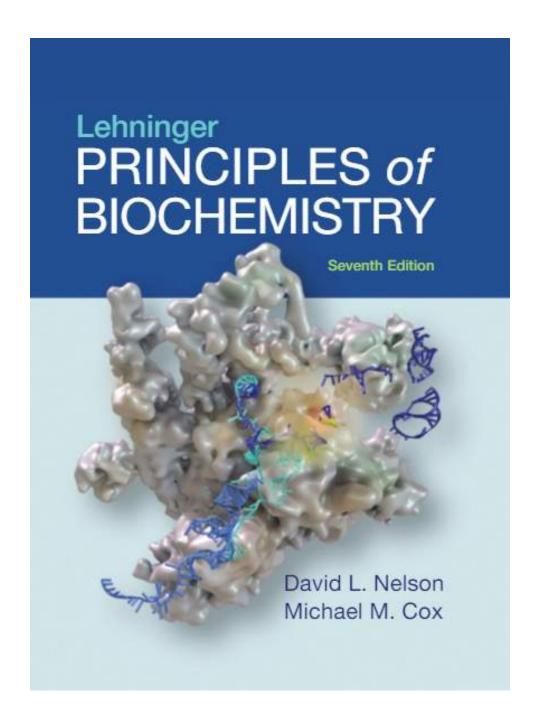


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What are enzymes

- Enzymes are catalysts.
 - increase reaction rates without being used up
- Most enzymes are proteins.
 - However, some RNA (ribozymes and ribosomal RNA)
 also catalyze reactions.
- The study of enzymatic processes is the oldest field of biochemistry, dating back to late 1700s.
- The study of enzymes has dominated biochemistry in the past and continues to do so.

Enzymes are macromolecular biological catalysts



The Structures of the Citric Acid Cycle

Acetyl-CoA This metabolic pathway is illustrated using protein structures from the Protein Data Bank. Illustration created with guidance from Fundamentals of Biochemistry. D. Voet, J. G. Voet, C. W. Pratt. (2002), John Wiley & Sons, Inc., New York, NY. Oxaloacetate Citrate L-Malate α-Ketoglutarate Succinate Succinyl-CoA

Also known as the Krebs cycle or the tricarboxylic acid cycle, the citric acid cycle is at the center of cellular metabolism. It plays a starring role in both the process of energy production and biosynthesis. The cycle finishes the sugar-breaking job started in glycolysis and fuels the production of ATP in the process. It is also a central hub in biosynthetic reactions, providing intermediates that are used to build amino acids and other molecules. Citric acid cycle enzymes are found in all cells that use oxygen, and even in some cells that don't.

Enzymes are extraordinary catalysts

高效催化剂!

TABLE 6-5

Some Rate Enhancements Produced by Enzymes

Cyclophilin	10 ⁵
Carbonic anhydrase	10 ⁷
Triose phosphate isomerase	10°
Carboxypeptidase A	10 ¹¹
Phosphoglucomutase	10 ¹²
Succinyl-CoA transferase	10 ¹³
Urease	10 ¹⁴
Orotidine monophosphate decarboxylase	10 ¹⁷

乳清酸脱羧酶(?)

Most enzymes are proteins

The Nobel Prize in Chemistry 1946



Sumner
Prize share: 1/2



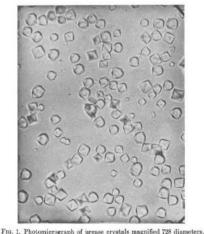
John Howard Northrop Prize share: 1/4



Wendell Meredith Stanley

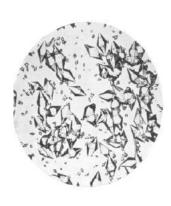
Prize share: 1/4

The Nobel Prize in Chemistry 1946 was divided, one half awarded to James Batcheller Sumner "for his discovery that enzymes can be crystallized", the other half jointly to John Howard Northrop and Wendell Meredith Stanley "for their preparation of enzymes and virus proteins in a pure form".



Octahedral crystals

of jack bean urease



Pepsin crystals

Some RNA can function as enzyme (Ribozyme): implications in the origin of life

The Nobel Prize in Chemistry 1989



Sidney Altman Prize share: 1/2



Thomas R. Cech Prize share: 1/2

RNase P

自剪切RNA(不算是真正的合酶,反应前后化学性质改变了)

Ribozyme

RNA message

The Nobel Prize in Chemistry 1989 was awarded jointly to Sidney Altman and Thomas R. Cech "for their discovery of catalytic properties of RNA"

RNA催化功能的发现支持了RNA世界假说

Cut (cleaved) RNA messages

Ribozyme-mediated cut

introduced into RNA message

Vocabularies

- Reactants in enzyme-catalyzed reactions are called substrates.
- Enzymes bring substrates together to form an enzyme-substrate complex on a particular region of the enzyme called the active site (catalytic site + binding site).
- Many enzymes require cofactors for activity. Cofactors are small molecules that some enzymes require for activity. The two main classes of cofactors are coenzymes (organic molecules derived from vitamins) and metals.
- Tightly bound coenzymes are called prosthetic groups.
- An enzyme with its cofactor is a holoenzyme. Without the cofactor, the enzyme is called an apoenzyme.

apo:empty(?)

PROTEIN STRUCTURE

Scaffold to support and position active site

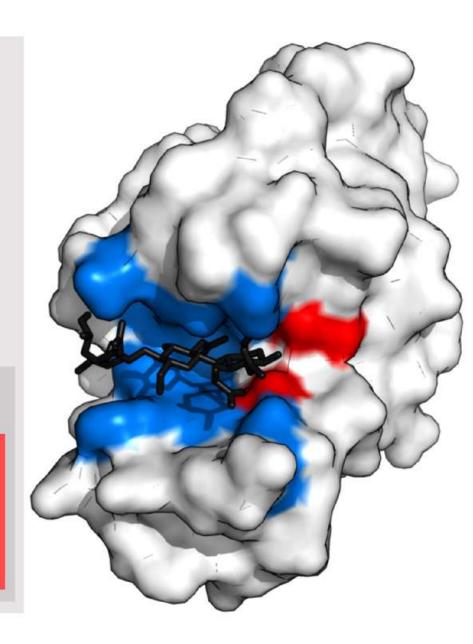
ACTIVE SITE

BINDING SITES

Bind and orient substrate(s)

CATALYTIC SITE

Reduce chemical activation energy



Cofactors and Coenzymes

Coenzyme	Examples of chemical groups transferred	Dietary precursor in mammals
Biocytin 生物胞素	CO ₂ 一碳单位载体!	Biotin 运搬
Coenzyme A	Acyl groups 乙酰基	泛酸 Pantothenic acid and other compounds
5'-Deoxyadenosylcobalamin (coenzyme B ₁₂) FAD	H atoms and alkyl groups H原子、烷基	Vitamin B ₁₂
Flavin adenine dinucleotide	Electrons	Riboflavin (vitamin B ₂)
Lipoate 硫辛酸 NAD	Electrons and acyl groups	Not required in diet
Nicotinamide adenine dinucleotide	Hydride ion (:H ⁻)	Nicotinic acid (niacin)
Pyridoxal phosphate 磷酸吡哆醛	Amino groups	Pyridoxine (vitamin B ₆)
Tetrahydrofolate 四氢叶酸	One-carbon groups	Folate
Thiamine pyrophosphate TPP	Aldehydes 醛基	Thiamine (vitamin B ₁)

Note: The structures and modes of action of these coenzymes are described in Part II.

Enzymes can be classified by the reactions they catalyze

TABLE 6-3 International Classification of Enzymes

		Class name	Type of reaction catalyzed	
脱氢酶	1	Oxidoreductases	Transfer of electrons (hydride ions or H atoms)	
转移酮	每 2	Transferases	Group transfer reactions	
水解酶	3	Hydrolases	Hydrolysis reactions (transfer of functional groups to water)	
裂合酶	4	Lyases	Cleavage of C—C, C—O, C—N, or other bonds by elimination, leavin bonds or rings, or addition of groups to double bonds	
异构酶	5	Isomerases	Transfer of groups within molecules to yield isomeric forms	
连接醛	6	Ligases	Formation of C—C, C—S, C—O, and C—N bonds by condensation reaction coupled to cleavage of ATP or similar cofactor	

IUBMB Enzyme Nomenclature

EC 2.7.1.1

2: class name (transferase);

7: subclass (phosphotransferase);

1: a hydroxyl group as acceptor; 羟基作为磷酸受体

1: D-hexose D-己糖

Reaction: ATP + D-hexose = ADP + D-hexose 6-phosphate

Accepted name: hexokinase

Other name(s): hexokinase type IV glucokinase; hexokinase D; hexokinase type IV; hexokinase (phosphorylating); ATP-dependent hexokinase; glucose ATP phosphotransferase

Systematic name: ATP:D-hexose 6-phosphotransferase

Comments: D-Glucose, D-mannose, D-fructose, sorbitol and D-glucosamine can act as acceptors; ITP and dATP can act as donors. The liver isoenzyme has sometimes been called glucokinase.

