



Enzymes III

Regulation

Prof. Mamoun Ahram



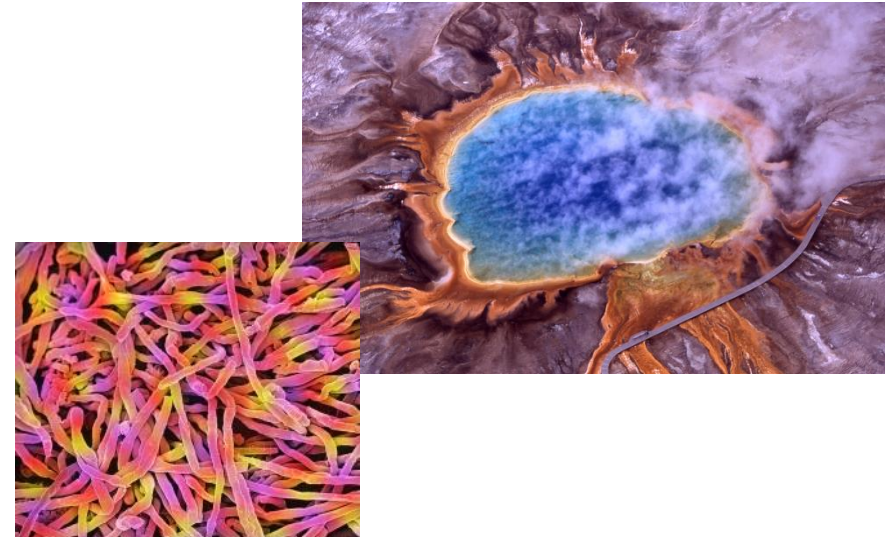
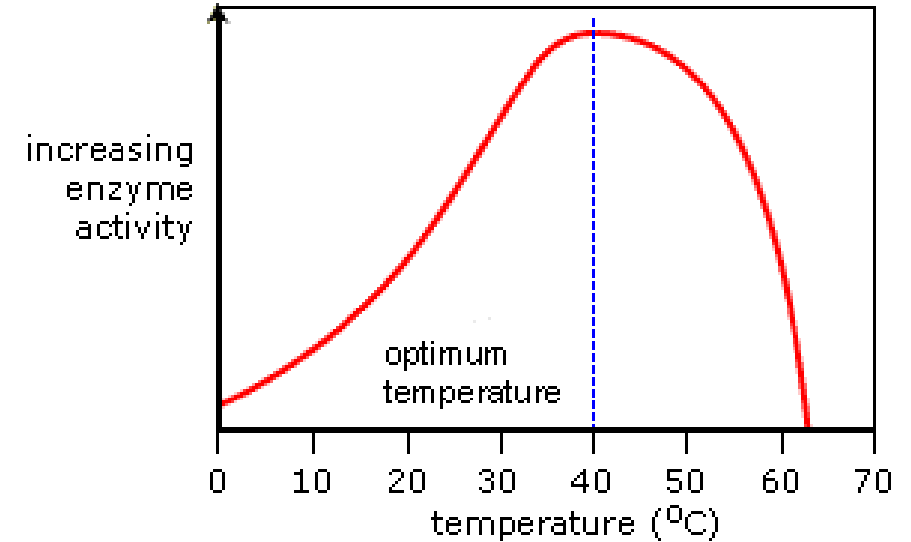
Mechanisms of regulation

- Non-specific and collective regulation (temperature, pH, diffusion, and expression)
 - Localization (compartmentalization) and enzyme complexing
 - Expression of isoenzymes
- Regulation of enzymatic activity
 - Inhibitors
 - Conformational changes
 - Modulators
 - Reversible covalent modification
 - Irreversible covalent modification
 - Allostery



Temperature

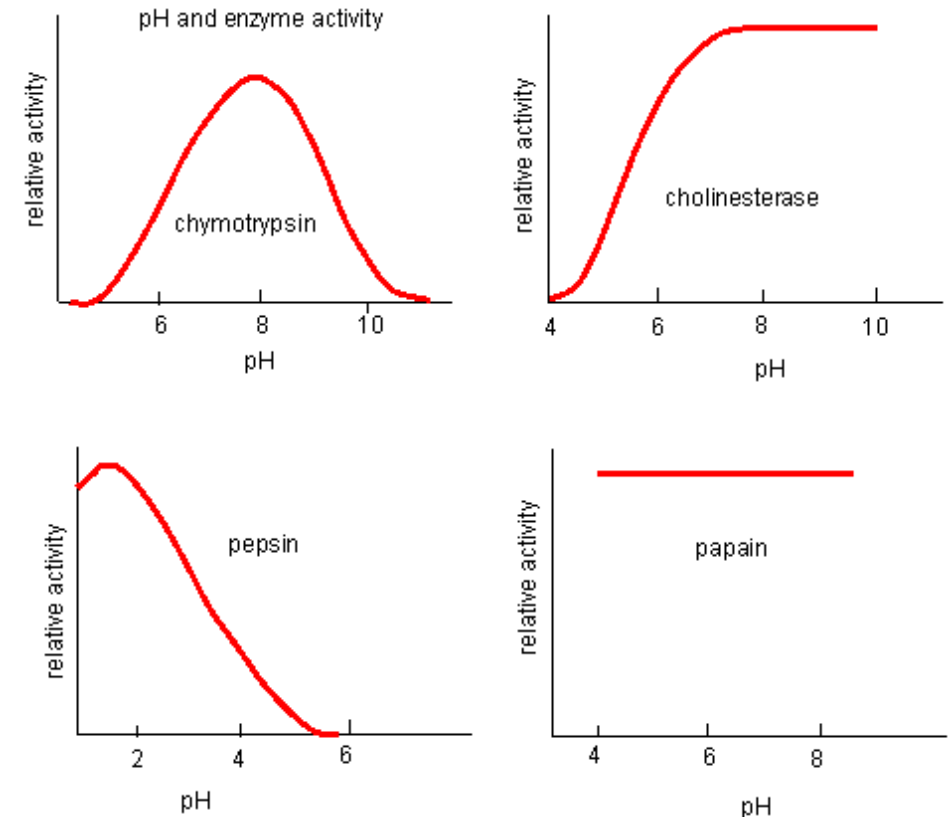
- Reaction rates increase with temperature due to increased kinetic energy of the molecules resulting in more collisions between enzymes and substrates.
 - However, high temperatures lead to protein denaturation.
- Each organism has an optimal temperature for its enzymes.
 - For thermophilic bacteria, the optimal temperature is as high as 65°C.





pH

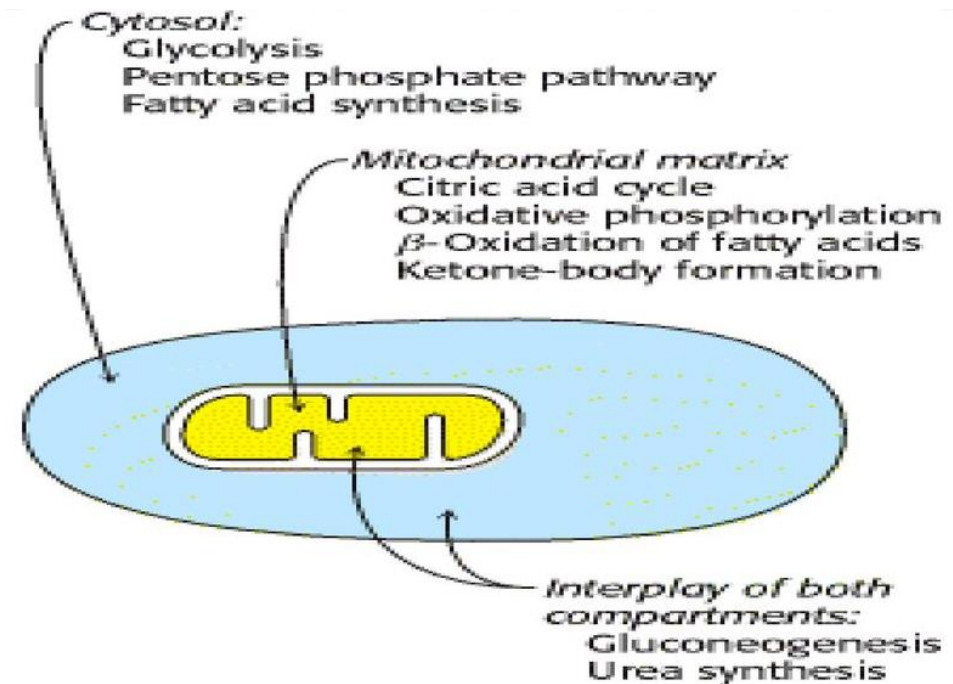
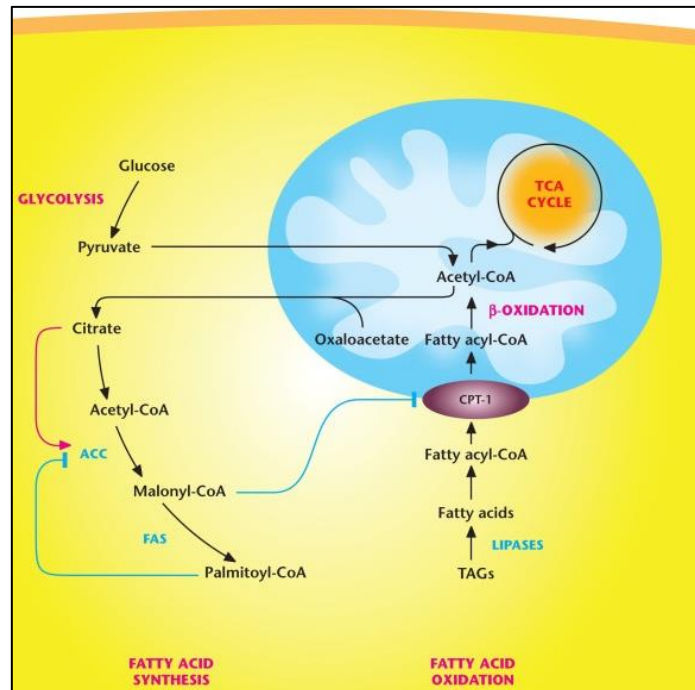
- pH alters the protonation state of the substrate and/or the enzyme and, hence, their binding.
- The effect of pH is enzyme-dependent.





Compartmentalization

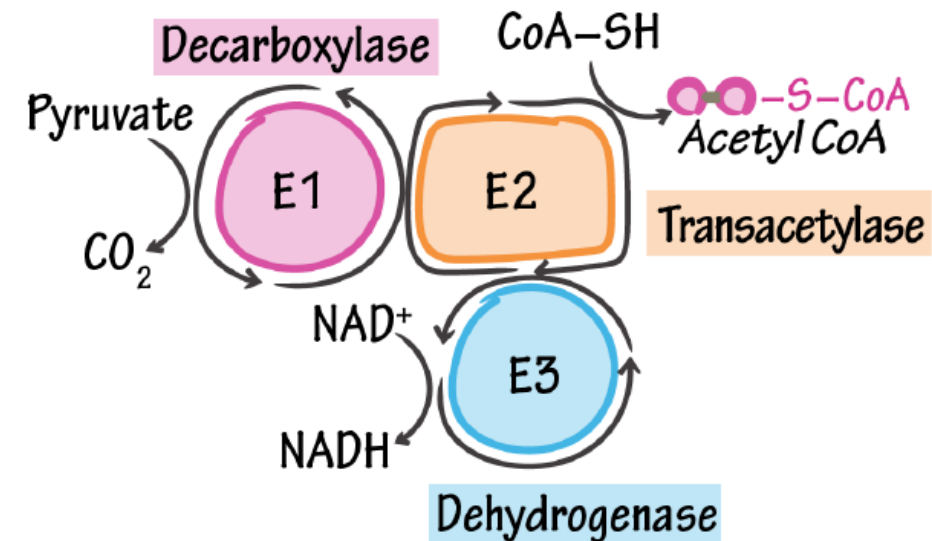
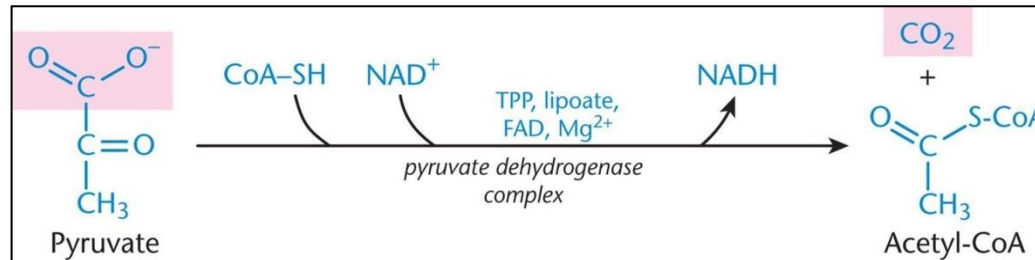
- Compartmentalization reduces the area of diffusion of both enzyme and substrate increasing the probability that they collide.
 - Example 1: lysosomal enzymes
 - Example 2: fatty acid metabolism
 - Synthesis occurs in cytosol, whereas break-down is mitochondrial.



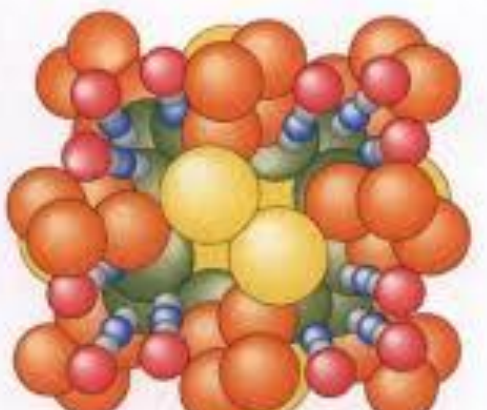


Enzyme complexing

- Formation of a complex of multiple enzymes also reduces diffusion.
- Example: Pyruvate dehydrogenase complex (mitochondria) is composed of 3 enzymes: decarboxylation, oxidation, & transfer of the acyl group to CoA.



(a)

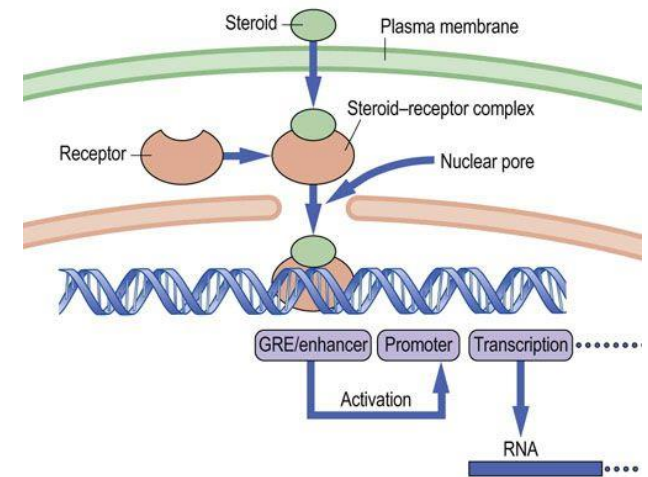


(b)



Regulation of enzyme amount

- Three mechanisms:
 - Enzyme synthesis at the gene level
 - Enzyme degradation by proteases
 - Synthesis of isozymes
- They are comparatively slow mechanisms for regulating enzyme concentration (hours-weeks).

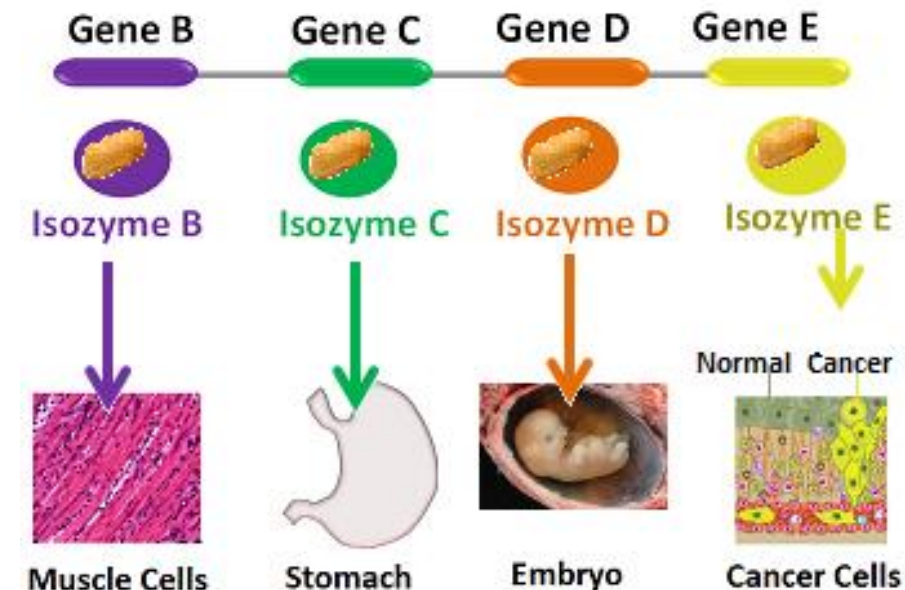
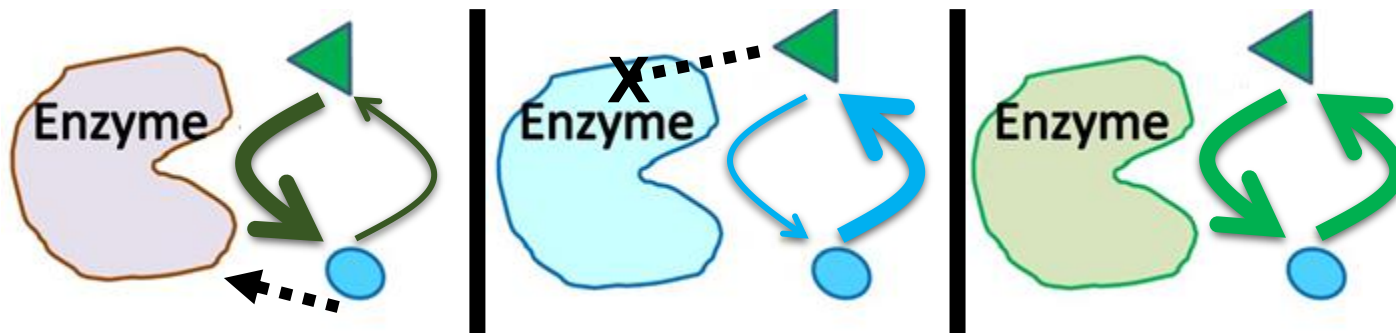


Enzyme	Half-life (days)
Catalase	1.4 days
Glucokinase	1.2 days
Lactate dehydrogenase	
LDH1 (heart)	1.6
LDH5 (liver)	16
LDH5 (muscle)	31



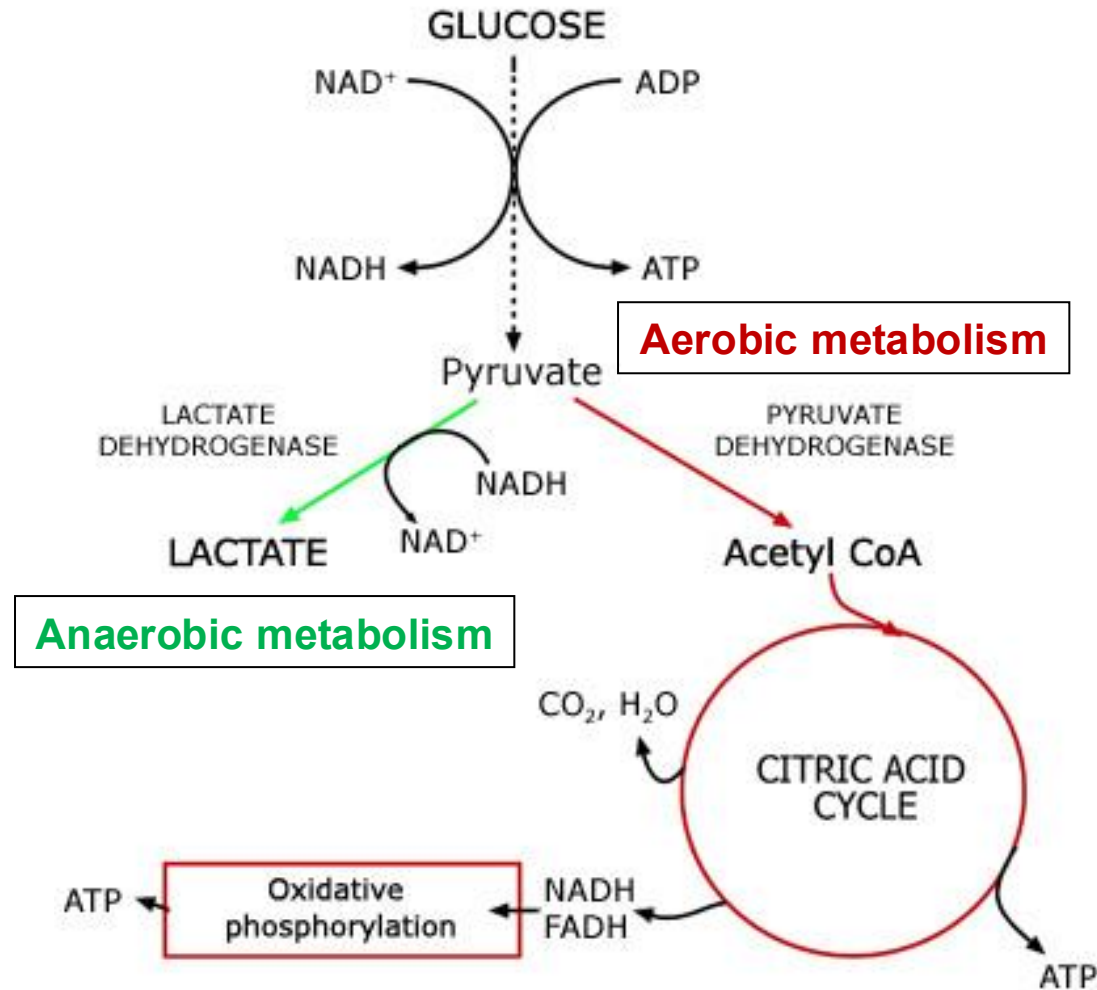
Isoenzymes (isozymes)

- Isoenzymes are enzymes that can act on the same substrate(s) and produce the same product(s).
- They are generated by different genes that are highly homologous (similar).
- Often, various isozymes are present in different tissues.
- They can be regulated differently .
- They can have different catalytic activities.





