamoyl aspartate + HPO₄²



Allosteric regulation



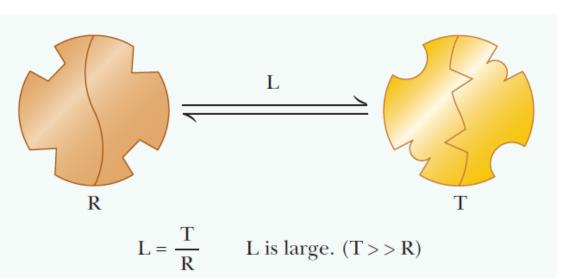
- What are allosteric enzymes? A multi-subunit enzyme with <u>catalytic subunit(s)</u> and regulatory subunit(s)
- Binding triggers a <u>conformational change</u> in the active site
- ➤ The <u>Michaelis-Menten model can't explain</u> the kinetic properties
- The effect of the modulators (<u>allosteric</u> modifiers)
- Homotropic vs. heterotropic
- The substrate concentration at half of the V_{max} is called ($\underline{K}_{0.5}$)
- Allosteric inhibitors have a much stronger effect on enzyme velocity

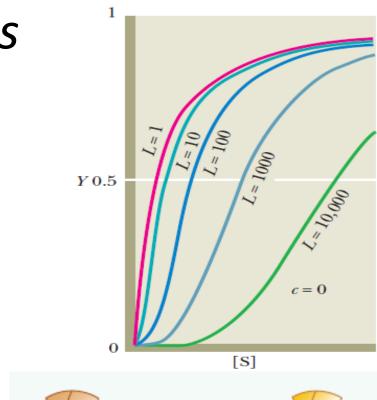


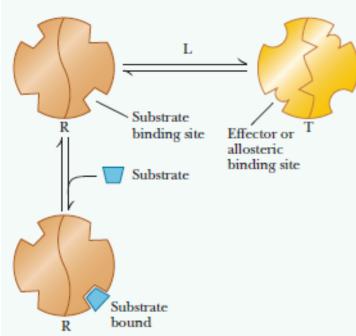
The effect of modifiers on $V_{max} \& K_{0.5}$

How do allosteric enzymes work?

- ➤ Two conformations: more active (R) & less active or inactive (T),
- ➤ The equilibrium ratio (T/R) is called L and assumed to be high
- ➤ As L (T/R) increases, the shape becomes more sigmoidal

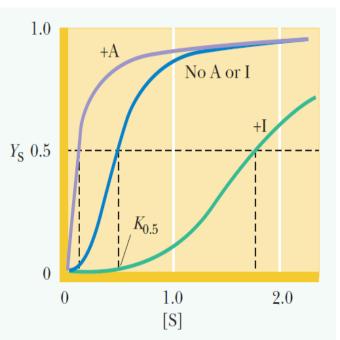


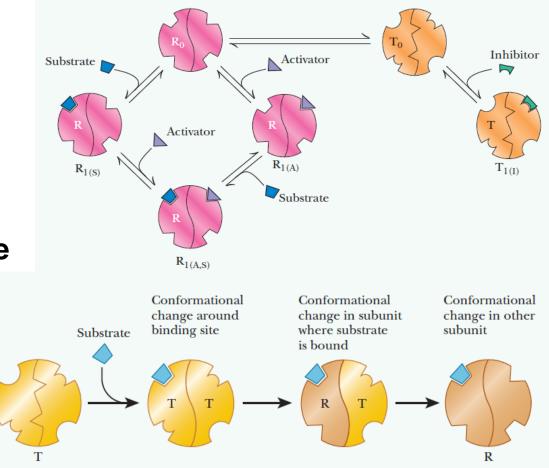


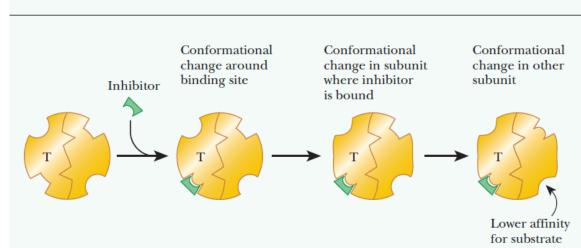


Concerted or sequential?

- Either substrate or activator must be increased to overcome the effects of the allosteric inhibitor
- Conformational change







Allosteric regulation – ATCase "synthesis of pyrimidine nucleotides"

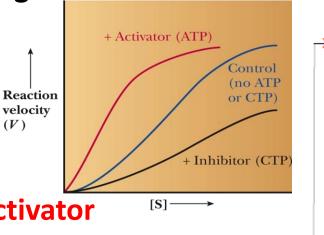
> ATCase and Hb are allosteric proteins (cooperative behavior)

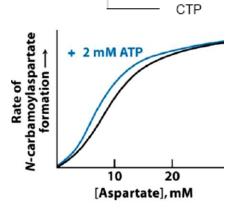
Catalytic can be separated from regulatory

(hyperbolic)

Cooperativity in relation to substrate

CTP is an inhibitor of ATCase (feedback inhibition), ATP is an activator





Regulatory dimer

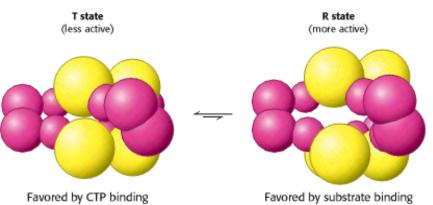
Catalytic trimer

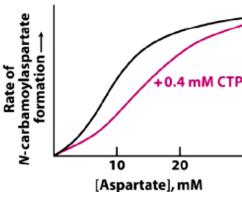
Aspartate

Carbamoyl phosphate

N-carbamoylaspartate

UTP





(V)