Links to other databases: BRENDA, EXPASY, GTD, KEGG, Metacyc, PDB, UM-BBD, CAS registry number: 9001-51-8

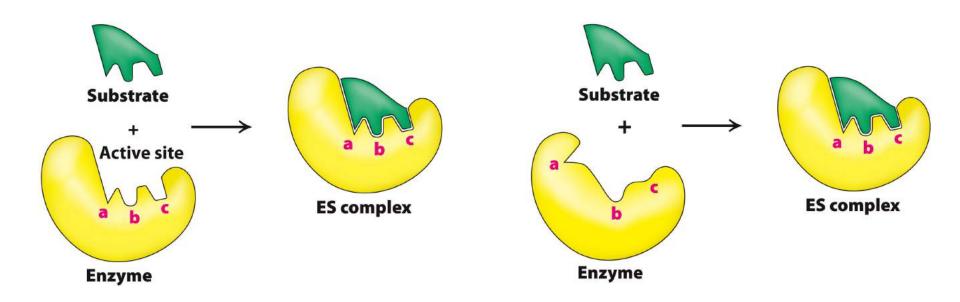
Enzymes display a high degree of specificity

NADP+ Unbound **Tetrahydrofolate Bound**

The specificity is due to the precise interaction of the enzyme and its substrate, achieved by binding pockets with complementary shape, charge and hydrophilic/hydrophobic properties of the substrates.

Dihydrofolate reductase

"Lock and key" vs "induced fit"

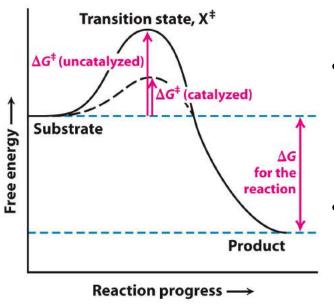


If so, there will not be catalysis.

Enzymes do not interact with their substrates like a lock and key.
Rather, the enzyme changes shape upon substrate binding, a phenomenon called induced fit.

Enzymes alter reaction rate, not equilibrium

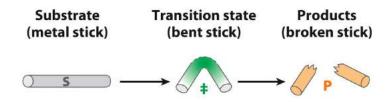
- A chemical reaction proceeds through a transition state, a molecular form that is no longer substrate but not yet product.
- The activation energy (ΔG^{\dagger}) is the difference between the energy levels of the ground state and the transition state.

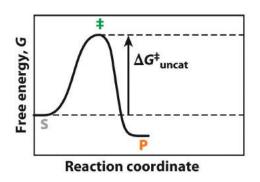


- Enzymes catalyze reaction by lowering down the activation energy.
- The reaction equilibrium is determined only by the free-energy difference between the products and reactants. Enzymes cannot alter this difference.
- In the presence of an enzyme, the reaction runs in the same direction as it would without the enzyme, just more quickly.

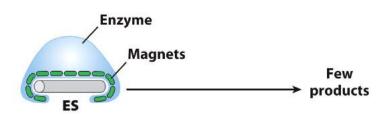
Enzymes facilitate formation of the transition state

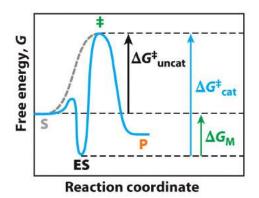
(a) No enzyme



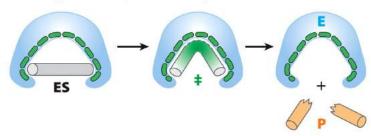


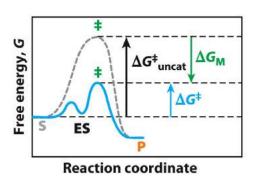
(b) Enzyme complementary to substrate





(c) Enzyme complementary to transition state







Common catalytic strategies

 General acid-base catalysis: A molecule other than water donates or accepts a proton. 广义酸碱催化

亲核基团

- Covalent catalysis: The active site contains a nucleophile that is briefly covalently modified. 共价催化
- Metal ion catalysis: Metal ions function in a number of ways, including serving as an electrophilic catalyst. 亲电催化
- Catalysis by approximation: The enzyme brings two substrates together in an orientation that facilitates catalysis.

临近定向效应

Proteases catalyze an energetically favorable, but kinetically difficult reaction

能量上有利,但是肽键稳定,不易反应

Chymotrypsin selectively hydrolyzes peptide bonds on the carboxyl side of large hydrophobic amino acids

Chymotrypsin is a proteolytic enzyme secreted by the pancreas that hydrolyzes peptide bonds selectively on the carboxyl side of large hydrophobic amino acids

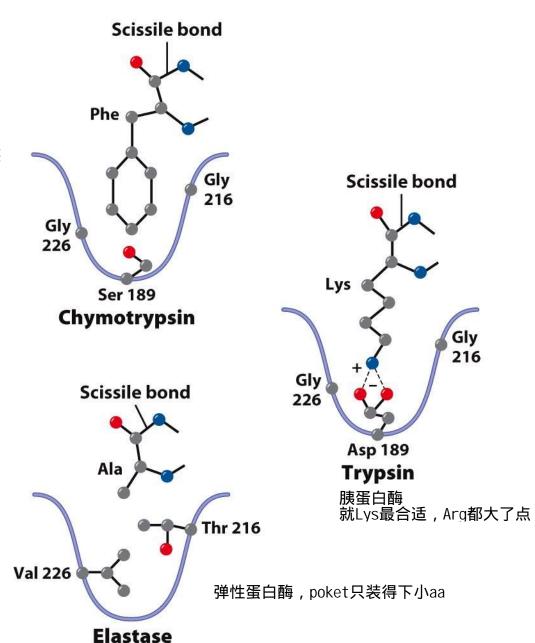
(b) (a) A chain 16 42 His⁵⁷ 58 **B** chain Asp¹⁰² (c) A chain **B** chain 122 136 146 149 168 182 C chain 191 Gly¹⁹³ Ser¹⁹⁵ (d) Gly¹⁹³ 201 Substrate Ser195 220 His⁵⁷ C chain 245 Hydrophobic pocket Asp¹⁰²

Chymotrypsin structure

- A binding site recognizes a large hydrophobic amino acids especially aromatic residues;
- A catalytic site contains a catalytic triad (Ser, His, Asp), which acts via a mixture of covalent and general acidbase catalysis to cleave a peptide bond.

Specificity of the serine proteases

口袋的形状及周围的aa决定了ser prE家族蛋白酶的特异性



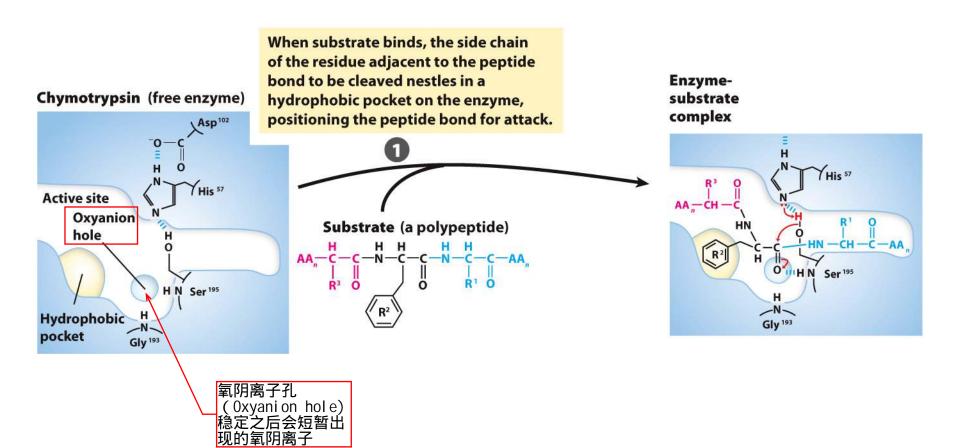
Catalytic triad 催化三联体

- Aspartate orients the histidine and renders it a better proton acceptor.
- Histidine removes a proton from serine 195, generating a highly reactive alkoxide ion (RO⁻).
- The alkoxide ion attacks the peptide bond of the substrate.