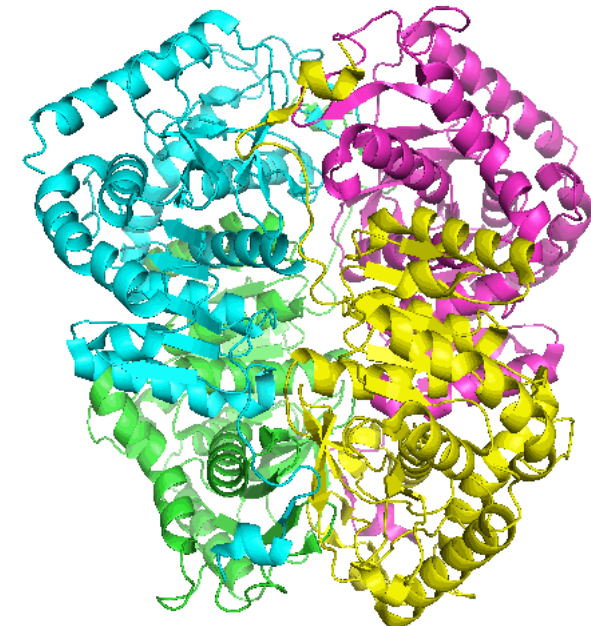
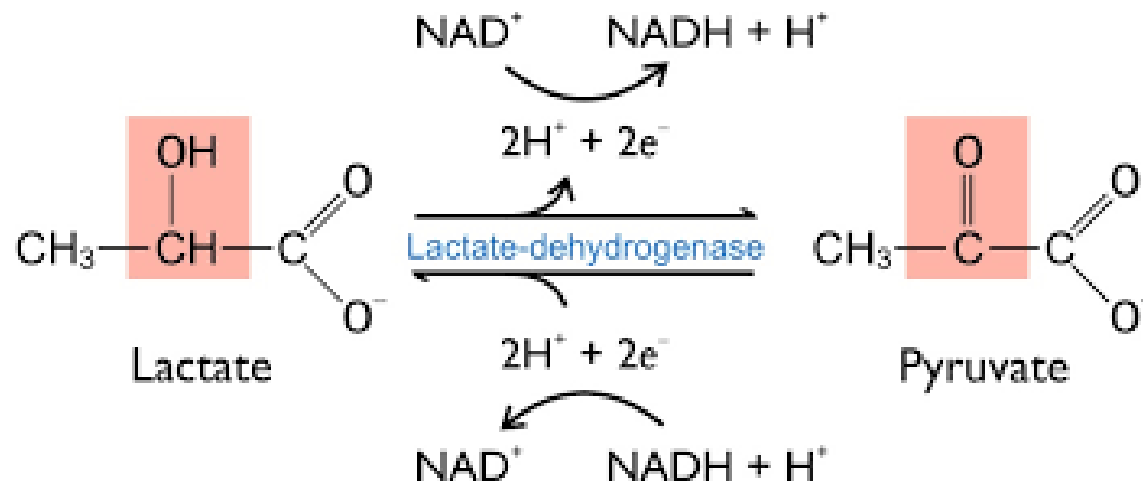
Aerobic vs. anaerobic metabolism

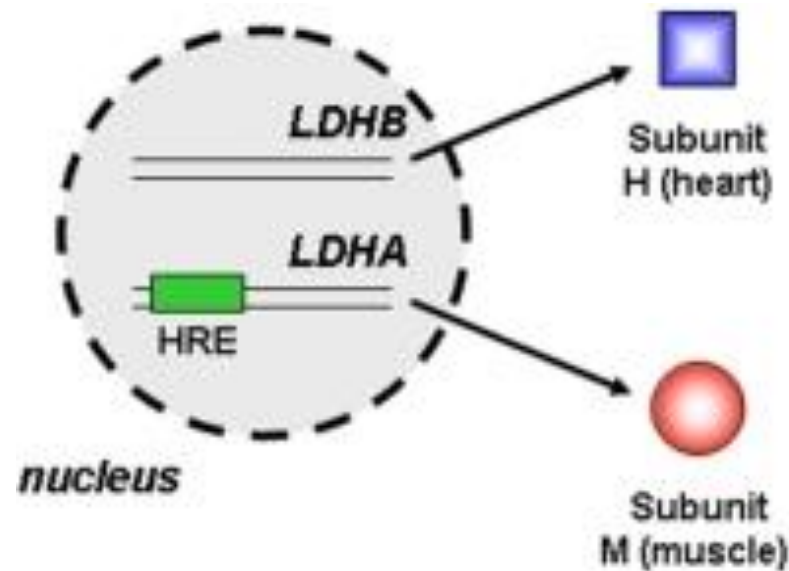




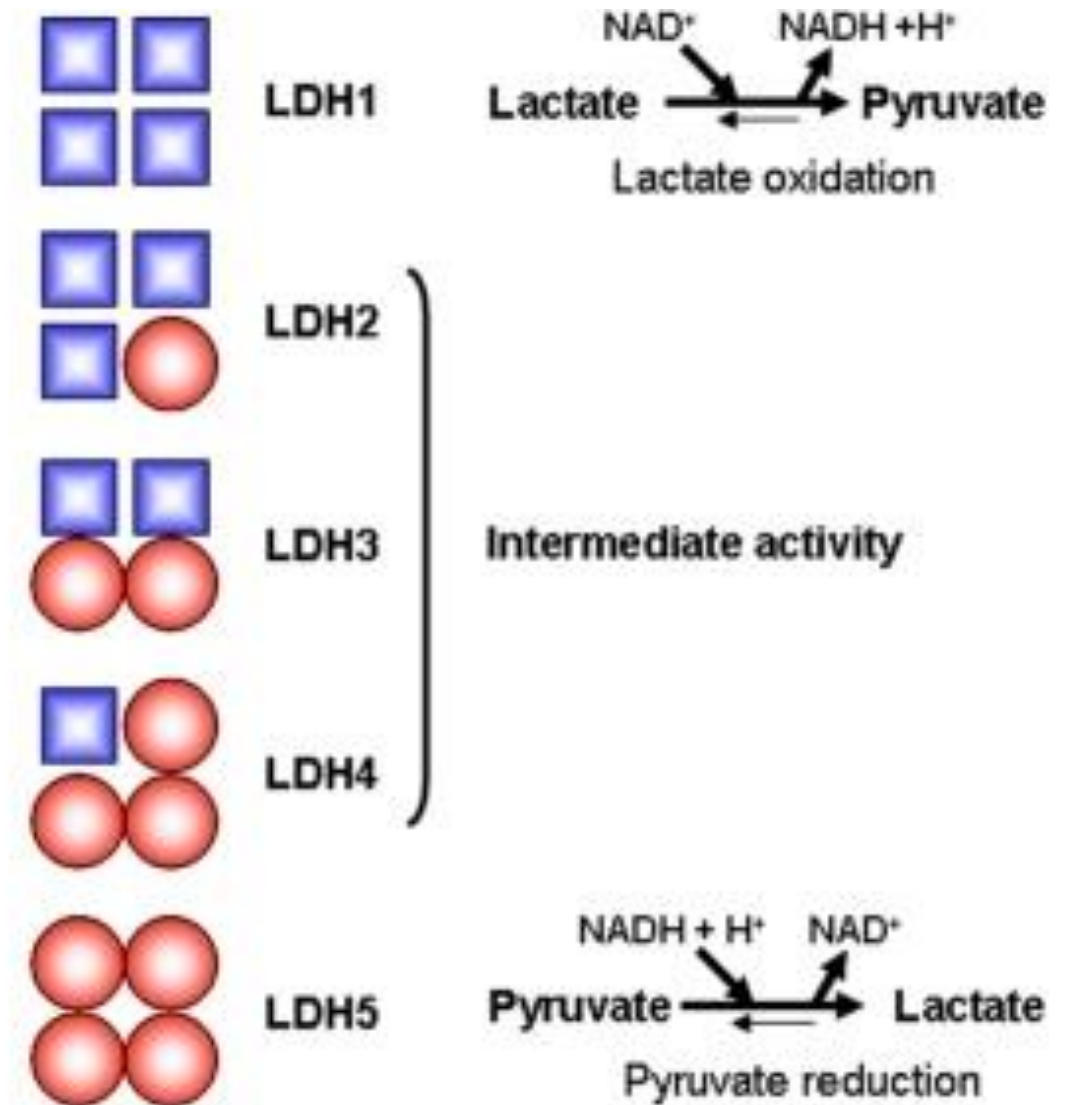
Lactate dehydrogenases (LDH)

- LDH is a **tetrameric** enzyme composed of a combination of one or two protein subunits: the H (heart) subunit and M (skeletal muscle) subunit.
- These subunits combine in various ways leading to 5 distinct isozymes (LDH1, LDH2, LDH3, LDH4, LDH5) with different combinations of the M and H subunits (H4, H3M, H2M2, HM3, and M4).
- The H4 isozyme or LDH1 is characteristic of that from heart tissue, and the M4 isozyme of LDH5 is typically found in skeletal muscle and liver.



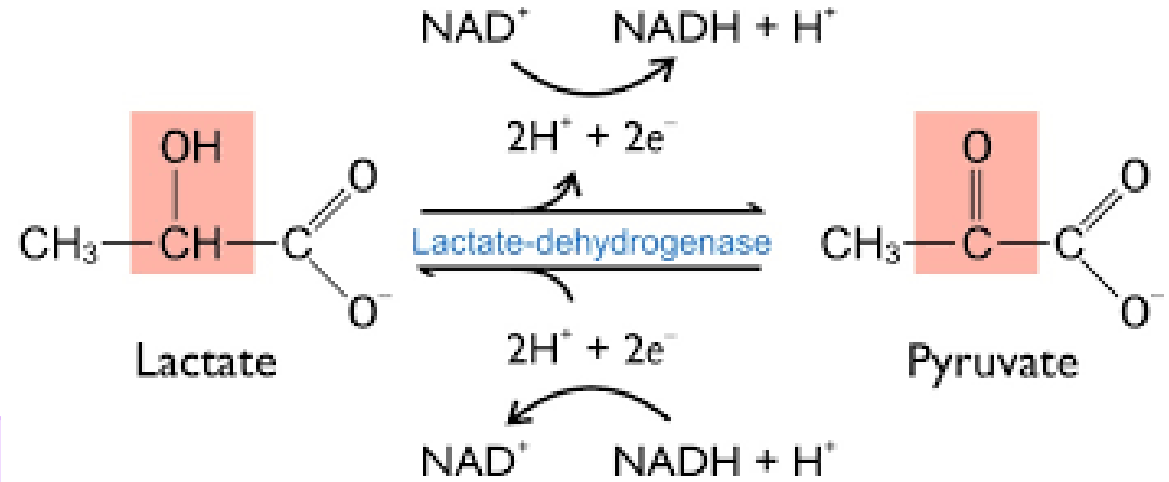


- Although the five isoforms catalyze the same reaction, they differ in their primary structure, kinetic properties, tissue distribution, affinity to the substrate (direction of the reaction), regulation, and isoelectric point.
- The M subunit has a higher affinity towards pyruvate, thus converting pyruvate to lactate (and NADH to NAD⁺).
- The H subunit has a higher affinity towards lactate, resulting in a preferential conversion of lactate to pyruvate (and NAD⁺ to NADH).





Logic behind tissue distribution



Isoenzyme	Structure	Present in
LDH1	(H₄)	Myocardium
LDH2	(H ₃ M ₁)	RBC
LDH3	(H ₂ M ₂)	Lungs
LDH4	(H ₁ M ₃)	Kidney
LDH5	(M₄)	Skeletal muscle, Liver

Muscles can function anaerobically, but heart tissues cannot.

Whereas the M4 isozyme catalyzes the reduction of pyruvate into lactate, the H4 enzyme catalyzes the reverse reaction.

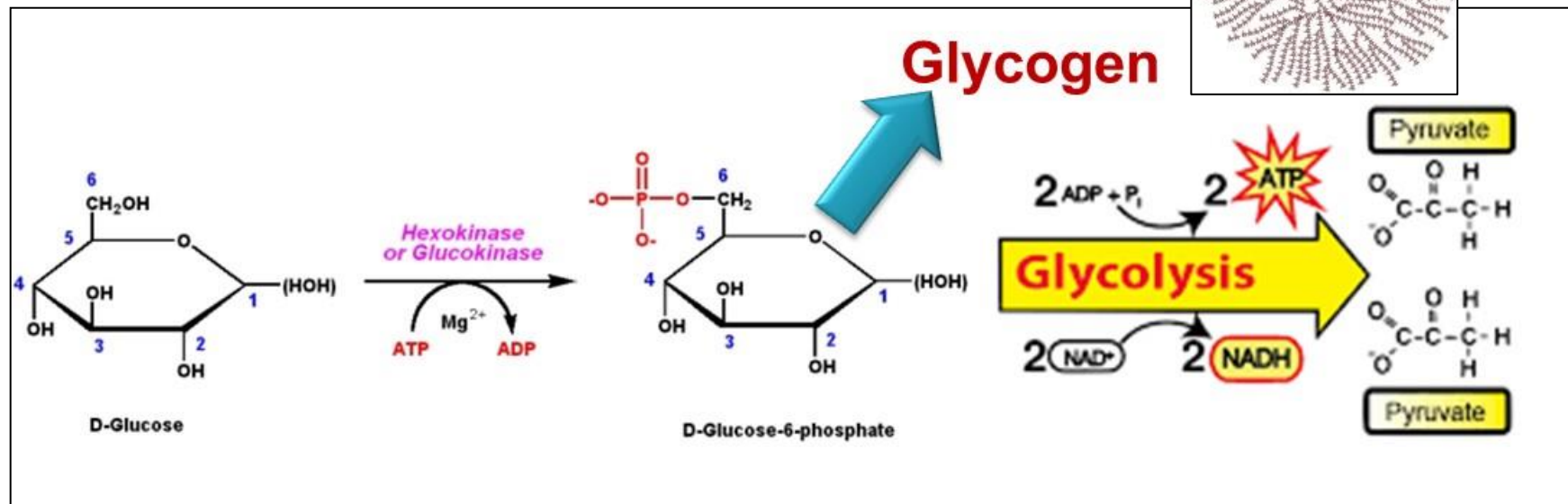
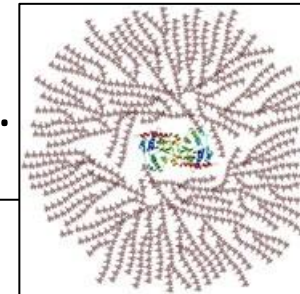


Hexokinase vs glucokinase

- Hexokinase and glucokinase (hexokinase IV) are allosteric isozymes that catalyze:



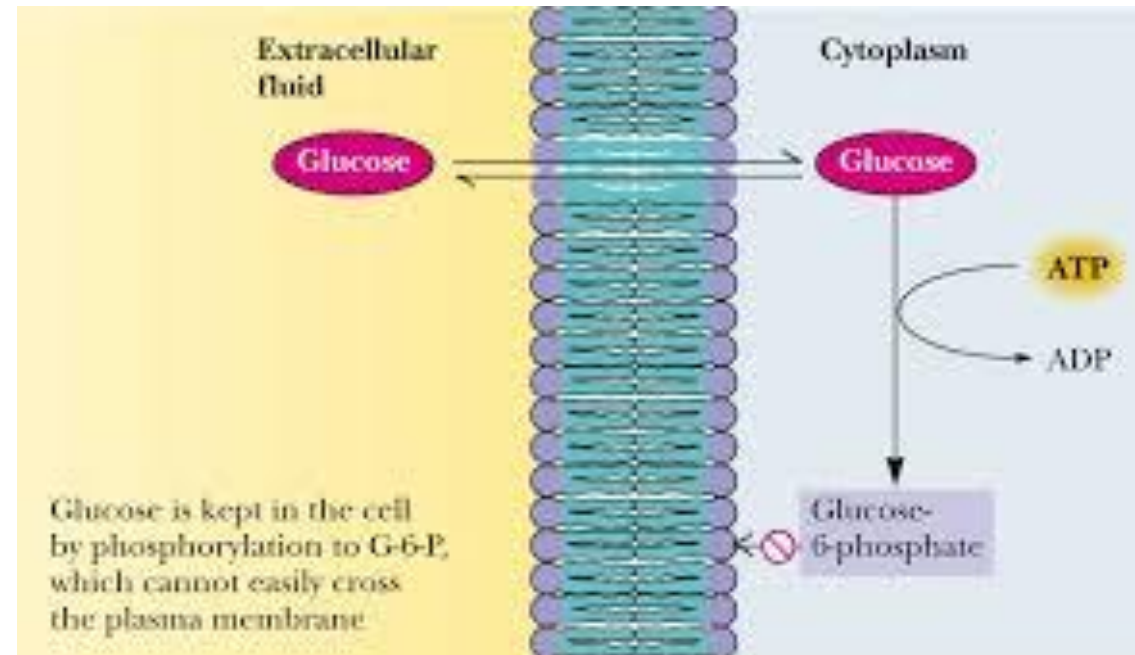
- Glucokinase is a liver (and pancreatic) enzyme, whereas hexokinase is a skeletal muscle enzyme.
 - The purpose of liver glucose is to store glucose as glycogen (or balance glucose level in the blood).
 - The purpose of skeletal muscle glucose is to produce energy.





Biological significance

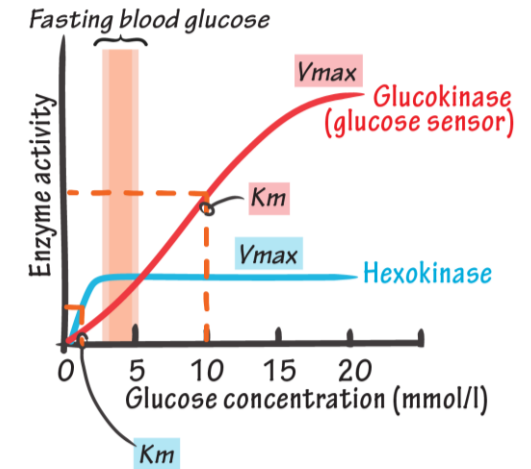
- Note: once glucose is phosphorylated, it cannot cross plasma membrane out of cells.
 - Liver: low efficiency enzyme to not store glucose and keep it to other organs.
 - Skeletal muscles: high efficiency enzyme to trap glucose immediately.





Regulation of hexokinase and glucokinase

- Note V_{max} and K_M values
- Regulation
 - Hexokinase is inhibited by glucose-6-phosphate, but glucokinase is not.
- Significance:
 - At fasting state, glucose is not stored.
 - At well-fed state, skeletal muscles do not consume all glucose in blood and liver can convert excess glucose to glycogen for storage.



K_m

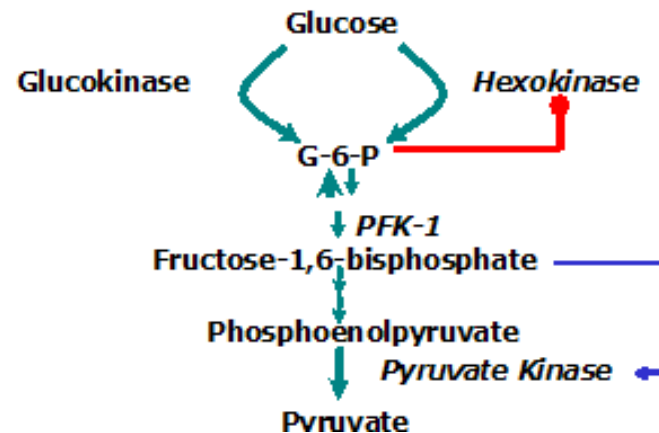
Glucokinase > Hexokinase

Spares glucose stores for brain, muscle & other tissues.

V_{max}

Glucokinase > Hexokinase

At fasting glc conc. – Hexokinase is at V_{max} , Glucokinase activity varies according to glc conc.



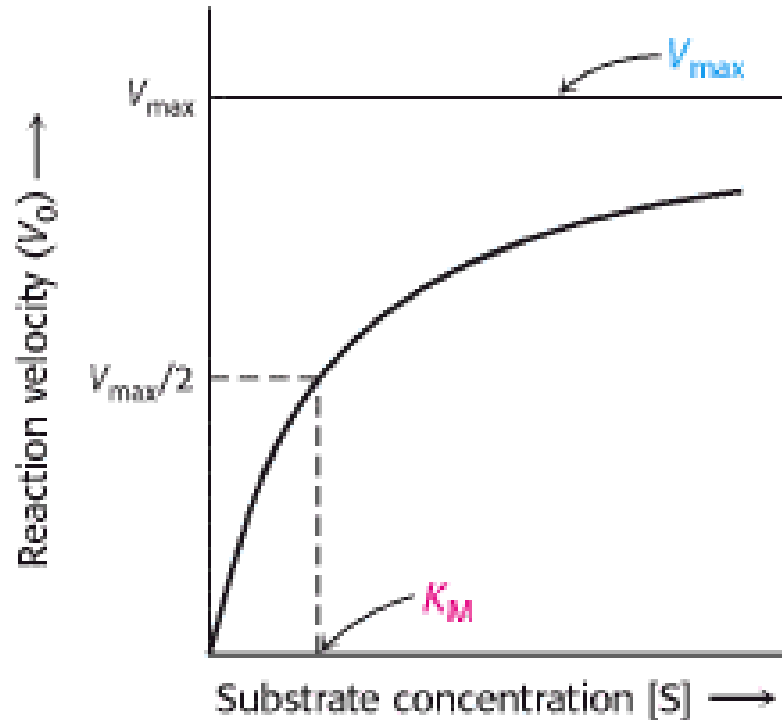
Regulation of enzymatic activity

But before, let's talk about this

A disadvantage of the Michaelis-Menten equation



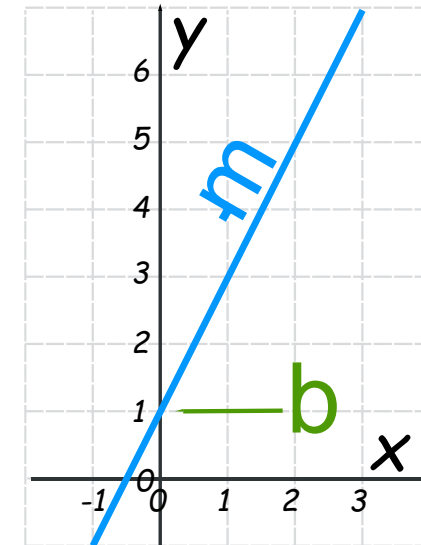
- Determination of K_M from hyperbolic plots is not accurate since a large amount of substrate is required in order to reach V_{max} .
- This prevents the calculation of both V_{max} and K_M .