Nucleophiles	Electrophiles
Negatively charged oxygen (as in an unprotonated hydroxyl group or an ionized carboxylic acid) —s — Negatively charged sulfhydryl Carbanion —c — — — — — — — — — — — — — — — — — —	Carbon atom of a carbo (the more electronegative oxygen of the carbonyl group pulls electrons away from the carbon) Protonated imine group (activated for nucleophilic attack at the carbon by protonation of the imine) Phosphorus of a phosphate group Proton R Proton Proton Proton Proton Proton

- An electron-rich atom is called a nucleophile (Lewis base).
- An electron-deficient atom is called an electrophile (Lewis acid).
- Nonbonded electrons are designated by dots.
- Curved arrows represent the movement of electron pairs. (A single-headed arrow represents the movement of a single electron.)

Chymotrypsin MechanismStep 1: Substrate Binding



Step 2: Nucleophilic Attack

Enzymesubstrate complex

AA -CH -C

R2

Interaction of Ser¹⁹⁵ and His⁵⁷ generates a strongly nucleophilic alkoxide ion on Ser¹⁹⁵; the ion attacks the peptide carbonyl group, forming a tetrahedral acyl-enzyme. This is accompanied by formation of

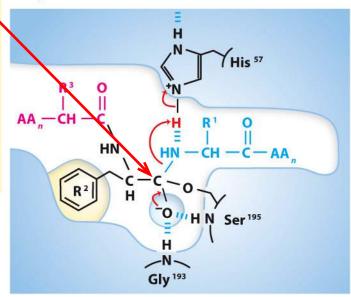
His 57

O'IIIHN Ser 195

Gly 193

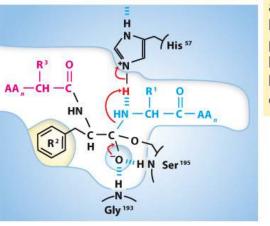
ashort-lived negative charge on the carbonyl oxygen of the substrate, which is stabilized by hydrogen bonding in the HN -CH -C-AA oxyanion hole.

Short-lived intermediate* (acylation)



Short-lived intermediate* (acylation)

Instability of the negative charge on the substrate carbonyl oxygen leads to collapse of the tetrahedral intermediate; re-formation of a double bond with carbon displaces the bond between carbon and the



amino group of the peptide linkage, breaking the peptide bond. The amino leaving group is protonated by His⁵⁷, facilitating its displacement.

Product 1

compared to C-O, C-N is easily
to break(peptide bond)

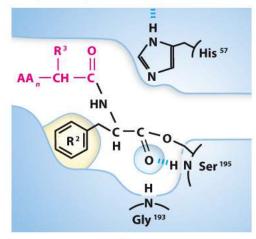
Step 3: Substrate Cleavage

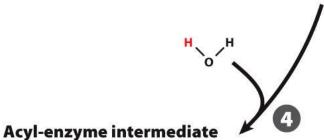
Acyl-enzyme intermediate

3

Step 4&5: Water Comes In and attacks

Acyl-enzyme intermediate



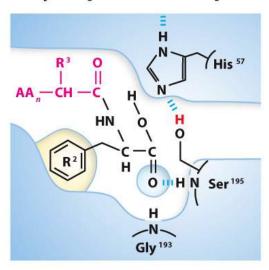


Short-lived intermediate * (deacylation)

6

An incoming water molecule is deprotonated by general base catalysis, generating a strongly nucleophilic hydroxide ion. Attack of hydroxide on the ester linkage of the acyl-enzyme generates a second tetrahedral intermediate, with oxygen in the oxyanion hole again taking on a negative charge.

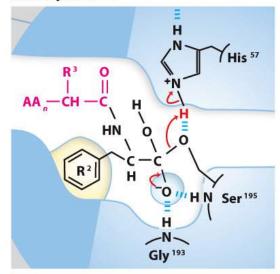
Enzyme-product 2 complex



6

Step 6: Break-off from the Enzyme

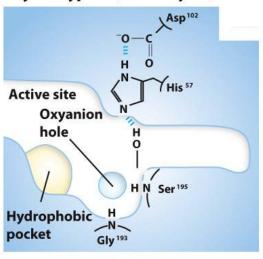
Short-lived intermediate * (deacylation)

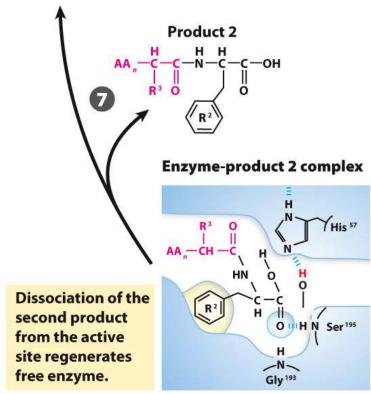


Collapse of the tetrahedral intermediate forms the second product, a carboxylate anion, and displaces Ser₁₉₅.

Step 7: Product Dissociates

Chymotrypsin (free enzyme)





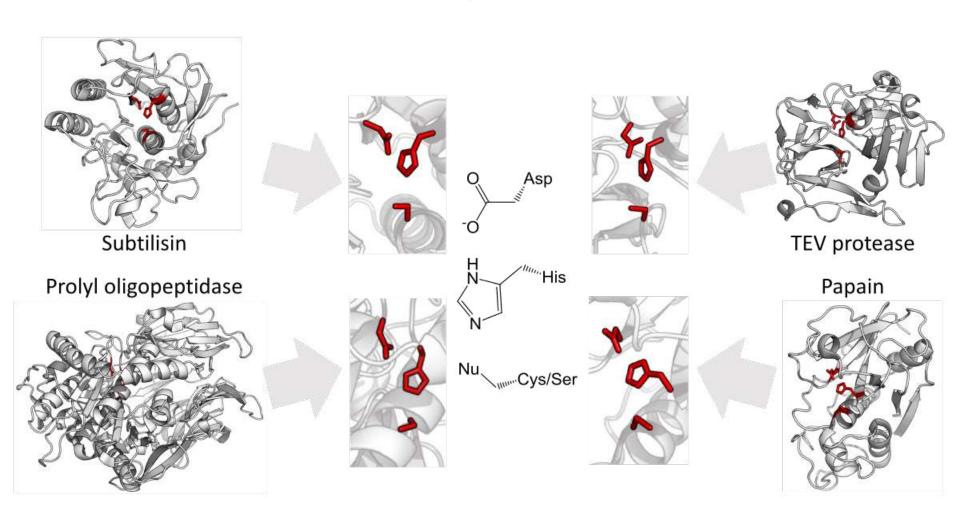
Catalytic triad

- An Acid-Base-Nucleophile triad is a common motif for generating a nucleophilic residue for covalent catalysis
- The acid residue (Asp, Glu) aligns and polarizes the base (His, Lys), which activates the nucleophile (Ser, Cys, Thr).
 The nucleophilic residue then attacks the substrate.
- An oxyanion hole in the enzyme (usually formed by backbone amides) stabilizes the negative charge on the alkoxide (RO⁻) during catalysis.
- Present in many hydrolases, including proteases, amidases, esterases, acylases, lipases, β-lactamases, etc.

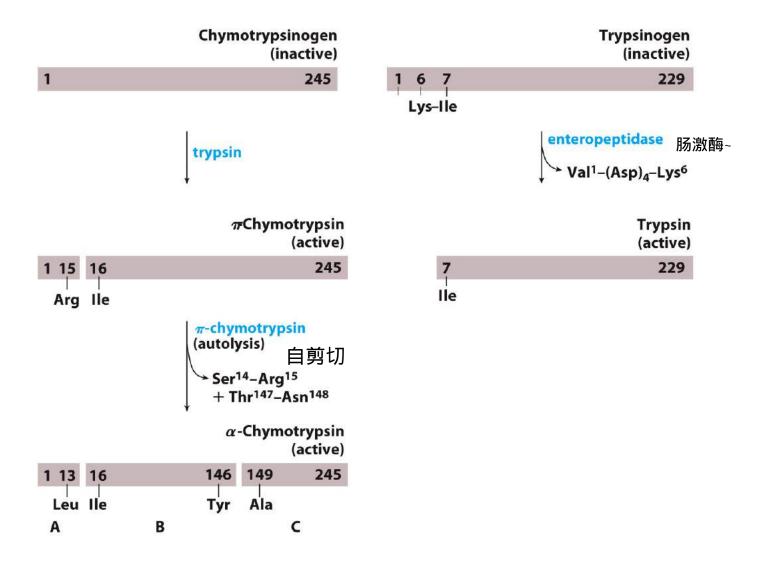
生成共价催化的亲核残基

Catalytic triad and Convergent evolution

催化三联体空间位置存在趋同演化



Zymogens are activated by irreversible covalent modification



Control of Enzymes

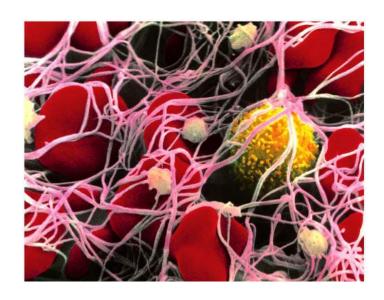
Five means to regulate enzymatic activity:

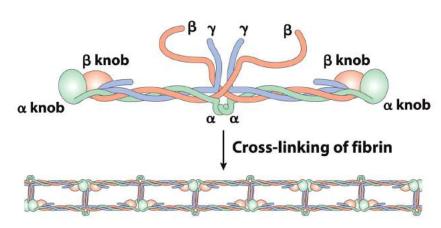
- 1. Multiple Forms of Enzymes 同工酶
- 2. Controlling the Amount of Enzyme Present
- 3. Proteolytic Activation
- 4. Reversible Covalent Modification
- 5. Allosteric Control

Many enzymes are regulated by multiple mechanisms.

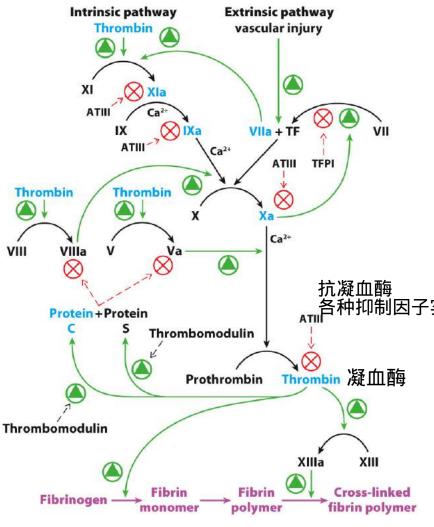
Blood clotting (Coagulation)

- Coagulation (also known as <u>clotting</u>) is the process by which blood changes from a liquid to a gel, forming a blood clot.
- A blood clot consists of aggregated platelets and red blood cells (erythrocytes), which are tied together by cross-linked fibrin.





The coagulation cascade



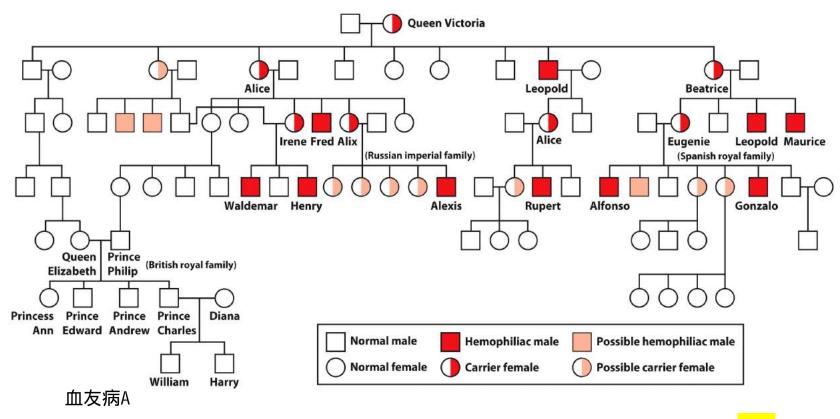
Blood clotting cascades can be initiated in two different ways that lead to a common end point.

- The extrinsic pathway is activated by the the tissue factor (TF).
- The intrinsic pathway is initiated by exposure of anionic surfaces of damaged tissue.

Most of the protein factors in the 实现对凝血级联反应的有效控制 coagulation cascade are designated by Roman numerals.

Many of these factors are chymotrypsinlike serine proteases that have <u>zymogen</u> <u>precursors</u> (the activated forms are indicated by a subscript "a").

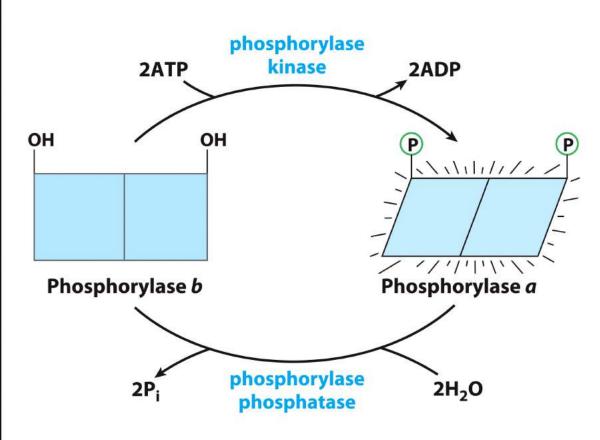
Coagulation defects can cause hemorrhage or thrombosis



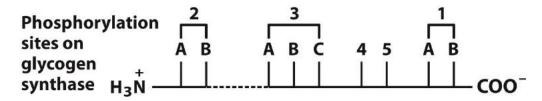
Hemophilia A, the royal disease, is caused by defect in the gene for factor VIII, which is located on the X chromosome

Covalent modification (Target residues) Phosphorylation (Tyr, Ser, Thr, His) ATP ADP Adenylylation 腺苷化 (Tyr) Adenine Acetylation (Lys, α -amino (amino terminus)) Acetyl-CoA HS-CoA Enzyme Enzyme Myristoylation $(\alpha$ -amino (amino terminus)) Myristoyl-CoA HS-CoA Enzyme Ubiquitination (Lys) **Activated ubiquitin** Activated ubiquitin HS- E2 Enzyme ADP-ribosylation ADP核糖基化 (Arg, Gln, Cys, diphthamide—a modified His) NAD nicotinamide Enzyme Enzyme Adenine Methylation (Glu) S-adenosyl- S -adenosylmethionine homocysteine Enzyme Enzyme -CH₃

Enzyme regulation by covalent modification



Multiple phosphorylation allow exquisite regulatory control

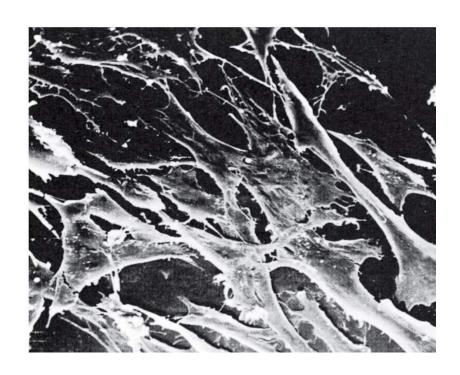


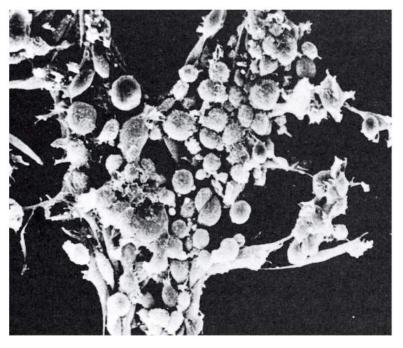
Kinase	Phosphorylation sites	Degree of synthase inactivation
Protein kinase A	1A, 1B, 2, 4	+
Protein kinase G	1A, 1B, 2	+
Protein kinase C	1A	+
Ca ²⁺ /calmodulin kinase	1B, 2	+
Phosphorylase <i>b</i> kinase	2	+
Casein kinase I	At least nine	+ + + +
Casein kinase II	5	0
Glycogen synthase kinase 3	3A, 3B, 3C	+ + +
Glycogen synthase kinase 4	2	+