Solution

$$y = mx + b$$

m is the slope
 b is the y-intercept



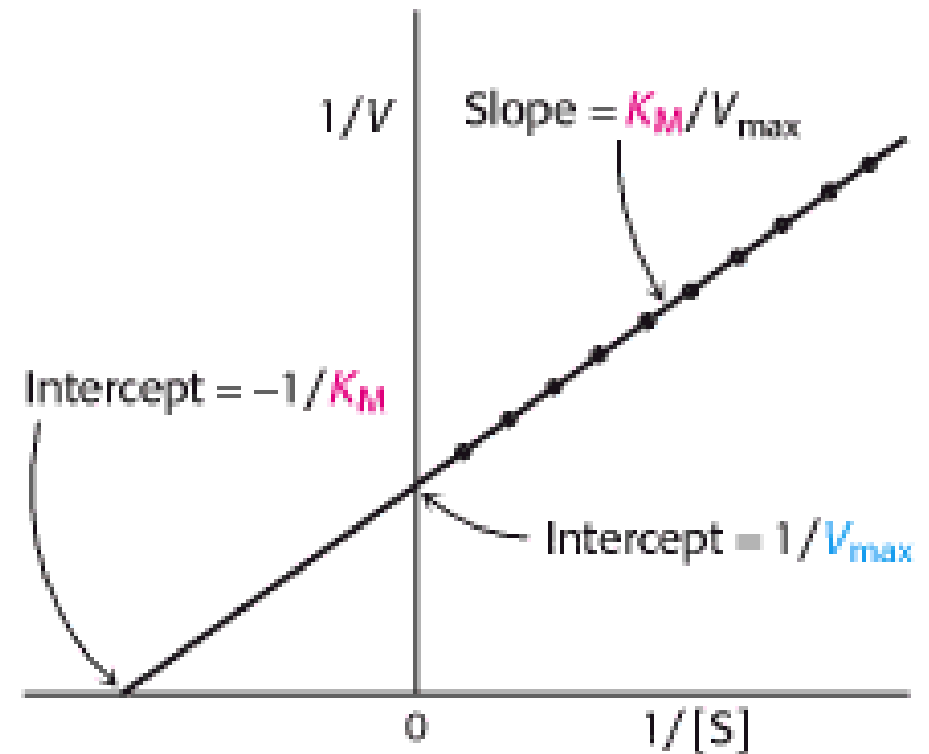


The Lineweaver-Burk or double-reciprocal plot

- A plot of $1/V_0$ versus $1/[S]$, called a Lineweaver-Burk or double-reciprocal plot, yields a straight line with an intercept of $1/V_{\max}$ and a slope of $K_M/V_{\max}$.
- The intercept on the x-axis is $-1/K_M$.

$$V_0 = V_{\max} \frac{[S]}{[S] + K_M}$$

$$\frac{1}{V_0} = \frac{1}{V_{\max}} + \frac{K_M}{V_{\max}} \cdot \frac{1}{[S]}$$

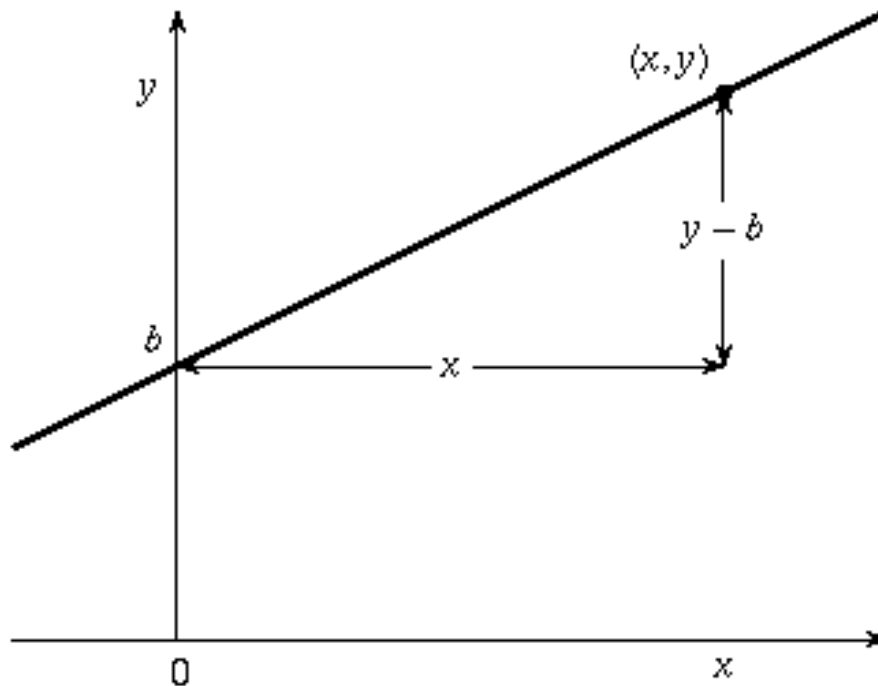




$$\frac{1}{V_o} = \frac{1}{V_{\max}} + \frac{K_M}{V_{\max}} \cdot \frac{1}{[S]}$$

$$y = b + mx$$

- y is y-axis = $1/V_o$
- x is x-axis = $1/[S]$
- m is slope = $K_M/V_{\max}$
- B is $1/V_{\max}$

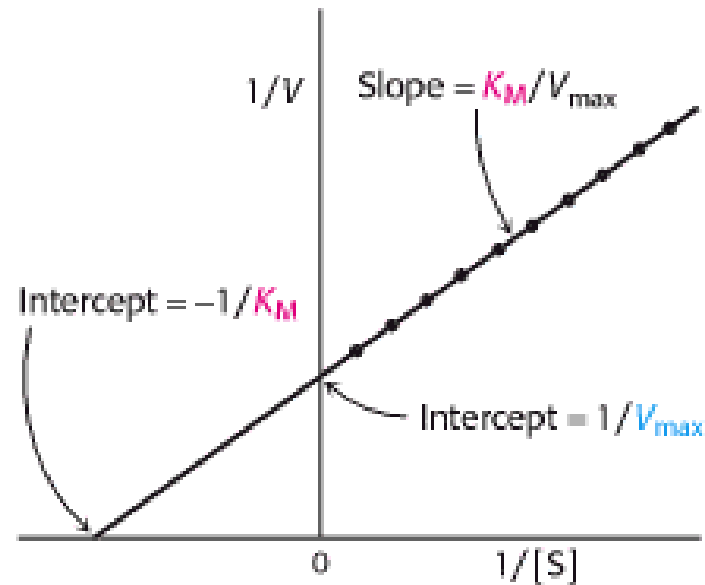




$$\frac{1}{V_0} = \frac{1}{V_{\max}} + \frac{K_M}{V_{\max}} \cdot \frac{1}{[S]}$$

$$y = b + mx$$

- If $x = 0$, then $y = b$ (x-axis is 0, then y-intercept = $1/V_{\max}$)





$$\frac{1}{V_0} = \frac{1}{V_{\max}} + \frac{K_M}{V_{\max}} \cdot \frac{1}{[S]}$$

$$y = b + mx$$

If $y = 0$, then $mx = -b$ (y-axis is 0, then x-intercept = $-1/K_M$)

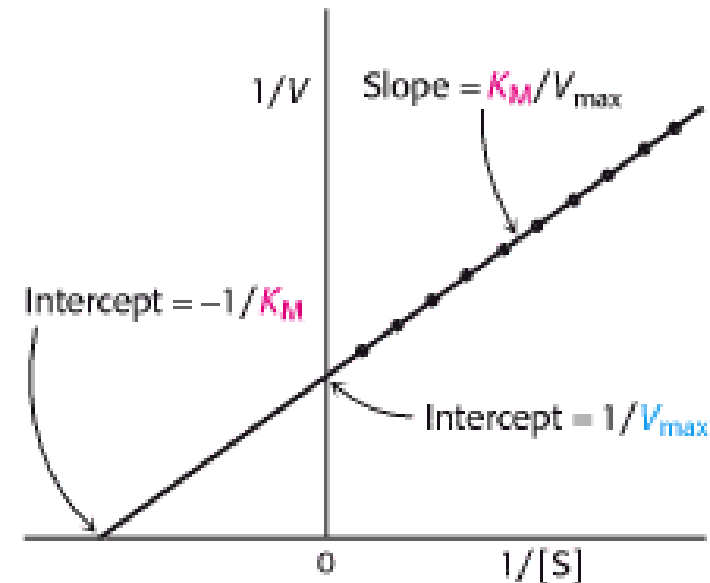
How?

$$0 = 1/V_{\max} + (K_M/V_{\max}) \cdot (1/[S])$$

$$-1/V_{\max} = (K_M/V_{\max}) \cdot (1/[S])$$

$$-1 = K_M \cdot (1/[S])$$

$$-1/K_M = 1/[S]$$



*Now, we can talk about regulation of enzyme activity and we will start with **inhibitors**.*



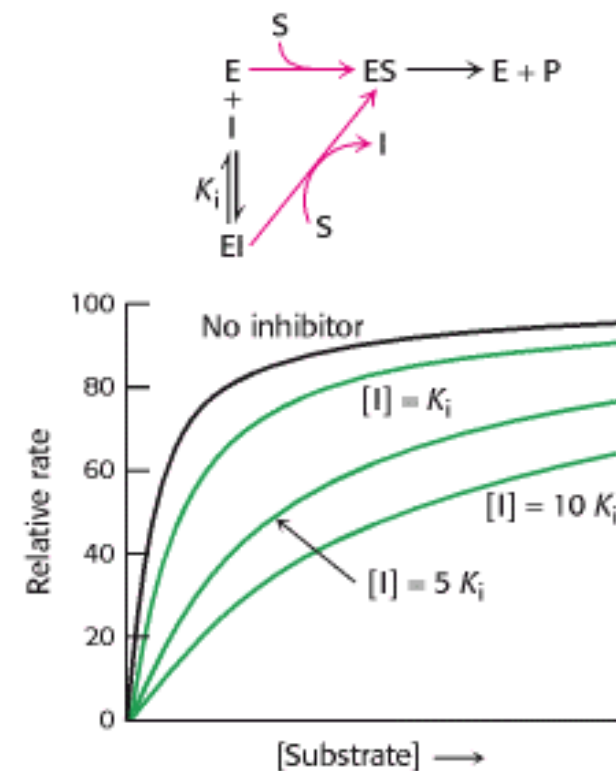
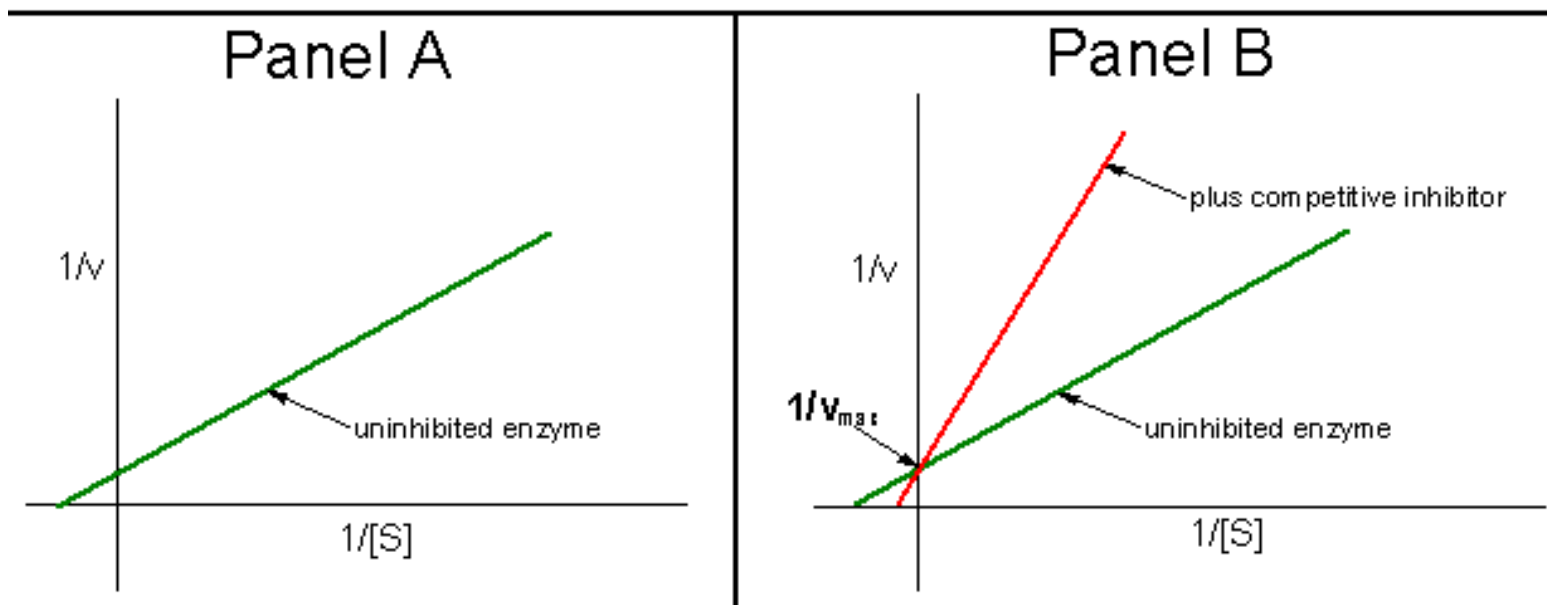
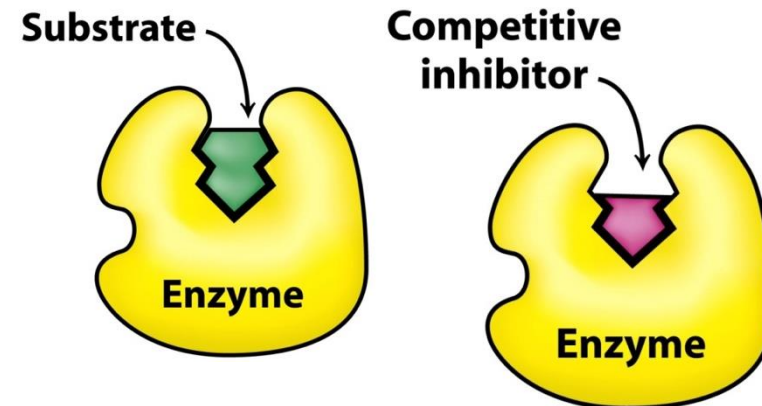
Enzyme inhibitors

- Enzyme inhibition can be either reversible or irreversible.
 - Reversible inhibitors rapidly dissociate from enzymes (e.g. non-covalent binding).
 - Competitive, noncompetitive, or uncompetitive inhibition.
 - An irreversible inhibitor is tightly bound (e.g. covalently) to the enzyme.
 - Lower concentration of active enzyme.



Competitive inhibition

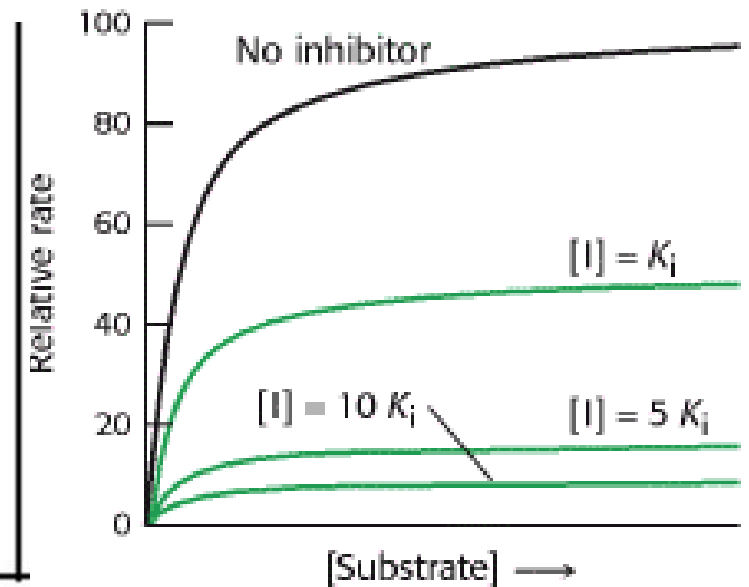
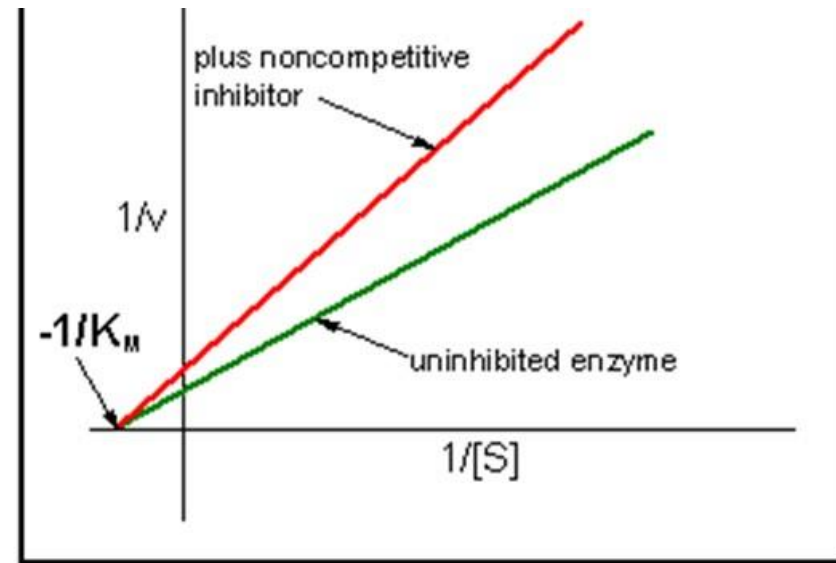
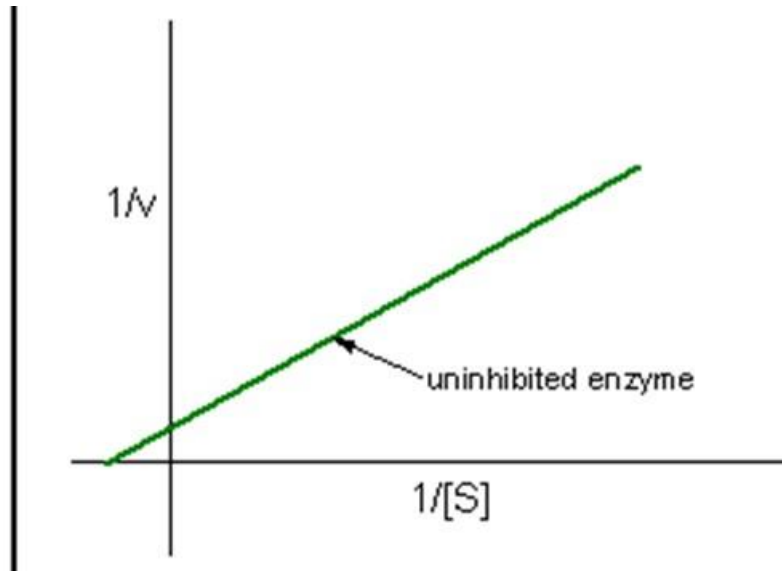
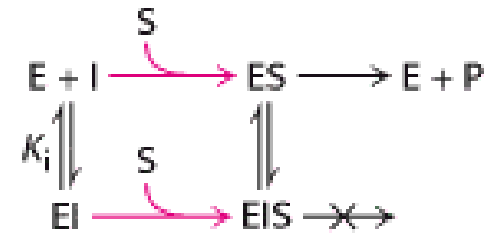
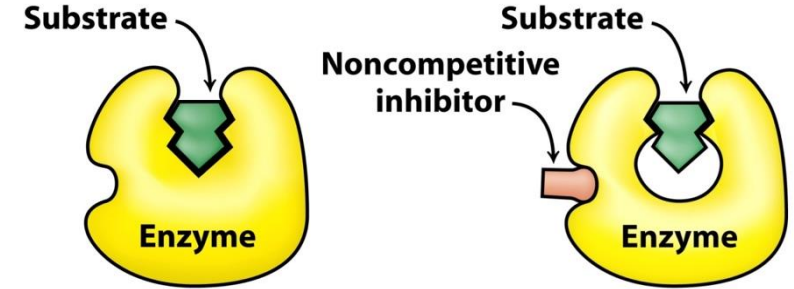
- Competitive inhibitors compete with the substrate for the active site.
 - Increasing substrate can overcome inhibition.
- Same V_{max} , but higher K_M





Noncompetitive inhibition

- Noncompetitive inhibitors bind E or ES complex at a site other than the catalytic site.
- Substrate can bind to the enzyme-inhibitor complex, but ESI cannot form a product.
- Lower V_{max} , but same K_M





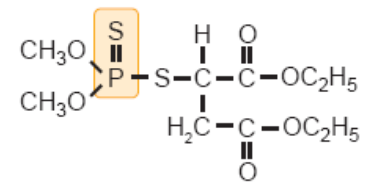
Mechanism-based inhibitors

Irreversible inhibitors

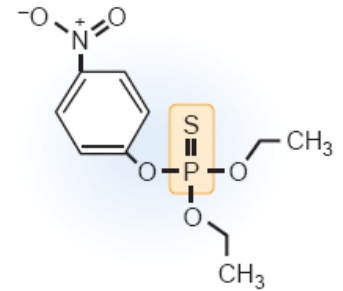
- Mechanism-based inhibitors mimic or participate in an intermediate step of the catalytic reaction.
- They include:
 - Covalent inhibitors
 - Transition state analogs
 - Heavy metals
- Irreversible inhibitors decrease the concentration of active enzyme.

Covalent inhibitors

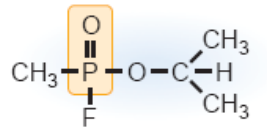
- They form covalent or extremely tight bonds with active site amino acids.
 - Example: di-isopropyl fluorophosphate (DFP) is an organophosphate
 - The nerve gas sarin
 - The insecticides malathion & parathion.
 - DFP inhibits acetylcholinesterase preventing the degradation of the neurotransmitter acetylcholine.



Malathion



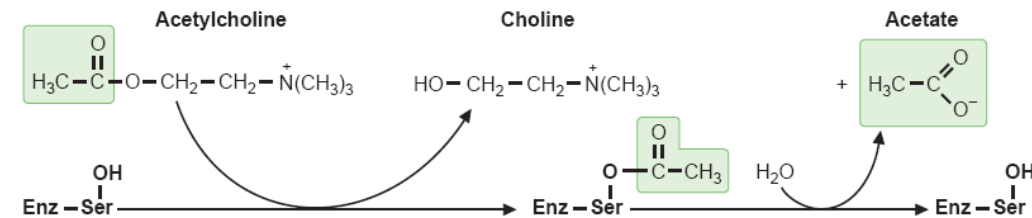
Parathion



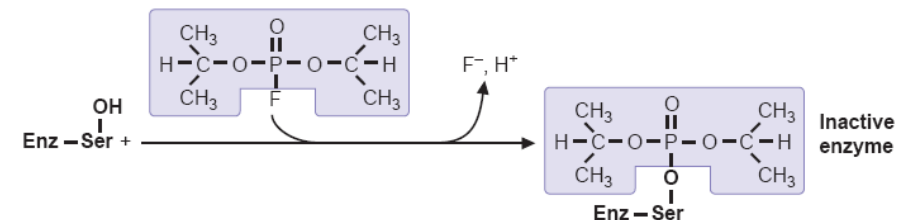
Sarin

DFP also inhibits other enzymes that use serine (ex. serine proteases), but not lethal.

A. Normal reaction of acetylcholinesterase



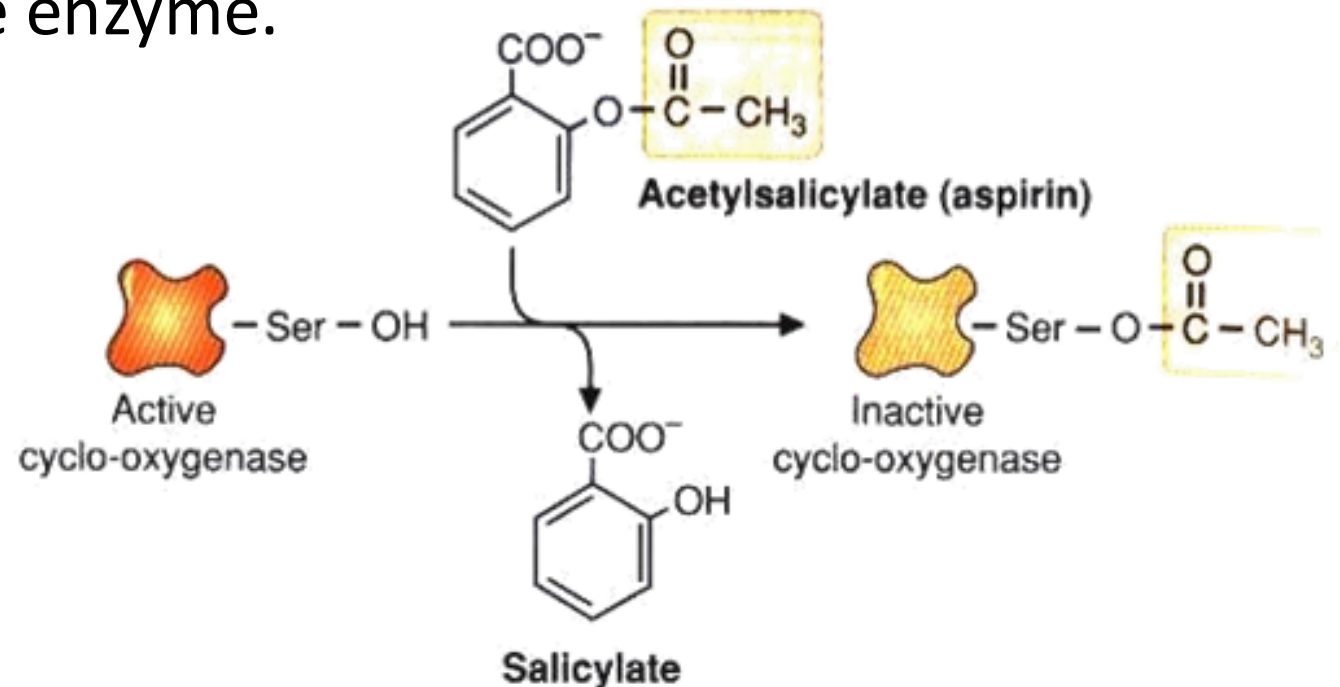
B. Reaction with organophosphorus inhibitors





Aspirin

- Aspirin (acetylsalicylic acid) acetylates an active site serine of cyclooxygenase.
- Aspirin resembles a portion of the prostaglandin precursor that is a physiologic substrate for the enzyme.

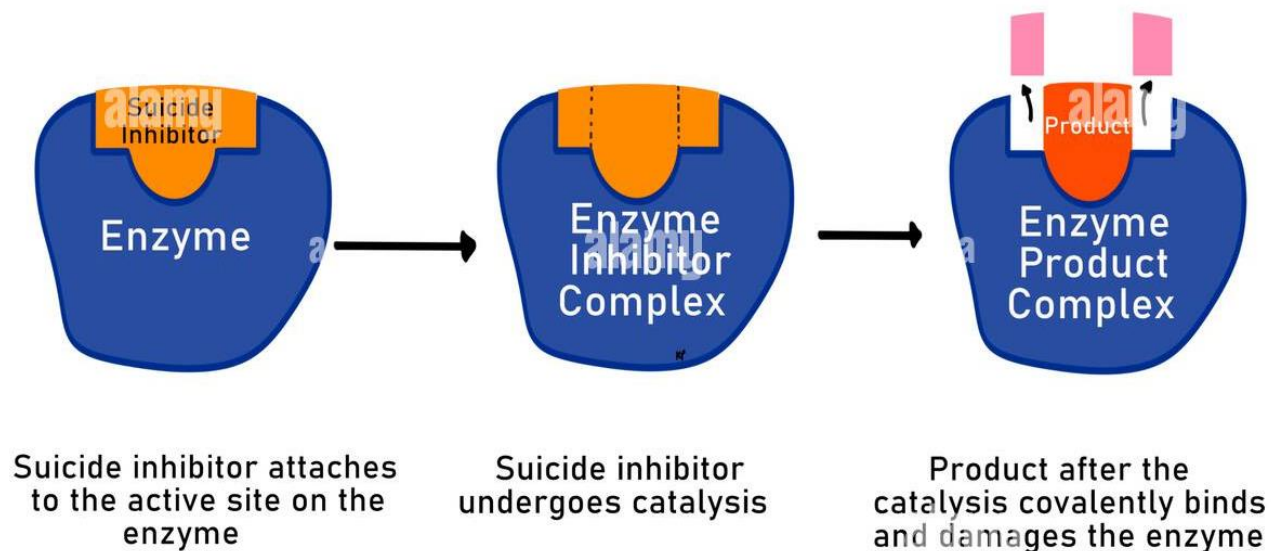




Substrate and transition-State analogs

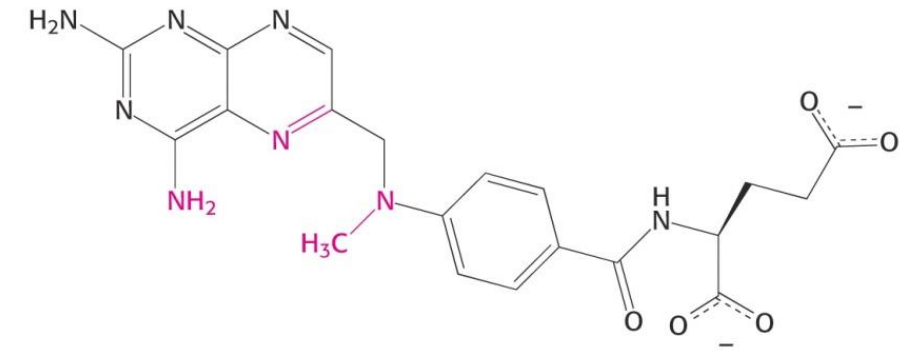
Suicide inhibitors

- They bind more tightly than substrates.
- Drugs cannot be designed that precisely mimic the transition state! (highly unstable structure).

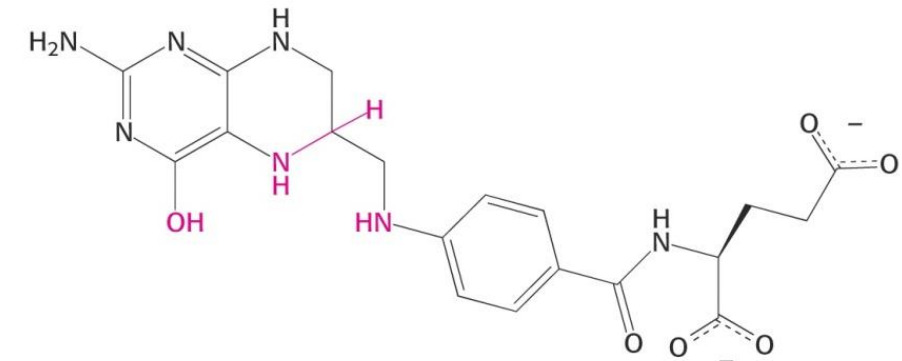


Methotrexate

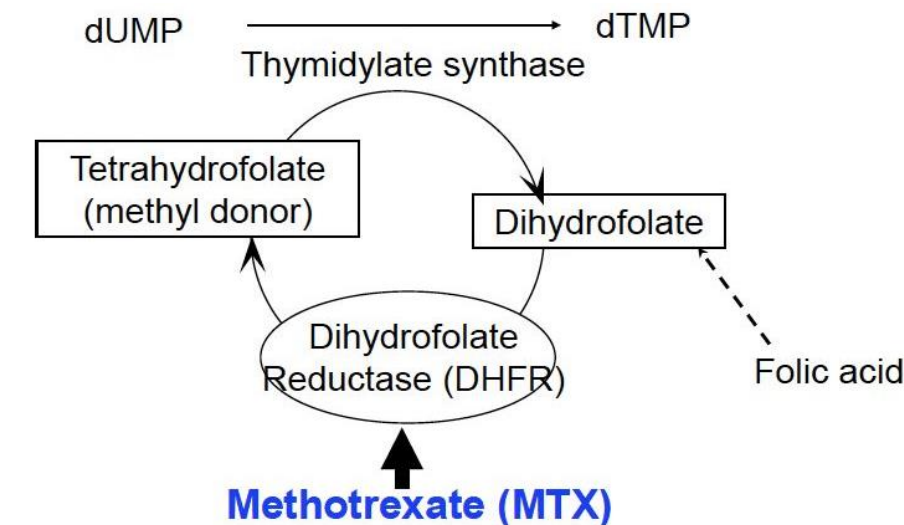
- Methotrexate is a synthetic inhibitor used to treat cancer.
- It is a structural analog of folate, a substrate for the enzyme dihydrofolate reductase, and a coenzyme for thymidylate synthase, both of which are responsible for the synthesis of nucleotides.
- It binds to dihydrofolate reductase 1000-fold more tightly than the natural substrate and inhibits nucleotide base synthesis.



Methotrexate



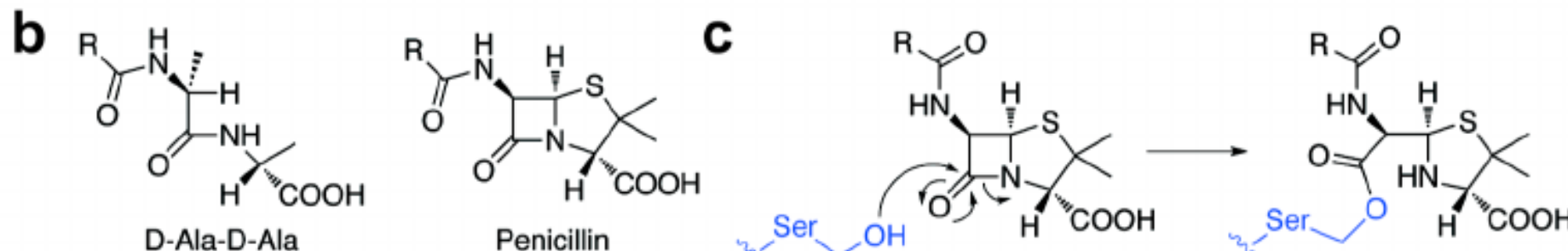
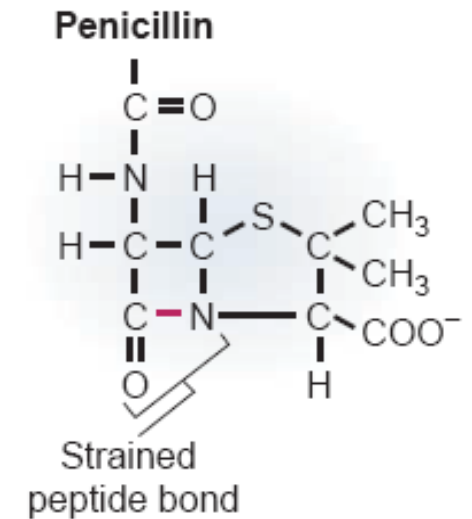
Tetrahydrofolate





Penicillin

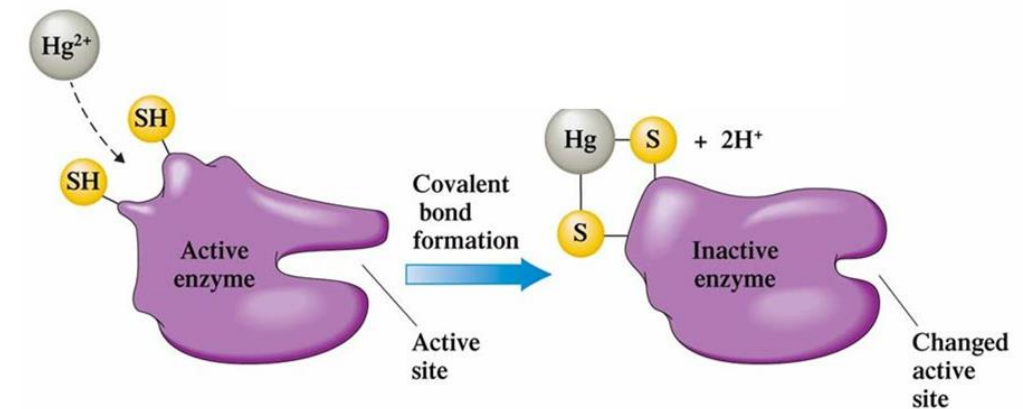
- It is a transition-state analog to glycopeptidyl transpeptidase, which is required for synthesis of the bacteria cell wall.
- The peptide bond in the β -lactam ring of penicillin looks like the natural transition-state complex.
- The active site serine attacks the highly strained β -lactam ring resulting in opening of the lactam. This reaction leads to irreversible covalent modification of the enzyme.





Heavy Metals

- Mercury (Hg), lead (Pb), aluminum (Al), or iron (Fe) result in tight binding to a functional group in an enzyme .
 - Nonspecific inhibition at high doses.
- Mercury binds to reactive sulfhydryl groups away from the active site and affect the binding of substrates.
 - Unknown enzymes in mercury toxicity.



- Lead replaces the normal functional metal in an enzyme such as calcium, iron, or zinc by an irreversible mechanism.
 - Its developmental & neurologic toxicity may be caused by its ability to replace Ca^{+2} in several regulatory proteins that are important in the central nervous system and other tissues.

Regulation through conformational
changes

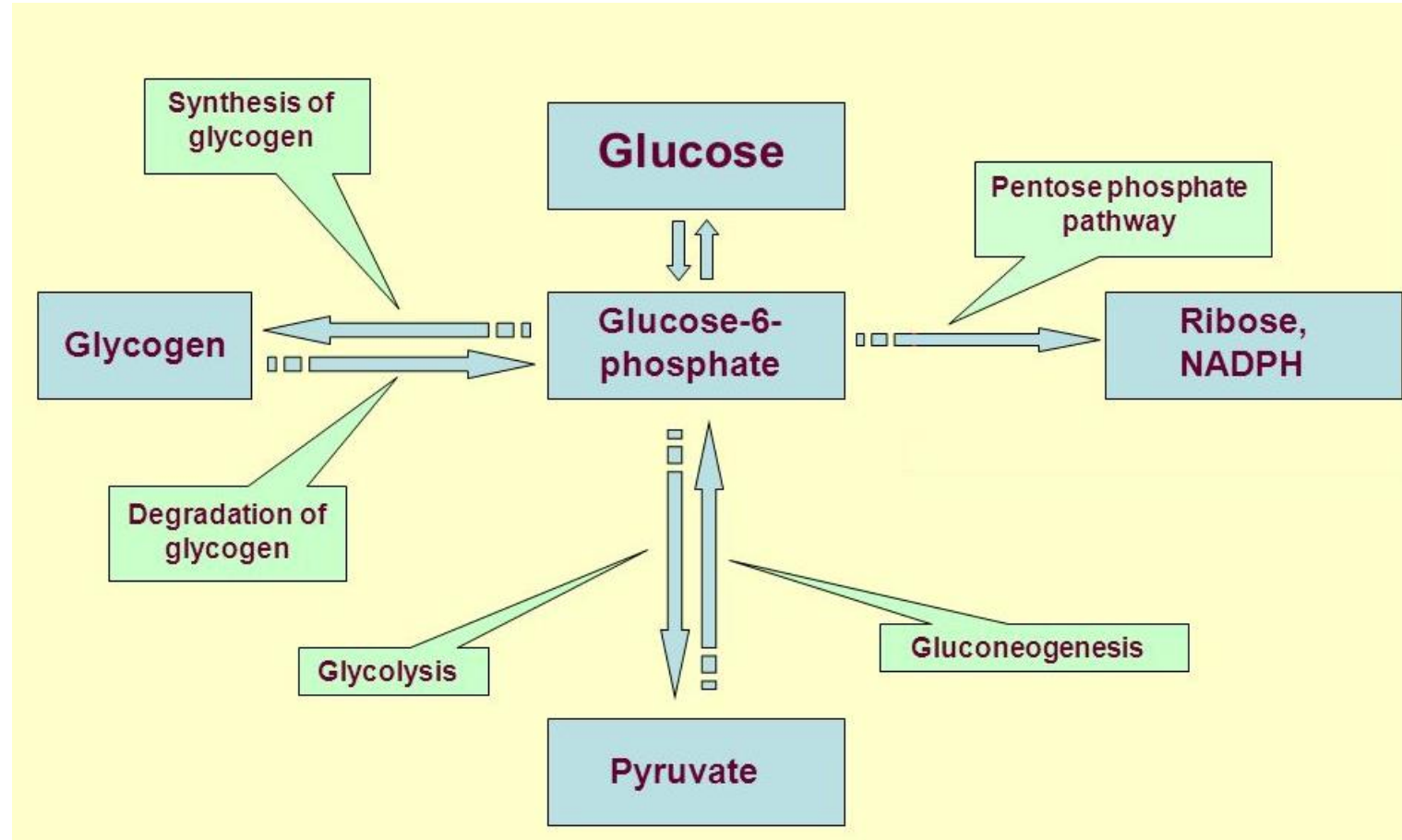


Regulation: conformational changes

- These regulatory mechanisms include
 - Covalent modification
 - Major structural changes (regulatory & catalytic subunits)
 - Protein-protein interactions
 - Proteolytic cleavage
 - Allostery
- Rapidly change from inactive to fully active enzyme.