多种磷酸化位点 多种激酶 可以实现对酶活性的精细调控

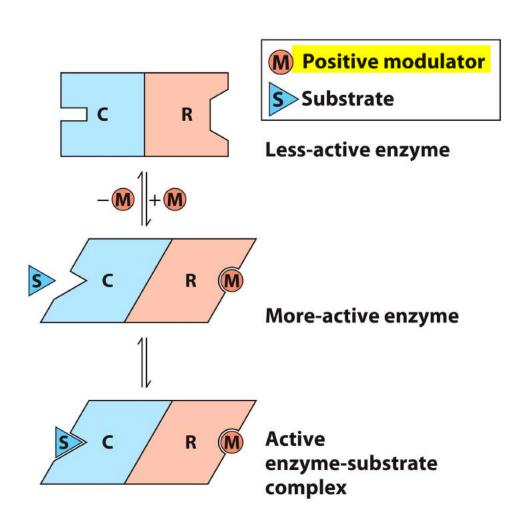
Loss of normal regulatory control can cause cancer

eg. some kinase lose control, stay active, the cell may keep mitoticing

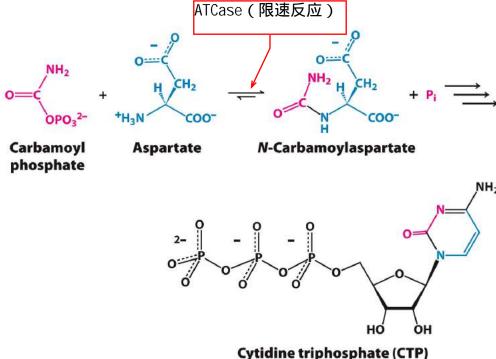




Allosteric enzymes

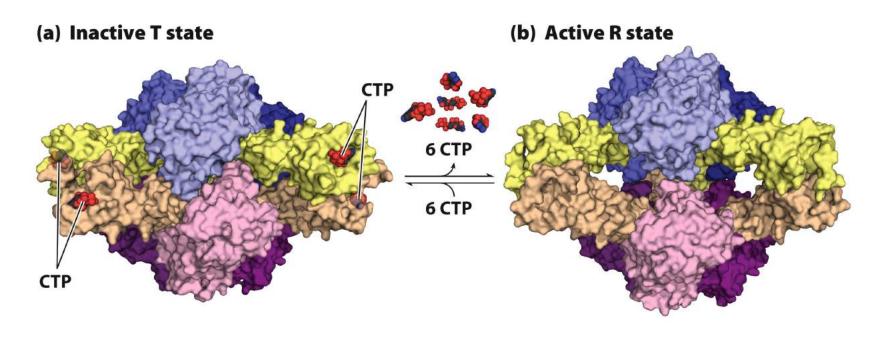


Aspartate transcarbamoylase is allosterically inhibited by the end product of its pathway



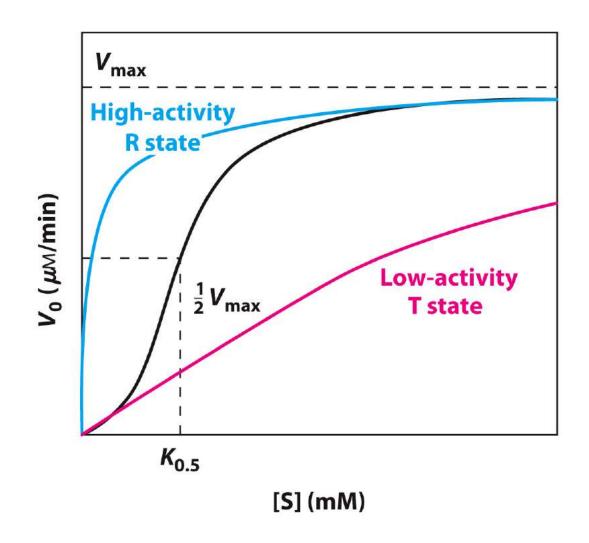
- Aspartate transcarbamoylase catalyzes the committed step, the condensation of aspartate and carbamoyl phosphate to form N-carbamoylaspartate, in pyrimidine synthesis.
- ATCase is activated by ATP and Asp (indicators of robust cellular metabolism), and inhibited by the end product of the pathway, CTP. 实现ATP\CTP数量的平衡
- ATP and CTP exert their effects by binding at distinct regulatory or allosteric sites on ATCase.

Allosteric regulation is mediated by conformational changes



- Native ATCase consists of six catalytic and six regulatory subunits (c_6r_6) .
- Free ATCase is in equilibirum between the T state (low activity) and the R state (high activity), with the T state being more favored.
- Binding of CTP to the regulatory site of ATCase alters the T-to-R equilibrium in favor of the T state.
- ATP and Asp alters the T-to-R equilibrium in favor of the R state.

The kinetic properties of allosteric enzymes can diverge from Michaelis-Menten behavior

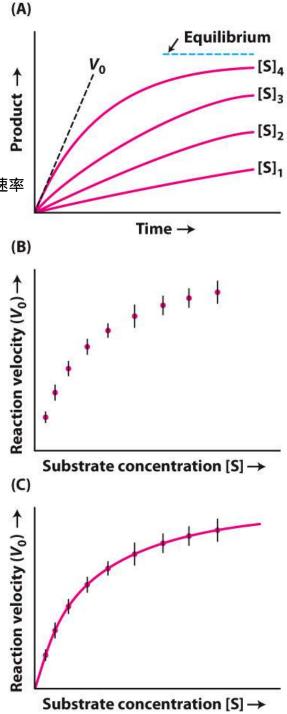


Kinetics is the study of reaction rates

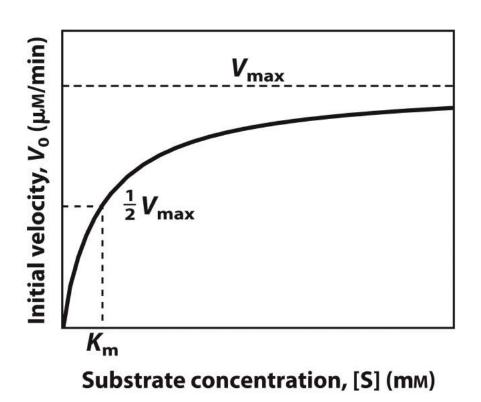
估算v0时的反应速率

Experiment:

- 1. Mix enzyme + substrate.
- Record rate of substrate disappearance and/or product formation as a function of time (the velocity of reaction).
- 3. Plot initial velocity versus substrate concentration.



The Michaelis-Menten equation



$$V_0 = V_{\text{max}} \frac{[S]}{[S] + K_{\text{M}}}$$

When $V_0 = \frac{1}{2} V_{max}$, $K_M = [S]$. K_M is the substrate concentration that yields $\frac{1}{2} V_{max}$.



Leonor Michaelis 1875–1949



Maud Menten 1879–1960

Consider a simple reaction in which the enzyme E catalyzes the conversion of $S \rightarrow P$.

$$E + S \stackrel{k_1}{\rightleftharpoons} ES \stackrel{k_2}{\rightleftharpoons} E + P$$

with k_1 , k_2 k_{-1} and k_{-2} being the rate constants for the indicated reaction steps. So as to ignore the reverse reaction of P \rightarrow S, we measure activity when [P] ≈ 0 .

$$E + S \xrightarrow{k_1} ES \xrightarrow{k_2} E + P$$

Under these conditions, the velocity is called the initial velocity or V_o.

初速度

$$V_0 = k_2 {
m [ES]}$$
 用产物生成的速率代表V0

At the **steady-state**, the rate of formation of ES is equal to the rate of its breakdown. Thus

$$k_1[E][S] = (k_{-1} + k_2)[ES]$$

This equation can be rearranged to

$$[E][S]/[ES] = (k_{-1} + k_2)/k_1$$

We can define a new constant, K_M, called the Michaelis constant.

$$K_{\rm M} = \frac{k_{-1} + k_2}{k_1}$$

Km的动力学含义

Thus

$$[E][S]/[ES] = (k_{-1} + k_2)/k_1$$

becomes

$$[ES] = \frac{[E][S]}{K_{M}}$$

The amount of free enzyme is equal to the total amount of enzyme present minus any enzyme bound to substrate.

$$[E] = [E]_T - [ES]$$

Substituting this equation for [E] in

$$[ES] = \frac{[E][S]}{K_{M}}$$

yields

$$[ES] = \frac{([E]_T - [ES])[S]}{K_M}$$

This equation can be rearranged to yield

[ES] =
$$[E]_T \frac{[S]}{[S] + K_M}$$

Recall that

$$V_0 = k_2[ES]$$

$$V_0 = k_2[E]_{\rm T} \frac{[S]}{[S] + K_{\rm M}}$$

The Michaelis-Menten equation

The maximal rate of catalysis, V_{max}, occurs when all of the enzyme is bound to substrate

$$[ES] = [E]_T$$

$$V_{\text{max}} = k_2[E]_{\text{T}}$$

Substituting the equation for
$$V_{\text{max}}$$
 into $V_0 = k_2[E]_T \frac{[S]}{[S] + K_M}$

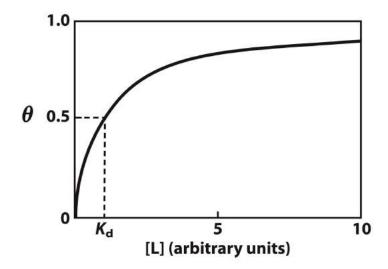
yields the Michaelis-Menten equation

$$V_0 = V_{\text{max}} \frac{[S]}{[S] + K_{\text{M}}}$$

Still remember K_d?