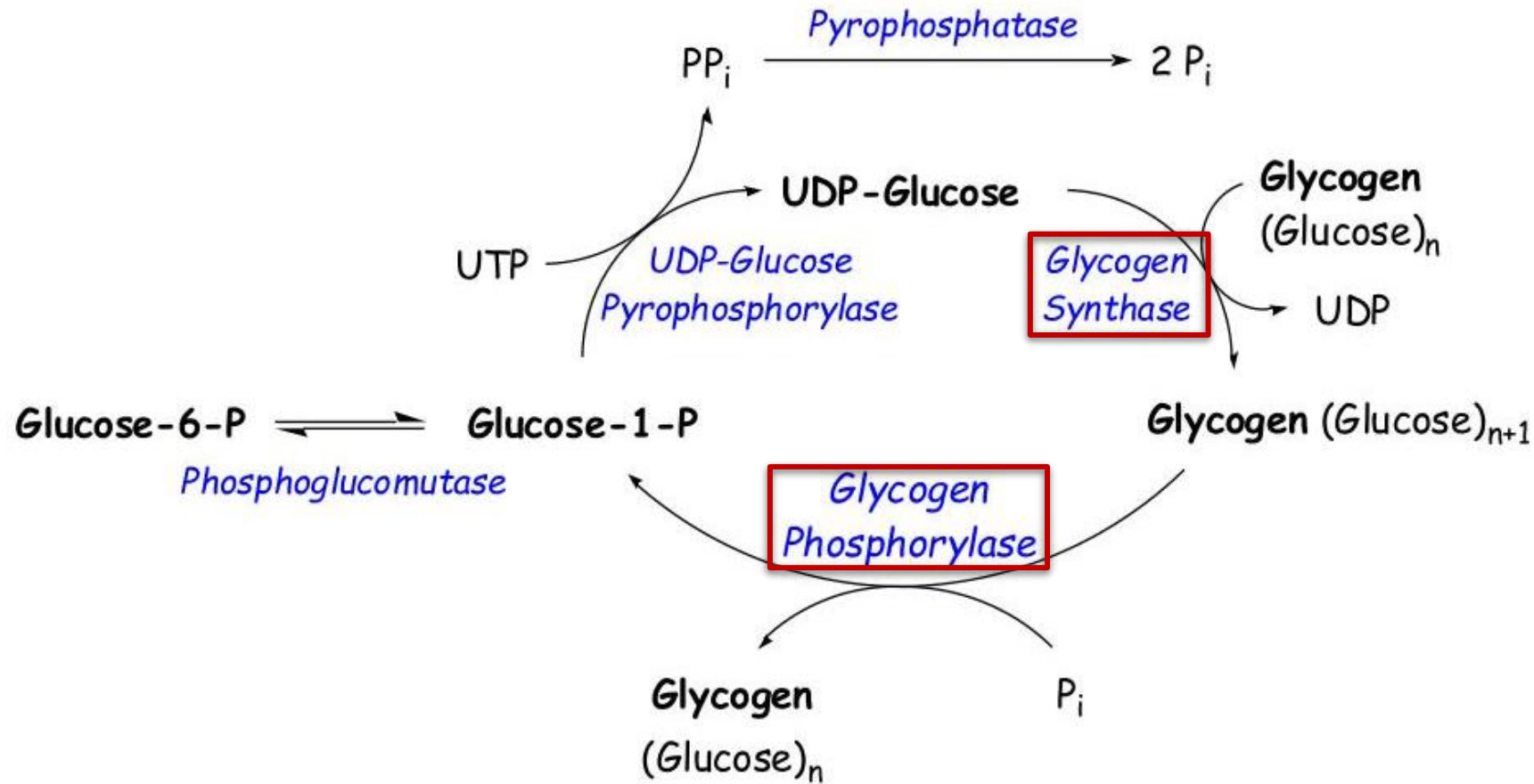


The different fates of glucose



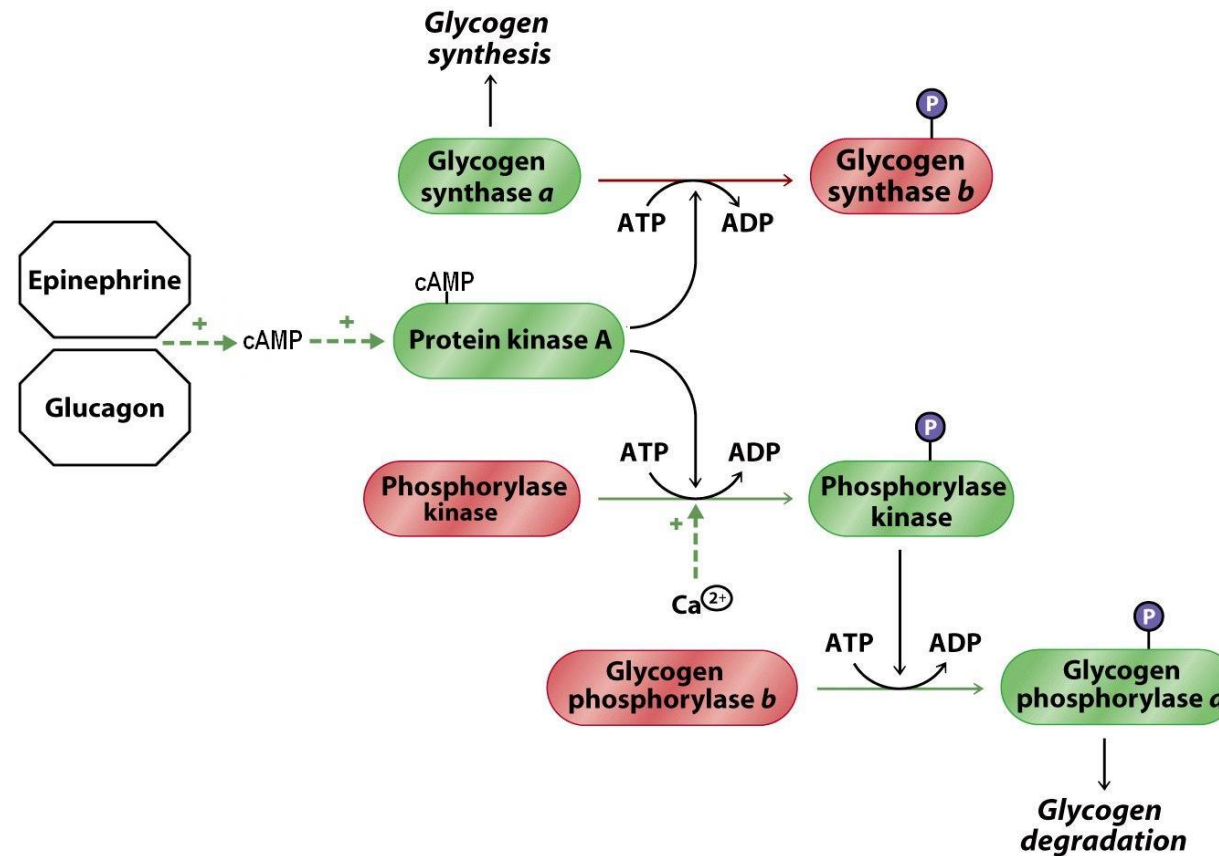


Metabolism of glycogen



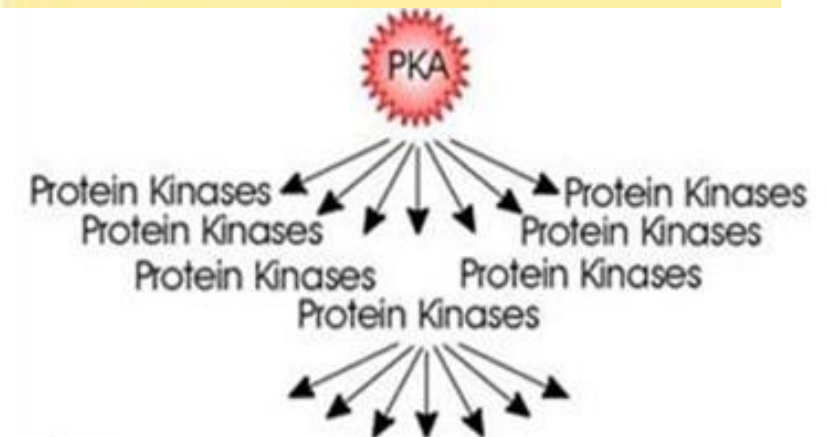
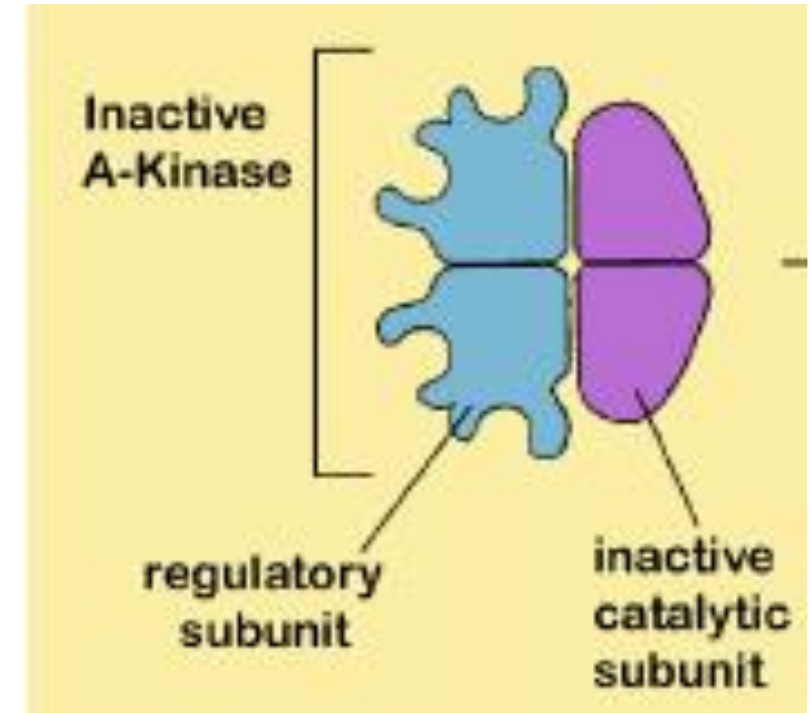


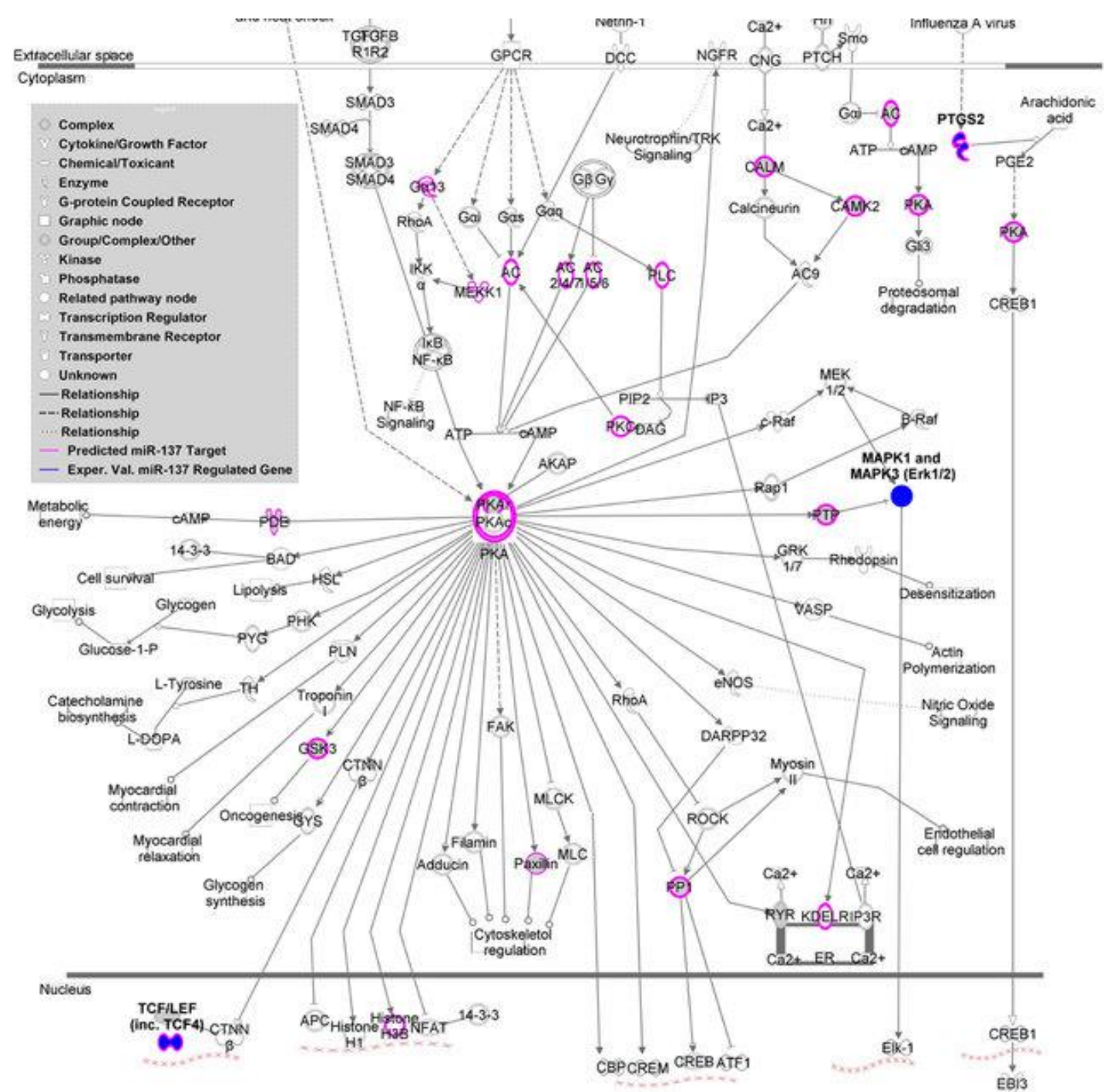
Regulation by phosphorylation



PKA-structure and regulation

- Protein kinase A (PKA), a serine/threonine protein kinase, phosphorylates several enzymes that regulate different metabolic pathways.
 - Example: glycogen phosphorylase kinase
- When inactive, PKA consists of four subunits
 - Two regulatory (R) subunits with high affinity for cAMP,
 - Two catalytic (C) subunits

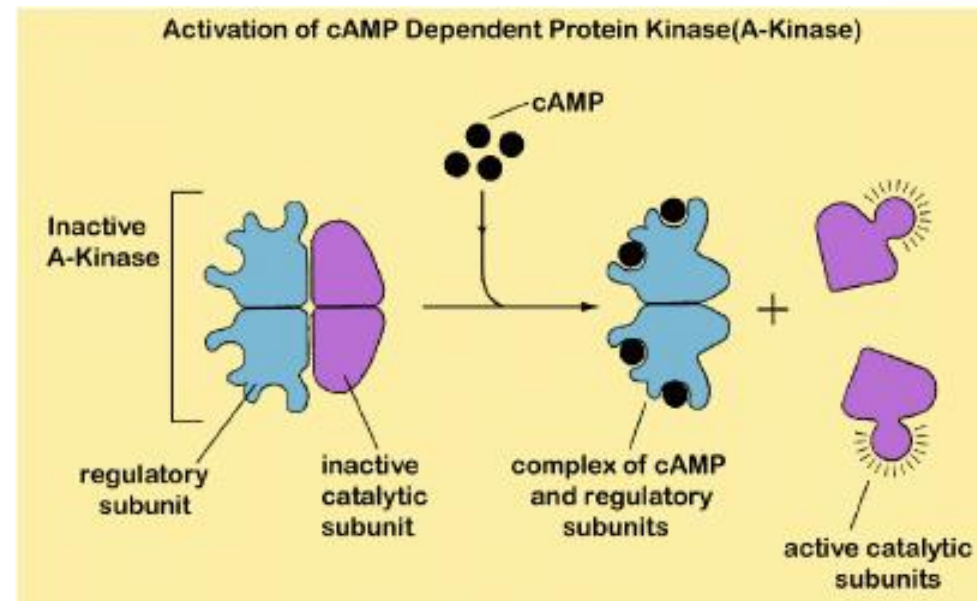
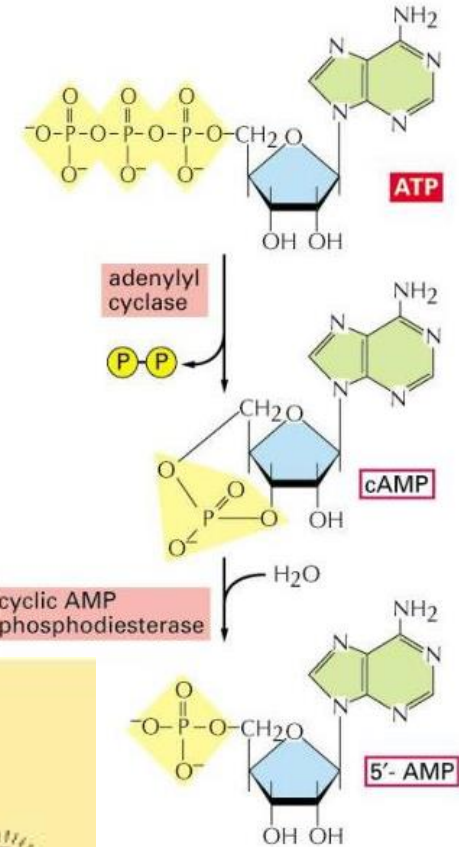






cAMP and protein kinase A (PKA)

- Small-molecule modulators can have dramatic effects on enzymes.
- For example, cAMP, which is structurally modified AMP, can activate protein kinase A (PKA).
- The binding of two molecules of cAMP to each regulatory subunit leads to the dissociation of R2C2 into an R2 subunit and two active C subunits.



Reversible covalent modification



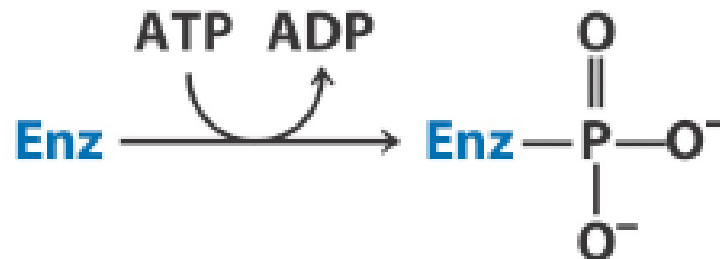
Advantage

- Rapid and transient
- A most common mechanism is enzyme phosphorylation (the covalent addition of a phosphate group to one of its amino acid side chains).
 - Usually serine, threonine, and tyrosine

Covalent modification (target residues)

Phosphorylation

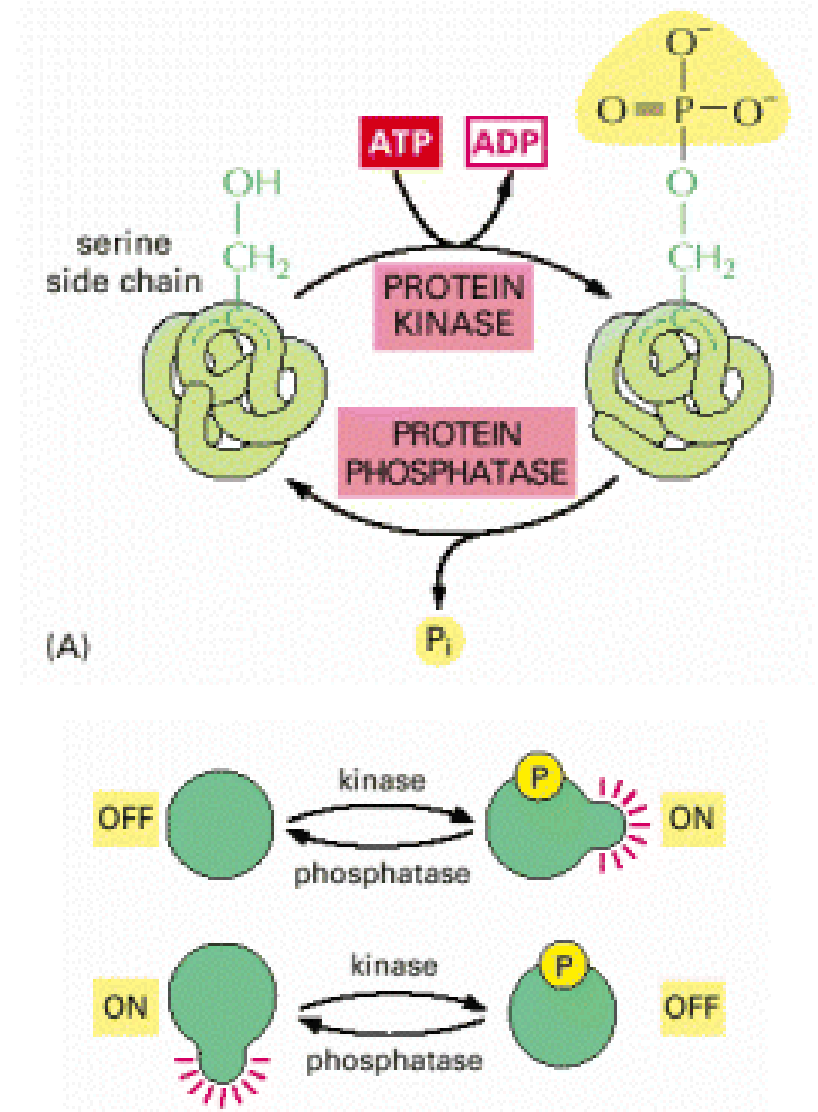
(Tyr, Ser, Thr, His)





Enzymes

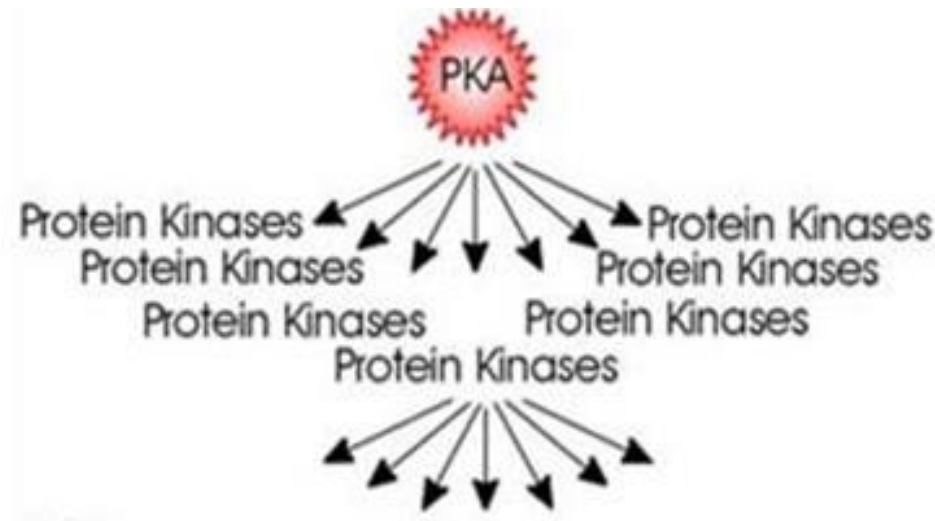
- ATP mostly is the phosphoryl donor in these reactions, which are catalyzed by protein kinases.
- The removal of phosphoryl groups (dephosphorylation) by hydrolysis is catalyzed by protein phosphatases.
- Note: dephosphorylation is not the reversal of phosphorylation.
- The addition or removal of a phosphate group to an enzyme may activate or inactivate these enzymes.





Why is phosphorylation effective?

- Formation or removal of new electrostatic interactions and/or hydrogen bonds altering substrate binding and catalytic activity.
- It can happen in less than a second or over a span of hours.
- Phosphorylation often causes highly amplified effects.



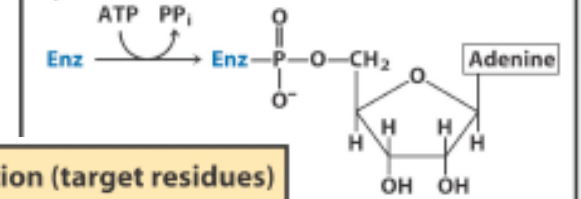


Others

- Adenylation (addition of adenylyl group (AMP)).
- Uridylylation (addition of uridylyl group).
- ADP-ribosylation (addition of adenosine diphosphate ribosyl group).
- Methylation of carboxylate side chains masking negative charges.
- Acetylation (from acetyl CoA) masking positive charges.