K_d equals to the molar concentration of free ligand concentration at which half of available binding sites are occupied.

$$\theta = \frac{\lfloor L \rfloor}{\lfloor L \rfloor + K_d}$$



K_M vs. K_d

$$E + S \xrightarrow{k_1} ES \xrightarrow{k_2} E + P$$

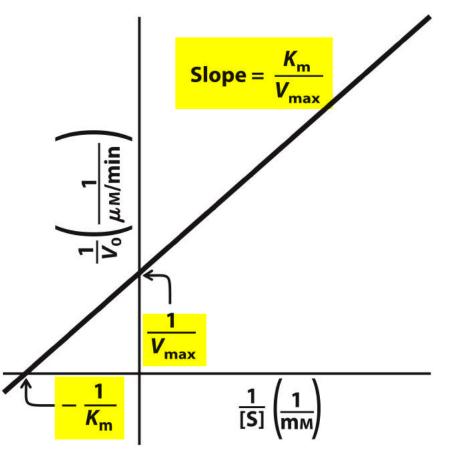
$$K_M = \frac{k_{-1} + k_2}{k_1}$$

$$Kd=k-1/k1$$

- If k_2 is rate-limiting, $k_2 << k_1$, $K_M = k_1/k_1$, which equals to the dissociation constant (K_d) of the ES complex. **Under this condition**, K_M represents a measure of affinity of the enzyme for its substrate in the ES complex (lower K_M , higher affinity and vice versa).
- If $k_2 >> k_1$, then $K_M = k_2/k_1$.
- If k_2 and k_1 are comparable, K_M is a complex function of all three rate constants.

The Lineweaver-Burk plot (Double-Reciprocal Plot)

双倒数作图



$$V = \frac{V_{\text{max}}[S]}{K_m + [S]}$$

Taking the reciprocal gives

$$\frac{1}{V} = \frac{K_m + [S]}{V_{\text{max}}[S]} = \frac{K_m}{V_{\text{max}}} \frac{1}{[S]} + \frac{1}{V_{\text{max}}}$$

Lineweaver & Burk (1934) The Determination of Enzyme Dissociation Constants, *J. Ame. Chem.Soc.* 56: 658–666.



Dean Burk (1904-1988)



Hans Lineweaver (1907-2009)

K_M is a constant for each substrate of an enzyme at a defined condition

TABLE 6-6	K _m for Some Enzymes and	d Substrates
-----------	--	--------------

Enzyme	Substrate	К _m (m м)
Hexokinase (brain) 己糖激酶	ATP D-Glucose D-Fructose	0.4 0.05 1.5
Carbonic anhydrase	HCO ⁻	26
Chymotrypsin	Glycyltyrosinylglycine N-Benzoyltyrosinamide	108 2.5
eta-Galactosidase	D- Lactose	4.0
Threonine dehydratase	լ-Threonine	5.0

Physiological implications of K_M: an example

Two enzymes play a key role in the metabolism of alcohol.

CH₃CH₂OH + NAD⁺
$$\stackrel{Alcohol}{\longleftarrow}$$
 CH₃CHO + NADH + H⁺

Some people respond to alcohol consumption with facial flushing and rapid heart beat, symptoms caused by excessive amounts of acetaldehyde in the blood. There are two different acetaldehyde dehydrogenase in most people, one with a low K_M and one with a high K_M . The low K_M enzyme is inactivated in susceptible individuals. The enzyme with the high K_M cannot process all of the acetaldehyde, and so some acetaldehyde appears in the blood.

The turnover number

$$k_{cat} = V_{max}/[Enzyme]$$

Km与酶浓度无关,但是Vmax与酶浓度有关 把酶浓度除了就是常数了!

k_{cat} is also called the **turnover number**. It is equivalent to the number of substrate molecules that are converted to product in a given unit of time on a single enzyme (when the enzyme is saturated with substrate)

TABLE 6-7	Turnover Number, <i>k</i> _{cat} , of Some Enzymes
-----------	--

Enzyme	Substrate	$\mathbf{k}_{\mathrm{cat}}(\mathrm{s}^{-1})$
Catalase	H ₂ O ₂	40,000,000
Carbonic anhydrase	HCO ₃	400,000
Acetylcholinesterase	Acetylcholine	14,000
$oldsymbol{eta}$ -Lactamase	Benzylpenicillin	2,000
Fumarase	Fumarate	800
RecA protein (an ATPase)	ATP	0.5

k_{cat}/K_M (specificity constant) is a measure of catalytic efficiency

TABLE 6-8 Enzymes for Which k_{cat}/K_m Is Close to the Diffusion-Controlled Limit (10° to 10° m⁻¹s⁻¹)

Enzyme	Substrate	K _{cat} (s ⁻¹)	К _м (м)	Κ_{cat}/K _m (м ⁻¹ s ⁻¹)
Acetylcholinesterase	Acetylcholine	1.4 × 10 ⁴	9 × 10 ⁻⁵	1.6 × 10 ⁸
Carbonic anhydrase	CO ₂ HCO ₃	1 × 10 ⁶ 4 × 10 ⁵	1.2×10^{-2} 2.6×10^{-2}	8.3×10^7 1.5×10^7
Catalase	H ₂ O ₂	4×10^7	$1.1 \times 10^{\circ}$	4×10^7
Crotonase	Crotonyl-CoA	5.7×10^3	2 × 10 ⁻⁵	2.8×10^8
Fumarase	Fumarate Malate	8×10^{2} 9×10^{2}	5×10^{-6} 2.5 \times 10 ⁻⁵	1.6×10^{8} 3.6×10^{7}
β -Lactamase	Benzylpenicillin	2.0×10^{3}	2 × 10 ⁻⁵	1 × 10 ⁸

Source: Fersht, A. (1999) Structure and Mechanism in Protein Science, p. 166, W. H. Freeman and Company, New York.

- The value of k_{cat}/K_M has an upper limit. It can be no greater than the rate at which E and S can diffuse together to form ES (k_1) .
- The most efficient enzymes have k_{cat}/K_M values near the diffusion-controlled limit of 10^8 to 10^9 M⁻¹S⁻¹. Such enzymes are catalytically perfect.

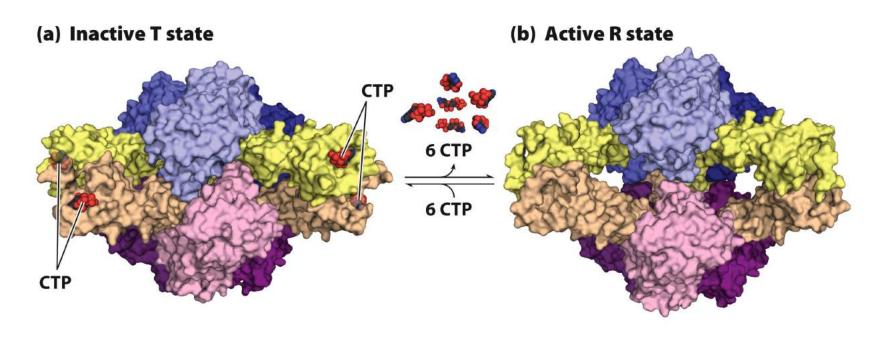
Not all enzymes display Michaelis-Menten behavior _{别构酶不遵循米氏方程!!}

High-activity R state V₀ (µM/min) **Low-activity** $\frac{1}{2}V_{\text{max}}$ T state $K_{0.5}$ [S] (mM)

Aspartate transcarbamoylase is allosterically inhibited by the end product of its pathway