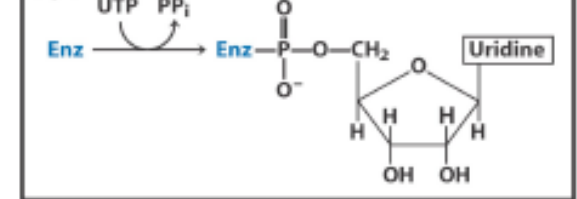
Covalent modification (target residues)

Adenylation (Tyr)



Covalent modification (target residues)

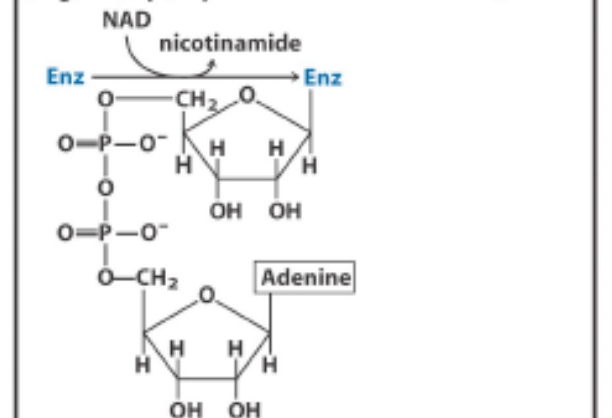
Uridylylation (Tyr)



Covalent modification (target residues)

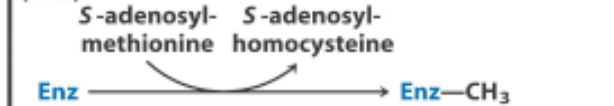
ADP-ribosylation

(Arg, Gln, Cys, diphthamide—a modified His)



Covalent modification (target residues)

Methylation (Glu)



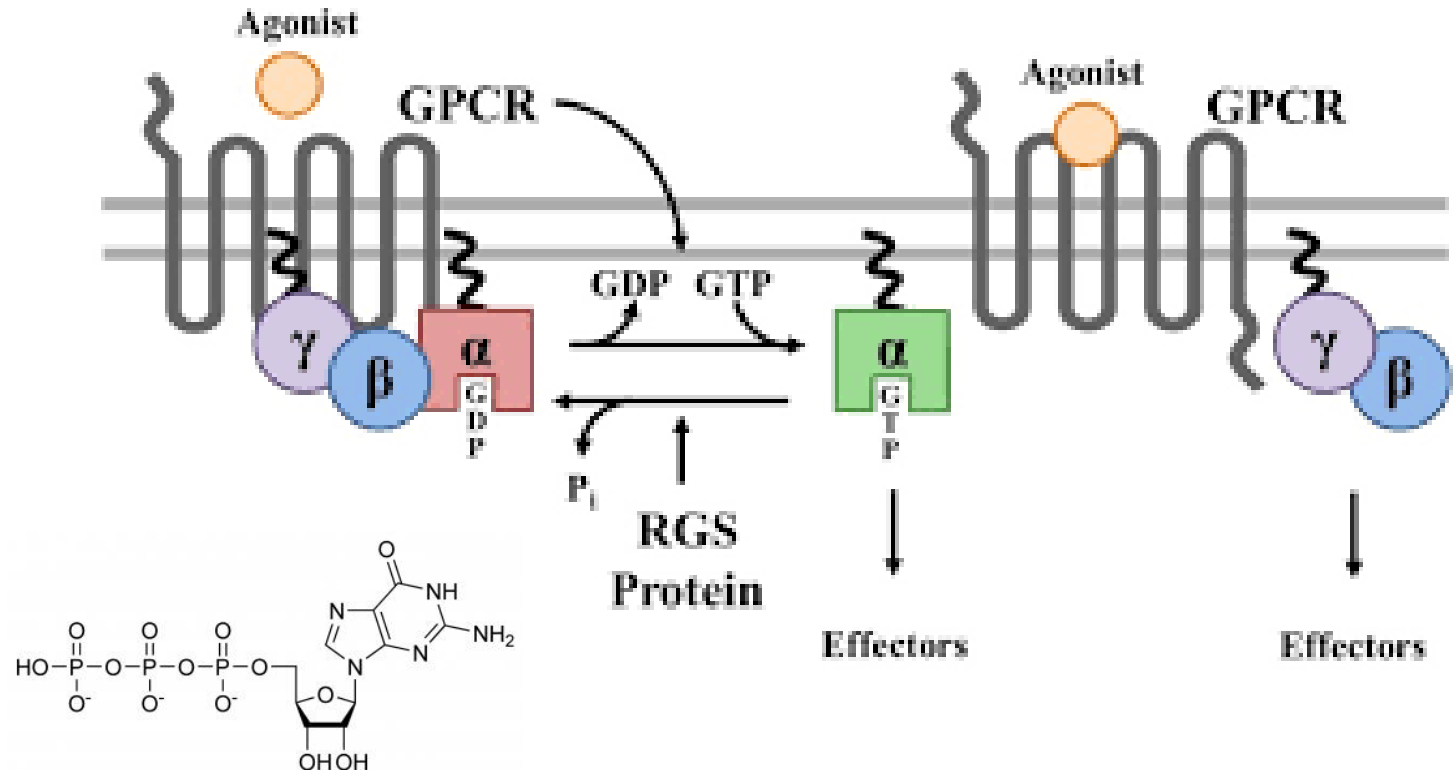


Large and small regulatory modulators

Trimeric large G proteins

- Trimeric G proteins: a family of membrane-bound proteins causing changes inside the cell. They communicate signals from hormones, neurotransmitters, and other signaling factors through G protein-coupled receptors (GPCRs)

- When they bind GTP (small), they are 'on', and, when they bind GDP, they are 'off'.
- The α subunit (large) binds to effectors stimulating or inhibiting them.

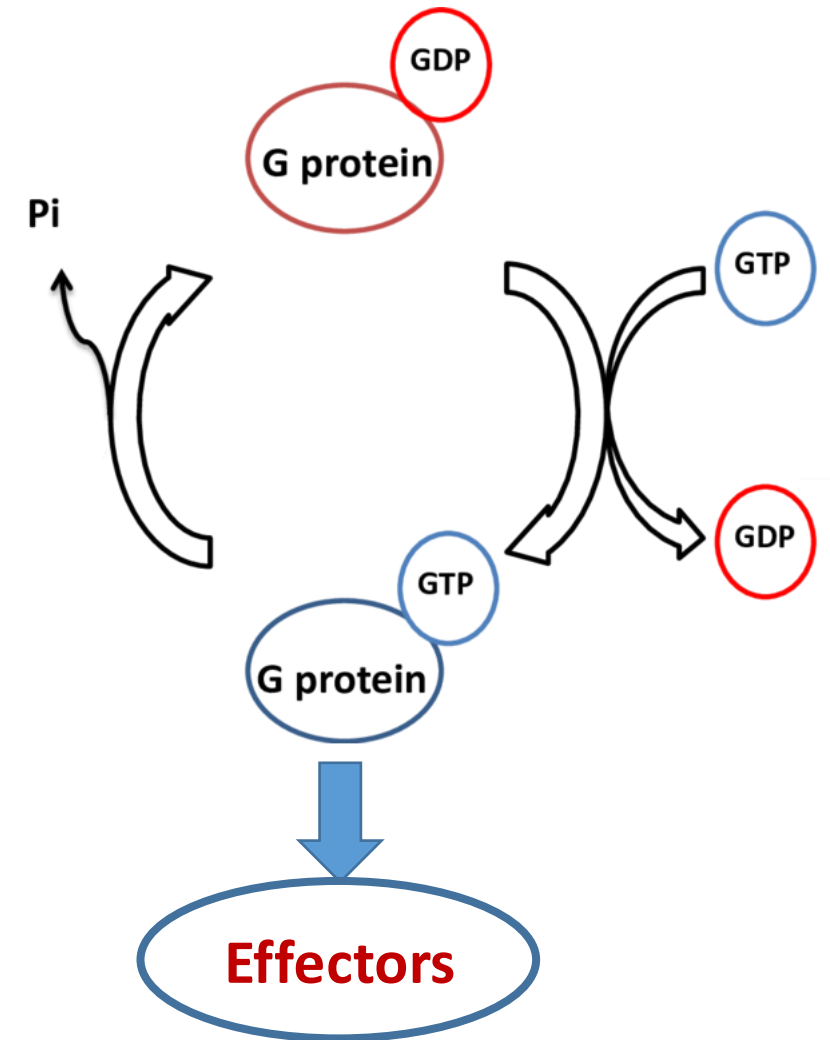




Large and small regulatory modulators

Small monomeric G proteins

- When GTP (small) is bound, the conformation of the small monomeric G protein (large) allows it to bind target proteins, which are then activated or inhibited.
- The small monomeric G protein hydrolyzes a phosphate from GTP to form GDP, which changes the G protein conformation and causes it to dissociate from the target protein.
- GDP is exchanged for GTP, which reactivates the small monomeric G protein.

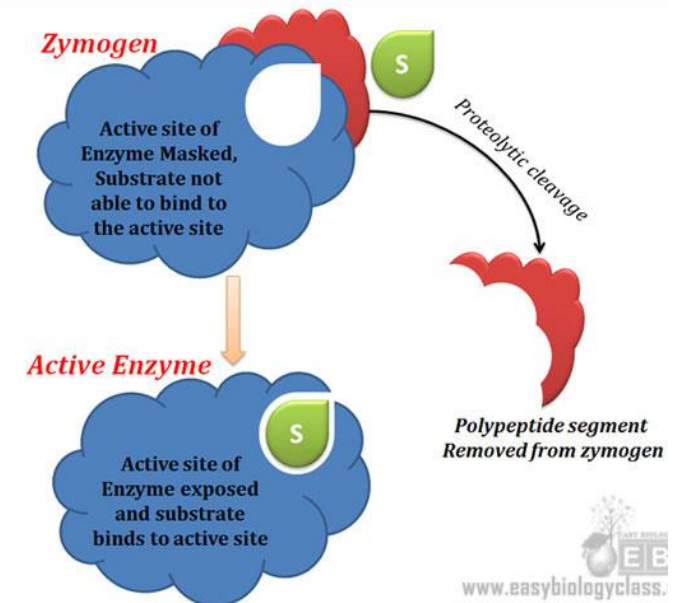
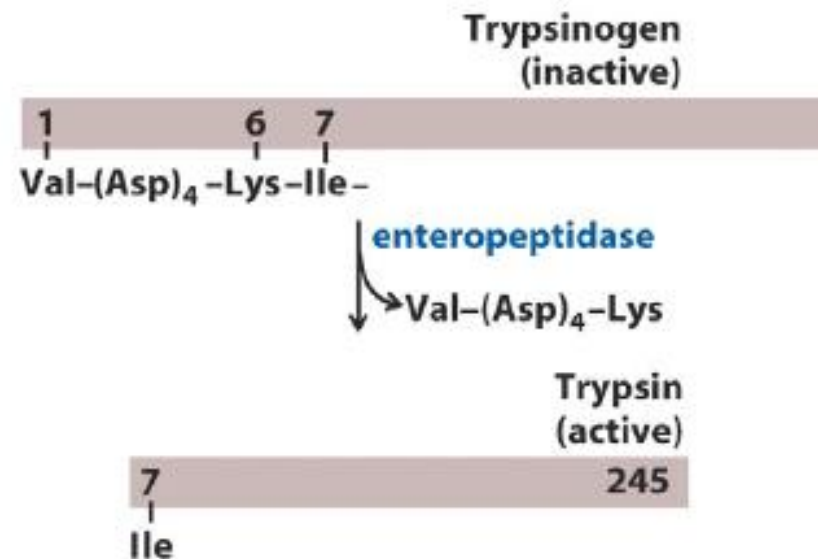


Irreversible covalent modification
(Proteolytic activation)



Zymogens

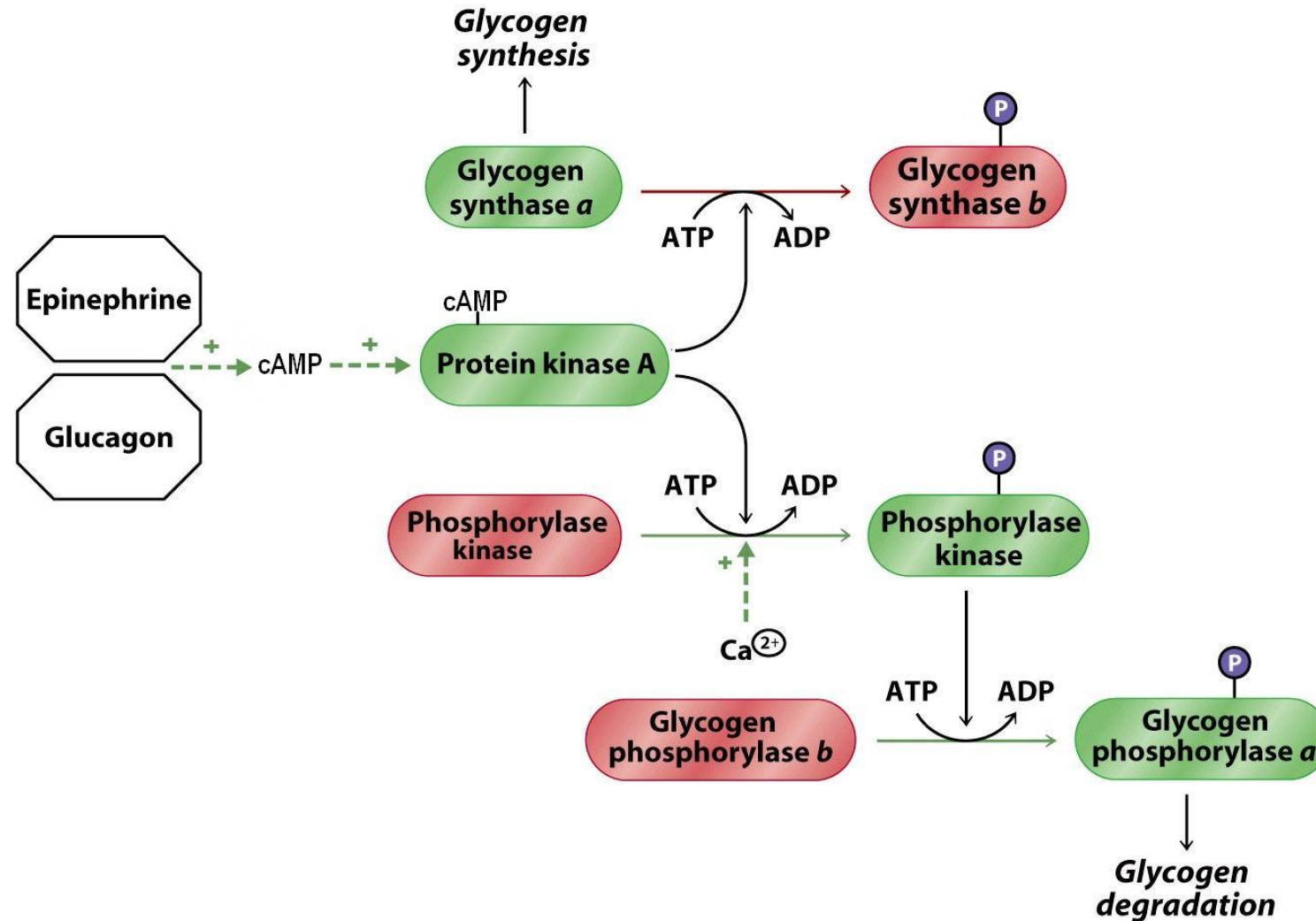
- Zymogens or proenzymes are inactive precursors of enzymes.
- Activation is done by irreversibly removing part of the enzyme (usually known as the pro region present at the N-terminus).
- Examples: digestive enzymes such as chymotrypsin, trypsin, and pepsin that get activated when food is ingested.
 - Trypsinogen (zymogen) is activated via removal of the first six amino acids at the N-terminus.

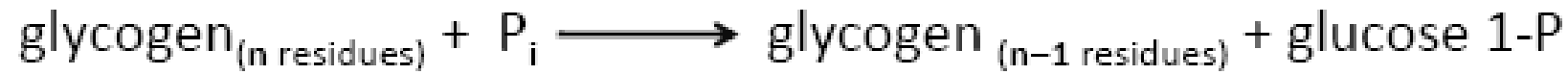


Allosteric regulation



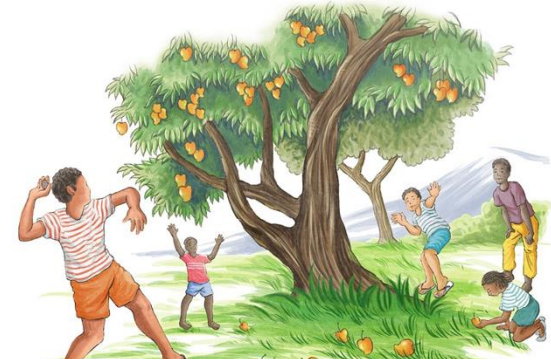
Phosphorylation cascade



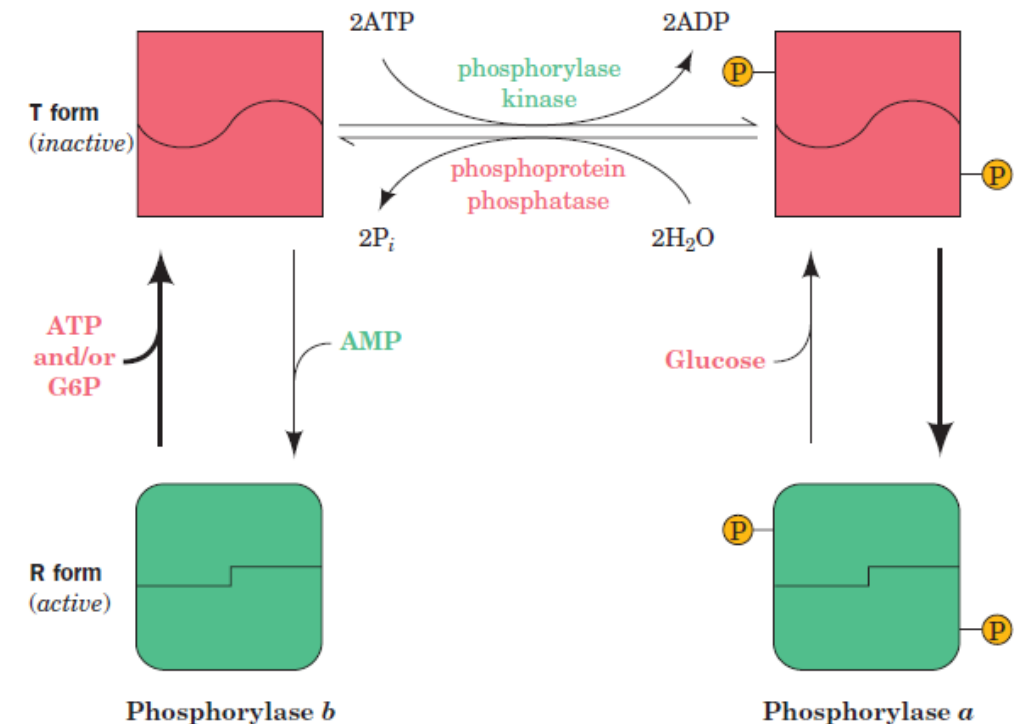


Example: Glycogen phosphorylase

- GP catalyzes removal of glucose molecules from glycogen.
- The enzyme exists in four forms:
 - T (inactive) and R (active) states
 - Phosphorylated (a) and dephosphorylated (b)



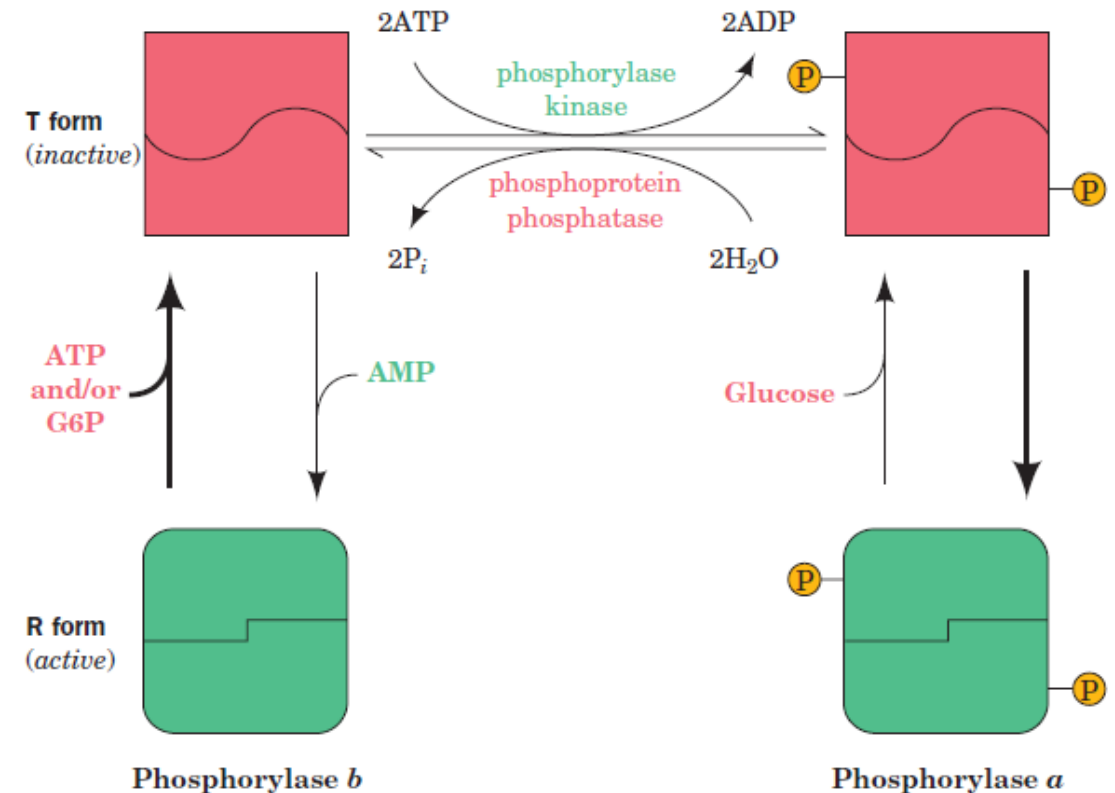
- *When phosphorylated, it is known as phosphorylase a.*
- *When dephosphorylated, it is known as phosphorylase b.*





The two forms of each form

- Both phosphorylase b and phosphorylase a exist in equilibrium between an active R state and a less-active T state.
- Phosphorylase b is usually inactive because the equilibrium favors the T state.
- Phosphorylase a is usually active because the equilibrium favors the R state.