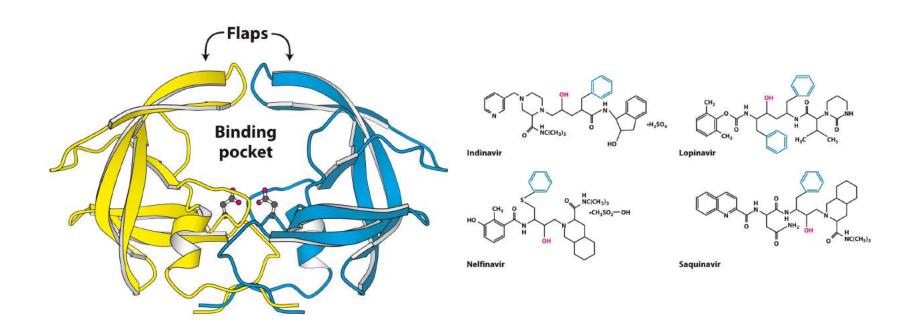
- Aspartate transcarbamoylase catalyzes the committed step, the condensation of aspartate and carbamoyl phosphate to form N-carbamoylaspartate, in pyrimidine synthesis.
- ATCase is activated by ATP and Asp (indicators of robust cellular metabolism), and inhibited by the end product of the pathway, CTP.
- ATP and CTP exert their effects by binding at distinct regulatory or allosteric sites on ATCase.

Allosteric regulation is mediated by conformational changes



- Native ATCase consists of six catalytic and six regulatory subunits (c_6r_6).
- Free ATCase is in equilibirum between the T state (low activity) and the R state (high activity), with the T state being more favored.
- Binding of CTP to the regulatory site of ATCase alters the T-to-R equilibrium in favor of the T state.
- ATP and Asp alters the T-to-R equilibrium in favor of the R state.

Enzyme inhibitors



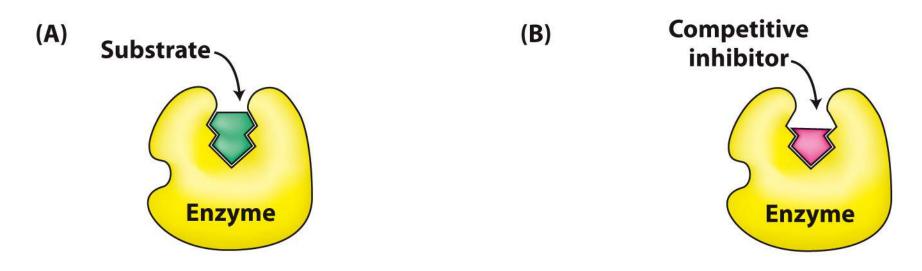
Enzymes can be inhibited by specific molecules

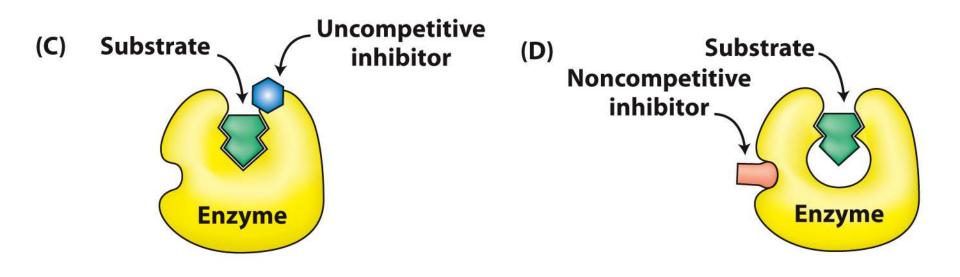
Reversible inhibition is characterized by a rapid dissociation of the enzyme-inhibitor complex.

There are three common types of reversible inhibition:

- **1.** Competitive inhibition: The inhibitor is structurally similar to the substrate and can bind to the active site, preventing the actual substrate from binding.
- 2. Uncompetitive inhibition: The inhibitor binds only to the enzyme-substrate complex in what is essentially substrate-dependent inhibition.
- 3. A **mixed inhibitor** also binds to an allosteric site, but it binds to either E or ES. In **Noncompetitive inhibition**, the inhibitor binds to either E or ES equally well.

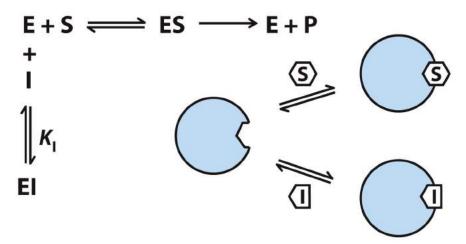
Irreversible enzyme inhibitors bind covalently, or noncovalently to the enzyme but with a negligible dissociation constant.





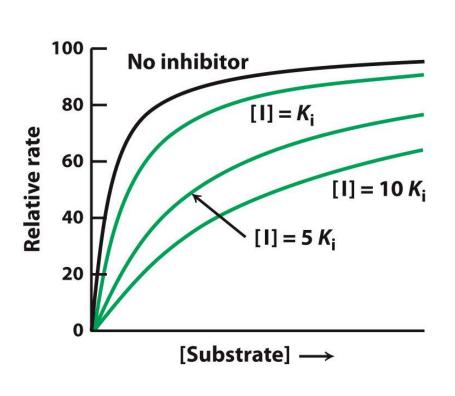
Competitive Inhibition

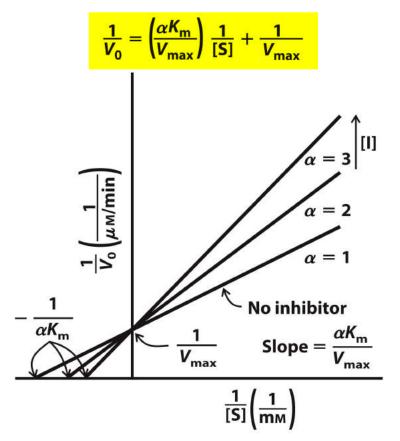
Competitive inhibition



- Competes with substrate for binding
- Does not affect catalysis
- No change in V_{max} (because the inhibition can be overcome by a sufficiently high concentration of substrate)
- Increase in apparent K_M