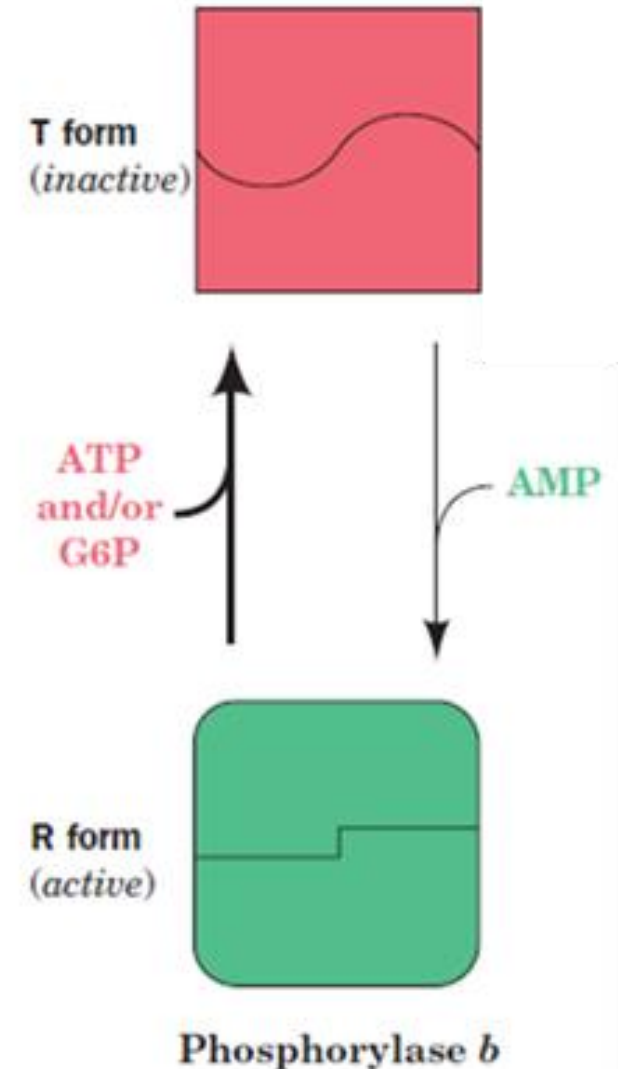
The transition of phosphorylase b between the T and the R state is controlled by the energy charge (ATP and AMP) of the muscle cell and availability of glucose-6-phosphate.



What do ATP and AMP do?

- Muscle phosphorylase b is active only in the presence of high concentrations of AMP, which binds to a nucleotide-binding site and stabilizes the conformation of phosphorylase b in the R state.
- ATP acts as a negative allosteric effector by competing with AMP and so favors the T state.

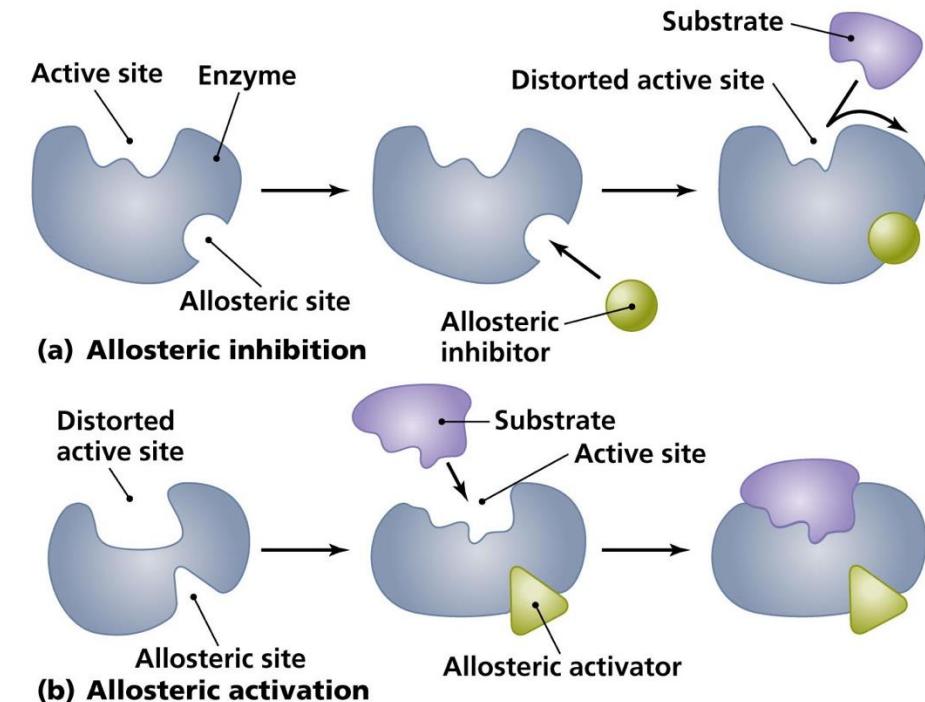
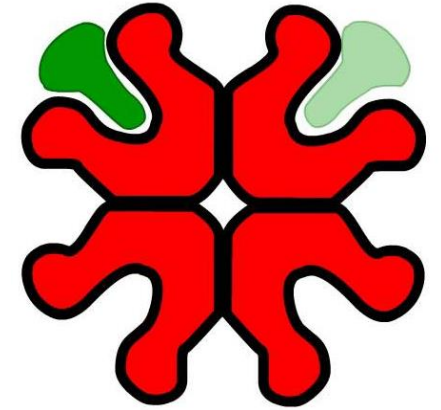
Glucose 6-phosphate also favors the T state of phosphorylase *b*, an example of feedback inhibition.





Allosteric enzymes and their modifiers

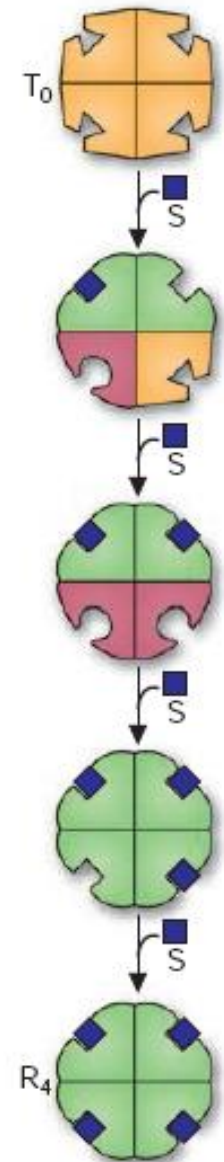
- Allosteric enzymes are multi-subunit proteins;
 - One subunit contains the active site (catalytic subunit) and another containing the regulatory site (regulatory subunit).
 - Multiple active sites can exist on multiple subunits.
- The binding of regulatory molecules triggers conformational changes in the active site via modifying non-covalent interactions.
- Allosteric enzymes bind modifiers at the allosteric site, a site that is physically separate from the catalytic site.
 - A negative allosteric modifier (inhibitor) causes the enzyme to have less activity.
 - A positive allosteric modifier (activator) causes the enzyme to be more active.





More on modifiers

- When the modifier is a molecule other than the substrate, then it is known as heterotropic.
- If the modifier is same as the substrate, then it called homotropic.
 - The binding of the substrate causes the enzyme to become more active and binds to a second substrate at a different active site with more ease.
 - This is called "positive cooperativity".
 - T to R conformation
 - There is also negative cooperativity.

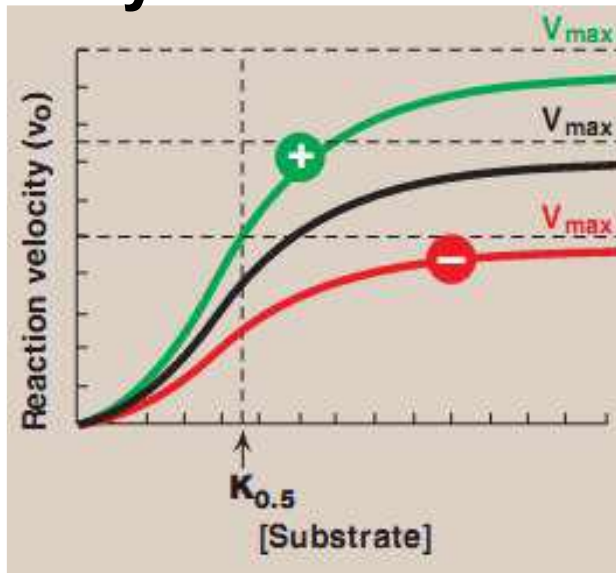




Types of allosteric enzymes

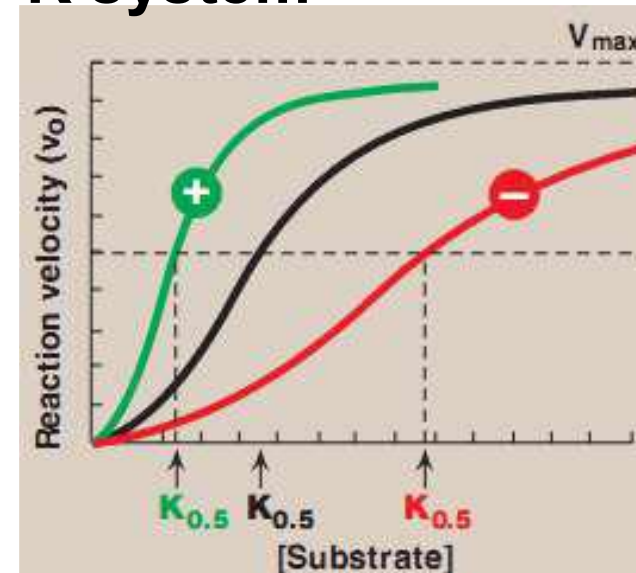
- The Michaelis-Menten model cannot explain the kinetic properties of allosteric enzymes.
- $K_{0.5}$ is used instead of K_M .

V system



Same $K_{0.5}$, Different V_{max} .

K system



Different $K_{0.5}$, same V_{max} .

Note near-hyperbolic plot with activators



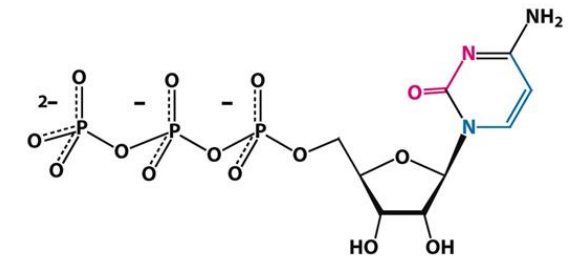
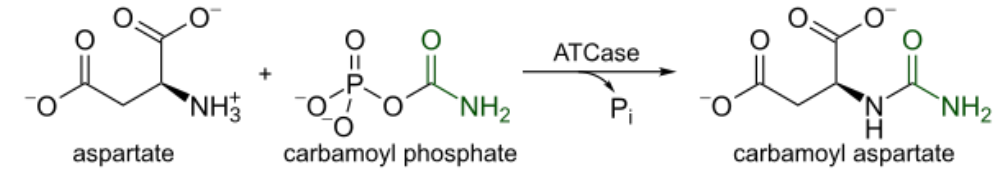
Allosteric enzymes and metabolism

- Allosteric inhibitors usually have a much stronger effect on enzyme velocity than competitive and noncompetitive inhibitors.
- Allosteric enzymes are not limited to regulation through inhibition whereby allosteric effectors may function as activators.
- The allosteric effector needs not bear any resemblance to substrate or product of the enzyme.
- The effect of an allosteric effector is rapid occurring as soon as its concentration changes in the cell.
 - Feedback regulation of metabolic pathways by end products or by signal molecules that coordinate multiple pathways.

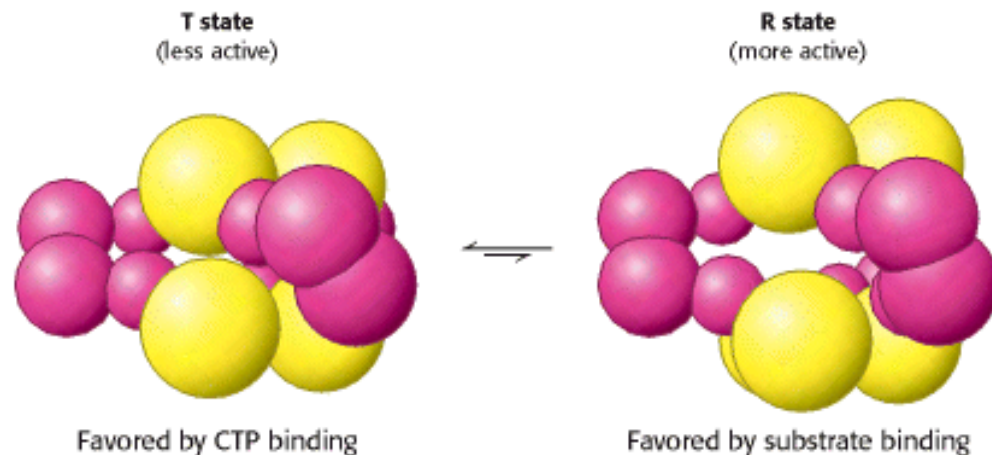


Aspartate transcarbamoylase

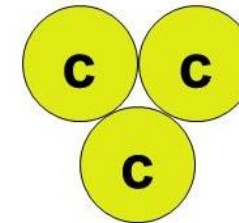
- Aspartate transcarbamoylase (ATCase) catalyzes the first step in the synthesis of pyrimidine nucleotides.
- ATCase consists of 12 polypeptide chains: six catalytic subunits (two trimers) and six regulatory subunits (three dimers).
- It exists in two forms: T state (less active) and R state (more active).



Cytidine triphosphate (CTP)



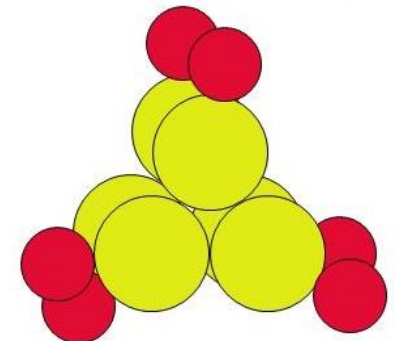
Catalytic Subunit:



Regulatory Subunit:



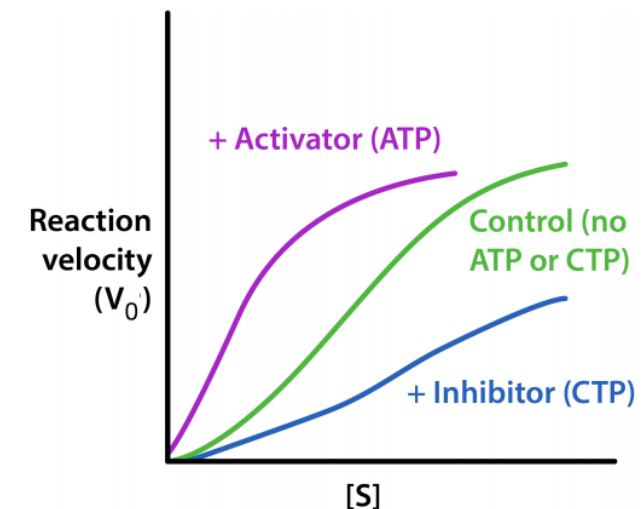
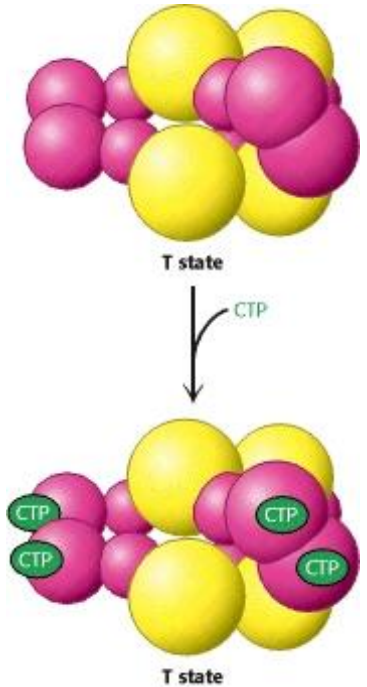
Active Complex: C_6r_6





Aspartate transcarbamoylase-regulation

- ATCase is inhibited by CTP, the end-product
 - inducing a major rearrangement of subunit positions
 - stabilizing the T state of the enzyme.
 - decreasing binding affinity for Asp (substrate) at active sites on catalytic subunits
 - increasing $K_{0.5}$ (K system)
 - Note: a non-competitive inhibitor changes $K_{0.5}$
 - On the other hand, ATP, a purine, heterotypically activates the enzyme in order to balance the rate of synthesis of purines and pyrimidines in cells.

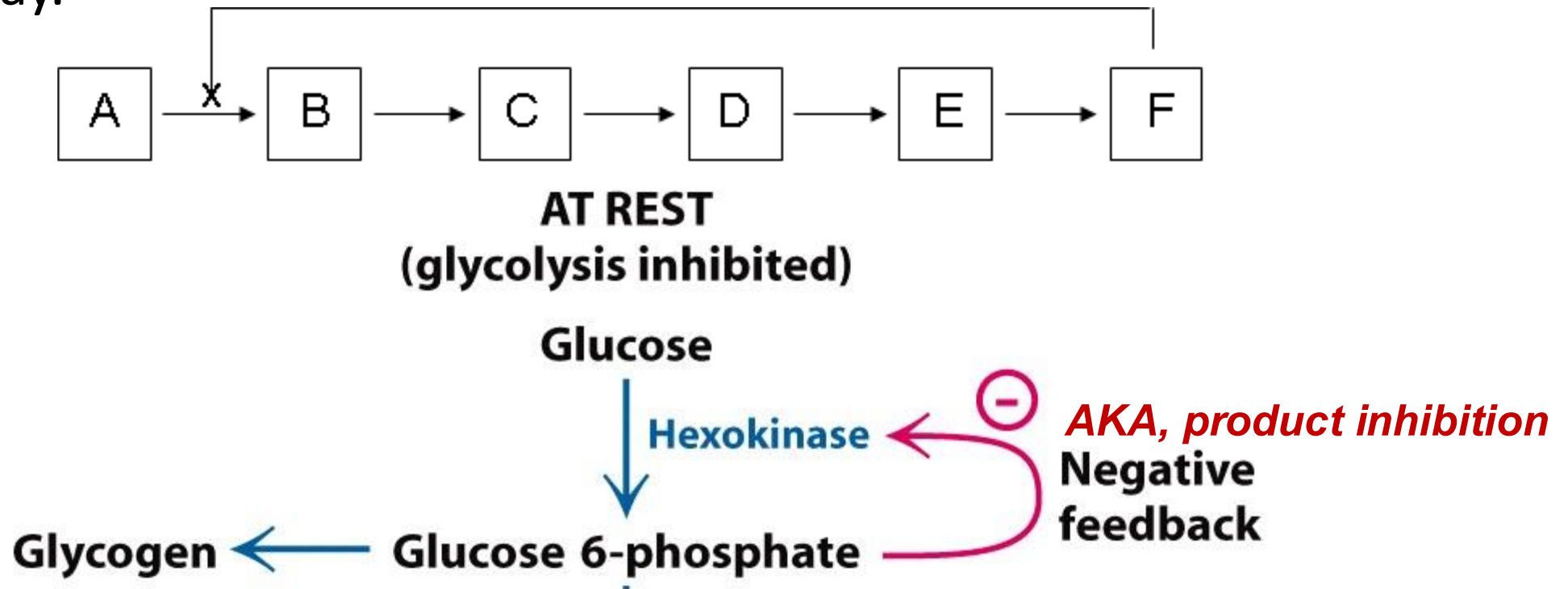


Modes of metabolic regulation



Feedback inhibition

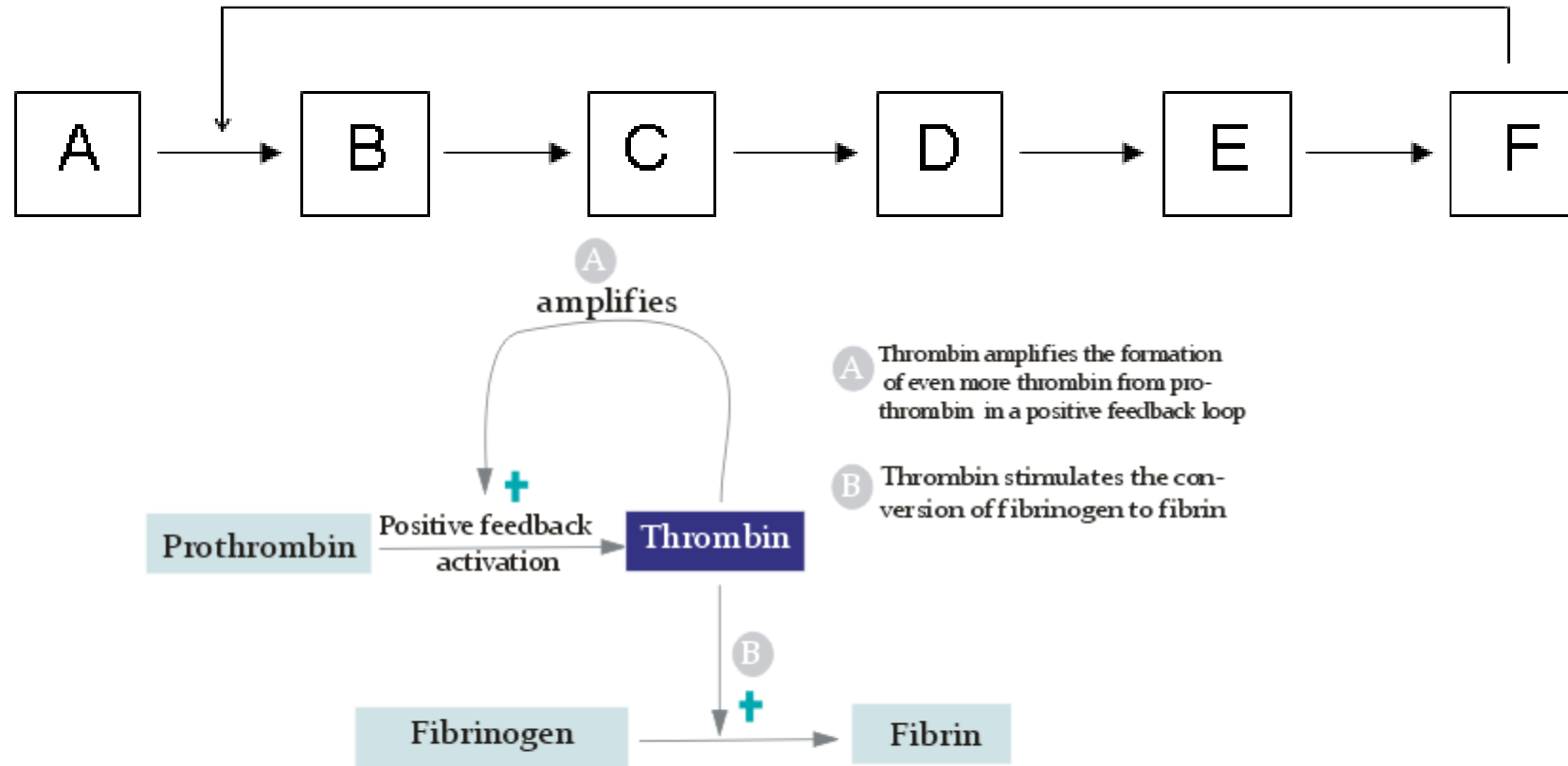
- Feedback inhibition or negative feedback regulation: an enzyme present early in a biochemical pathway is inhibited by a late product of pathway.