Competitive Inhibition

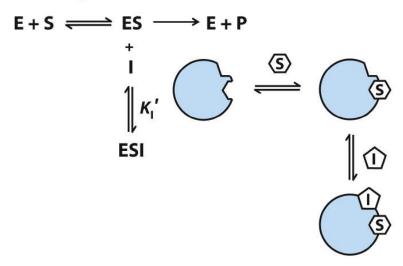




Uncompetitive Inhibition

反竞争性抑制剂

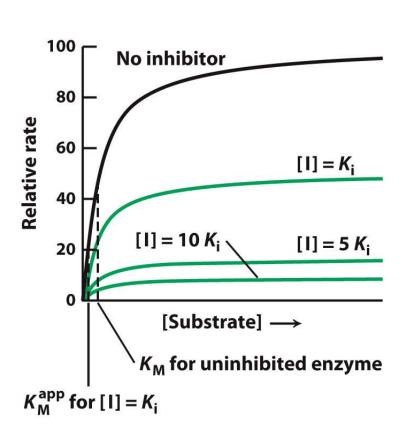
Uncompetitive inhibition

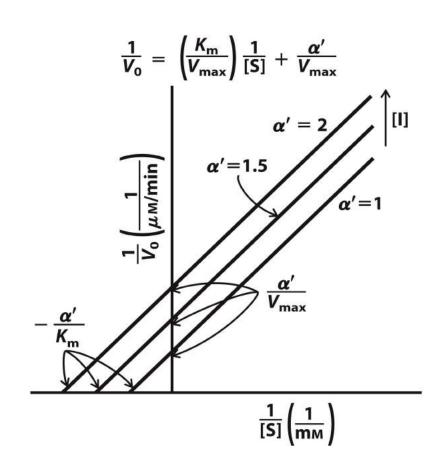




- Only binds to ES complex
- Decrease in V_{max}
- Apparent decrease in K_M

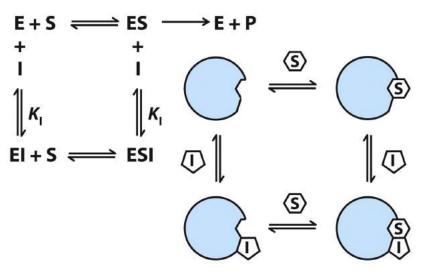
Uncompetitive Inhibition

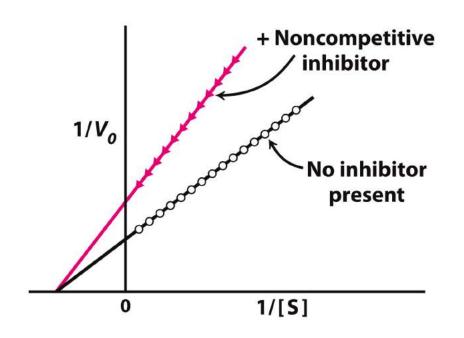




Noncompetitive inhibition 非竞争性抑制剂

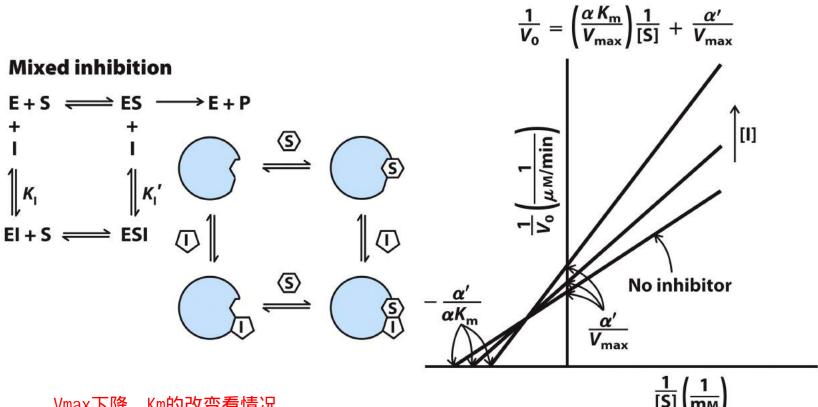
Noncompetitive inhibition





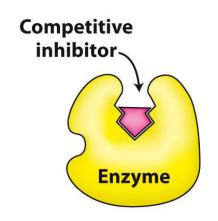
- K_M is not changed.
- V_{max} is lower.
- Lineweaver-Burk: lines intersect at the x-axis.

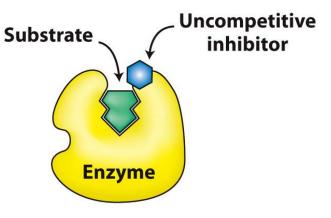
A mixed inhibitor binds to either E or ES

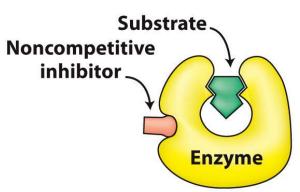


(结合E强点还是结合ES强点) 结合E强:Km升高,交点在第二

合ES强:Km降低,交点在第







$$E+S \Longrightarrow ES \longrightarrow E+P \qquad E+S \Longleftrightarrow ES \longrightarrow E+P$$

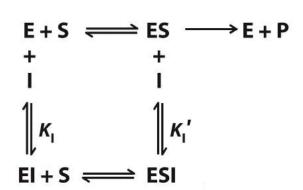
$$\uparrow \qquad \qquad \uparrow \qquad \qquad \uparrow \qquad \qquad \downarrow \\ ||\kappa_1| \qquad \qquad ||\kappa_1'| \qquad ||\kappa_1'| \qquad ||\kappa_1'| \qquad \qquad ||\kappa_1'| \qquad ||\kappa_1$$

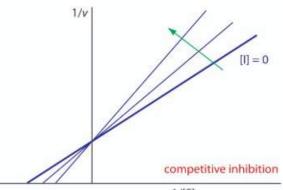
$$E + S \Longrightarrow ES \longrightarrow E + I$$

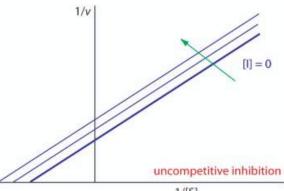
$$\downarrow I$$

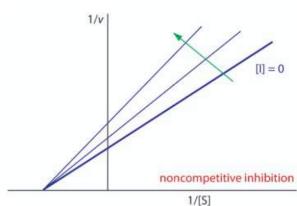
$$\downarrow K_{I}'$$

$$ESI$$





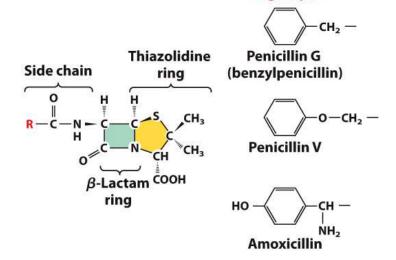








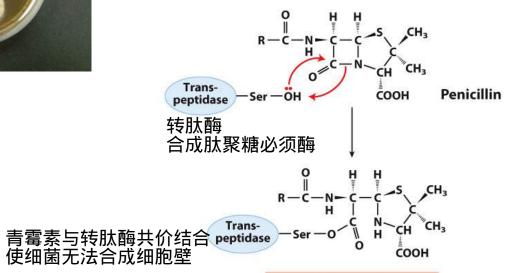
Alexander Fleming 1945 Nobel Prize



R groups

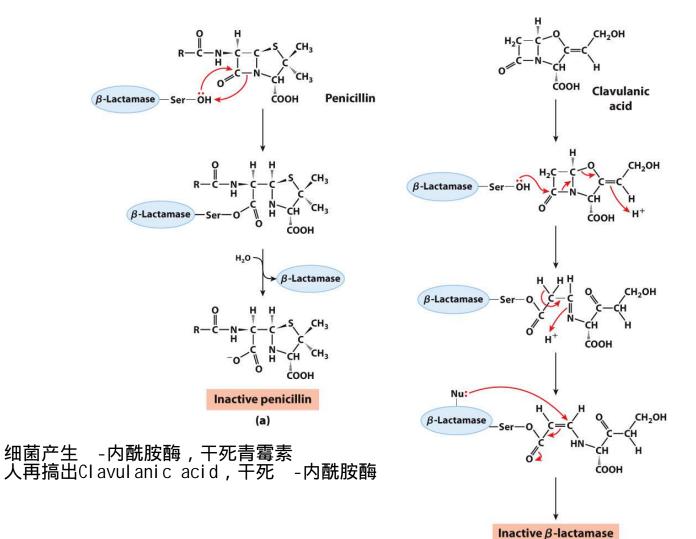
General structure of penicillins

(a)



Stably derivatized, inactive transpeptidase

Chemical warfare between us and bacteria continues



(b)

Most biochemical reactions include multiple substrates

$$A + B \Longrightarrow P + Q$$

There are two classes of multiple substrate reactions: sequential and double-displacement reactions.

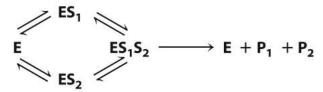
Sequential reactions, which may be random or ordered, are characterized by the formation of a ternary complex consisting of the enzyme and both substrates.

Double-displacement reactions are characterized by the formation of a substituted enzyme intermediate.

(a) Enzyme reaction involving a ternary complex

Ordered
$$E + S_1 \rightleftharpoons ES_1 \rightleftharpoons ES_1S_2 \longrightarrow E + P_1 + P_2$$

Random order



(b) Enzyme reaction in which no ternary complex is formed

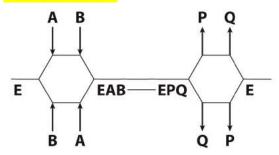
$$E + S_1 \Longrightarrow ES_1 \Longrightarrow E'P_1 \stackrel{P_1}{\Longrightarrow} E' \stackrel{S_2}{\Longleftrightarrow} E'S_2 \longrightarrow E + P_2 \qquad \qquad \stackrel{A}{\downarrow} \qquad \qquad \stackrel{P}{\downarrow} \qquad \qquad \downarrow$$

(c) Cleland nomenclature

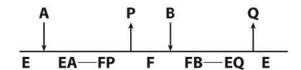
Ordered bi bi



Random bi bi



(d) Ping-Pong in Cleland nomenclature



Enzyme kinetics allows to distinguish between different kinetic mechanisms



(a) Enzyme reaction involving a ternary complex

Random order

$$E = \underbrace{ES_1}_{ES_2} S_2 \longrightarrow E + P_1 + P_2$$

Ordered
$$S_2$$

 $E + S_1 \Longrightarrow ES_1 \Longrightarrow ES_1S_2 \longrightarrow E + P_1 + P_2$

(b) Enzyme reaction in which no ternary complex is formed

$$E + S_1 \rightleftharpoons ES_1 \rightleftharpoons E'P_1 \rightleftharpoons E'S_2 \longrightarrow E + P_2$$