Feedback activation

- Positive feedback regulation: a product stimulates the activity of an enzyme.

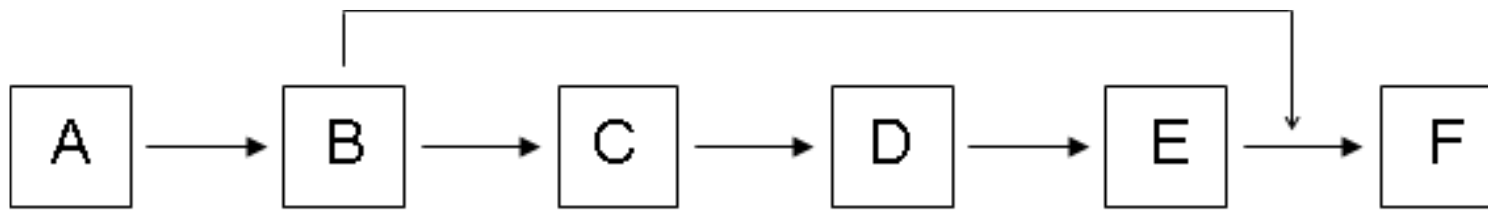


Positive feedback activation of more prothrombin into thrombin



Feed-forward activation

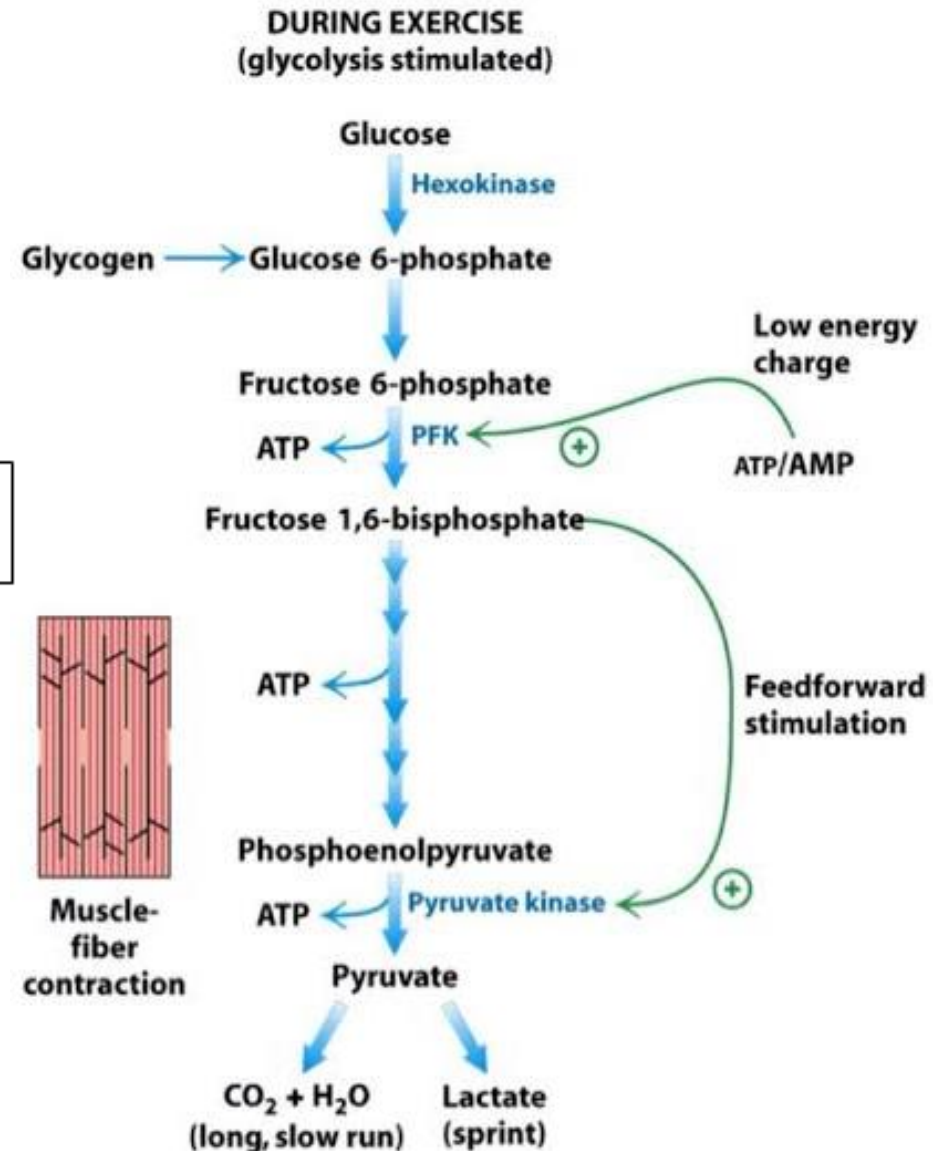
- Feed-forward regulation: a substrate produced early in a pathway activates an enzyme downstream of the same pathway.



- Glycolysis
- Poisoning



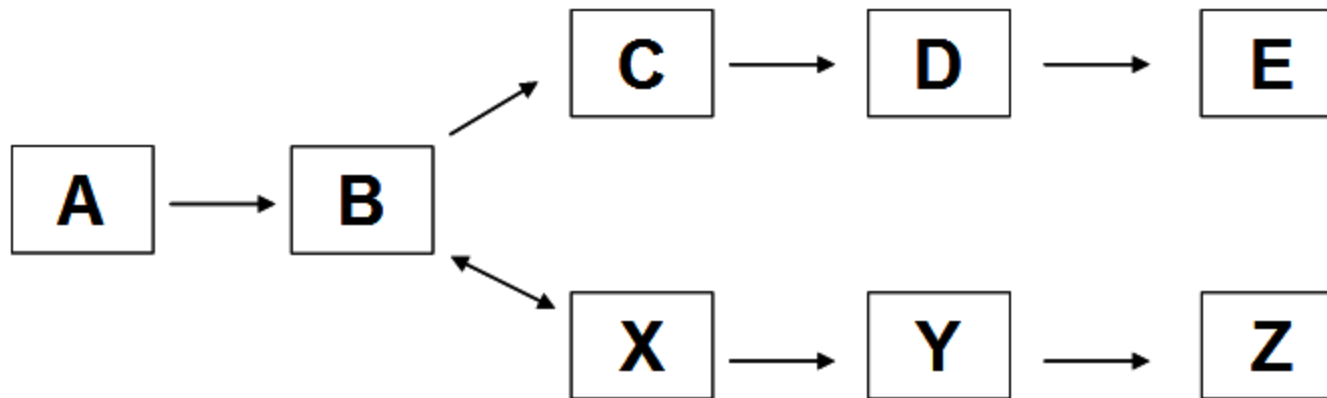
"Oh no! Get this poison out of here!"
"A lot more substrate coming through!"





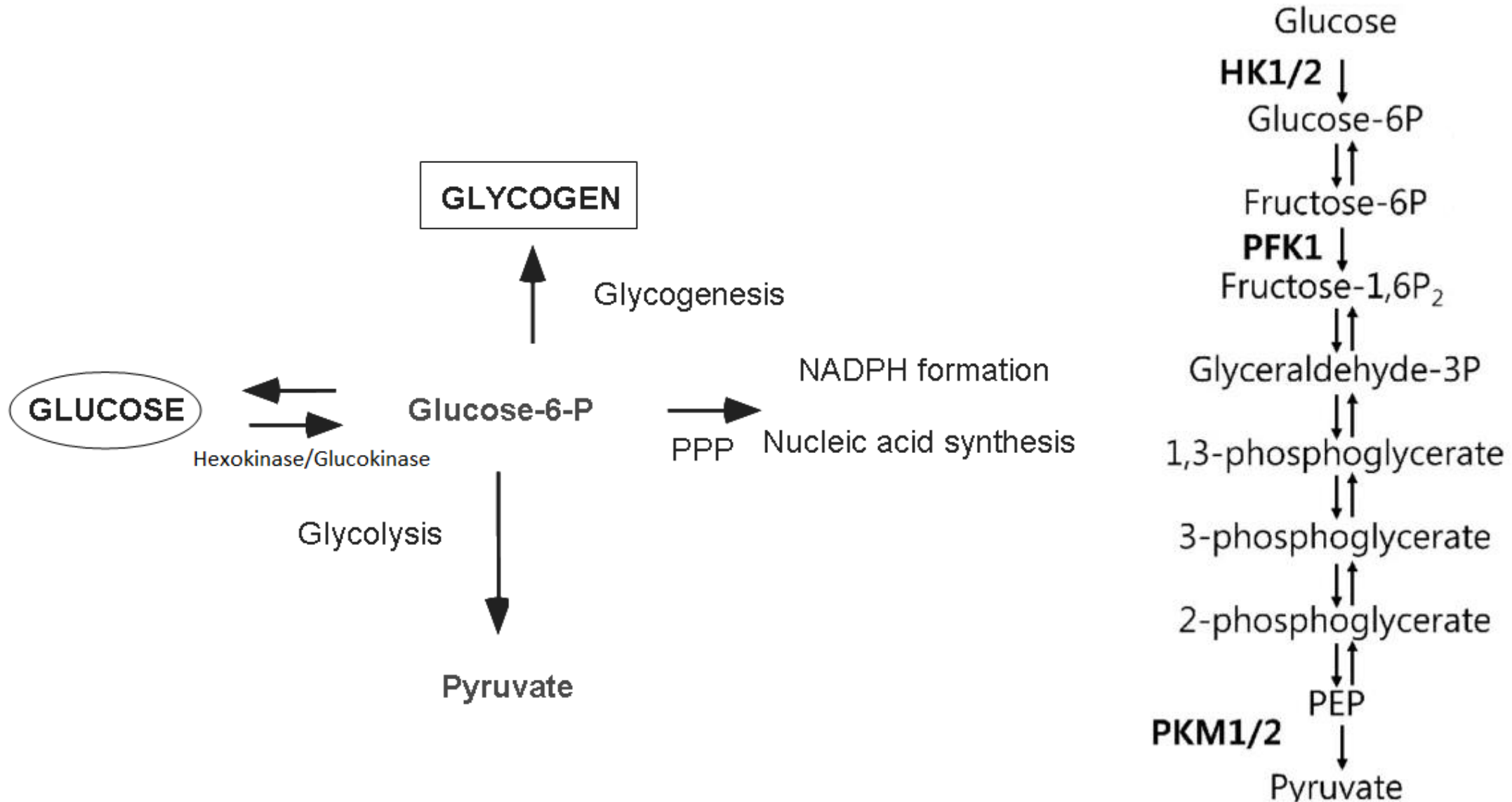
A committed step

- A committed step in a metabolic pathway is the first irreversible reaction that is unique to a pathway and that, once occurs, leads to the formation of the final substrate with no point of return.
- Committed steps are exergonic reaction.
- For example, the committed step for making product E is ($B \rightarrow C$), not ($A \rightarrow B$).





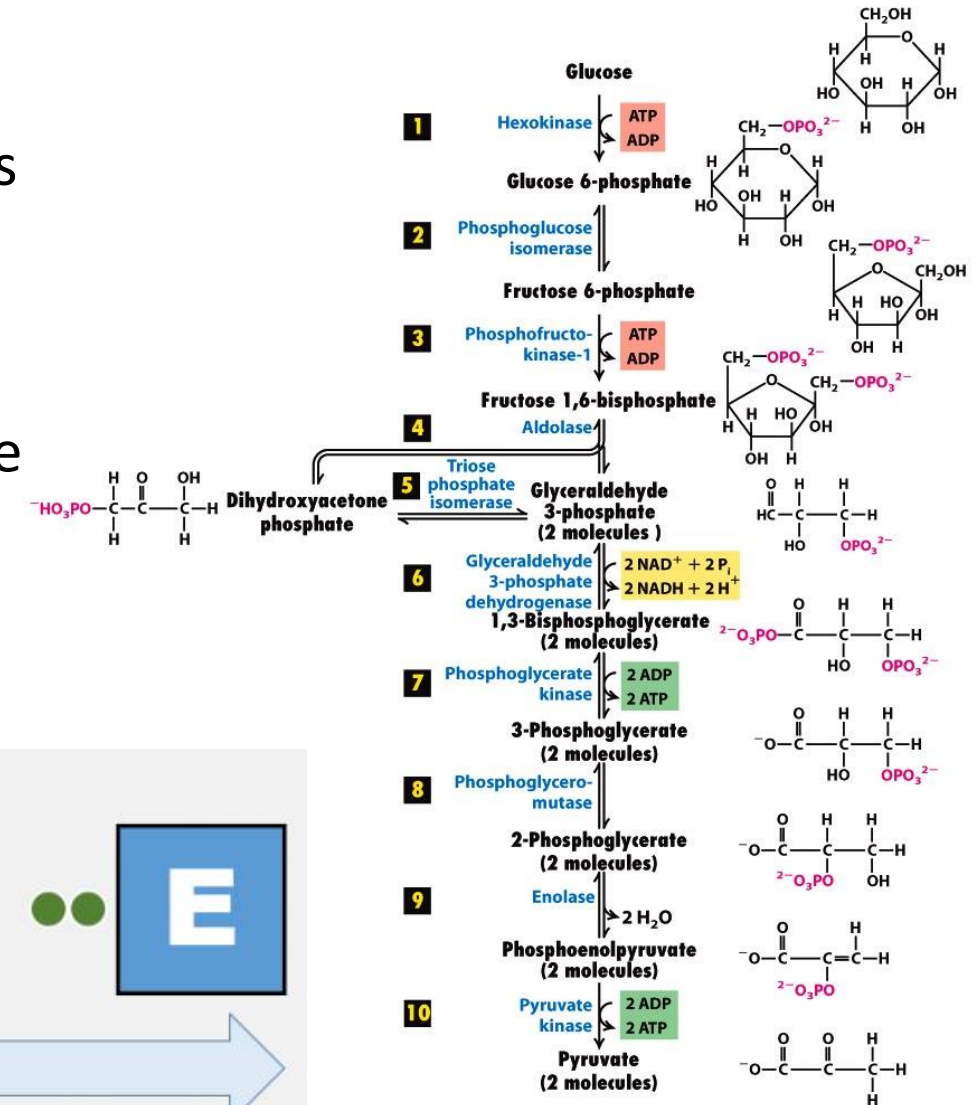
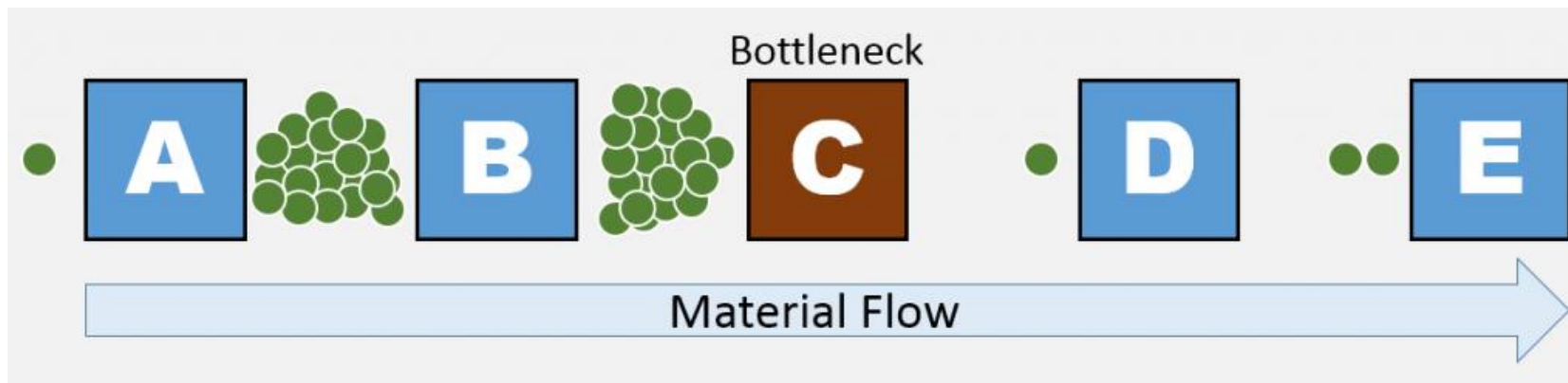
PFK, not HK/GK, is the committed step





Rate-limiting reactions

- Rate-limiting reactions slow down rate of reactions because:
 - requirement for high amount of energy
 - strict regulation of enzymes
 - high K_m values of enzyme towards its substrate
- These reactions are also usually, but not necessarily, committed steps.

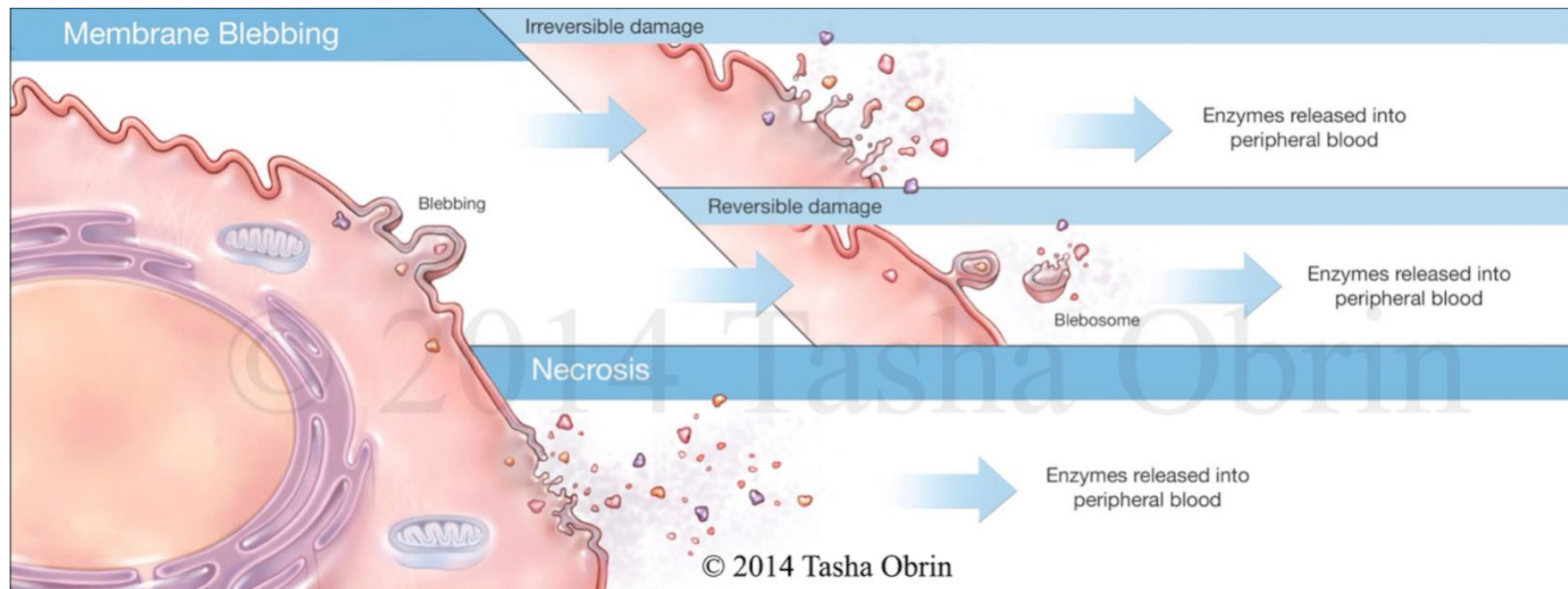


Enzymes in disease diagnosis



Concept

- The presence of enzymes in serum indicates that tissue or cellular damage.
- The measurement enzyme amount in serum is of diagnostic significance.





Example: Creatine phosphokinase (CPK)

- CPK is found primarily in heart and skeletal muscle as well as the brain.
- Three tissue-specific isozymes of CPK:
 - CPK3 (CPK-MM)
 - CPK2 (CPK-MB)
 - CPK1 (CPK-BB)

Serum	Skeletal Muscle	Cardiac Muscle	Brain
0 trace BB <6% MB >94% MM	0 trace BB 1% MB 99% MM	0% BB 20% MB 80% MM	97% BB 3% MB 0%MM