

ENZYMES: Binding & Catalysis

A. Binding

B. Catalysis

C. Nomenclature

D. Catalysis

1. Transition State Theory
2. Catalytic strategies (What)
3. Mechanistic strategies (How)

E. Quantifying the Catalytic Power: Kinetics

1. Review
2. Enzyme Kinetics
3. Initial rate (v_0) vs. $[S]$ for enzymic reaction;
4. ES complex
5. Rate expression; Michaelis-Menten Kinetics (M-M)
6. Meaning of rate expression (M-M eqn)
7. Collection and manipulation of data
 - a. Lineweaver-Burk; double reciprocal; $1/v_0$ vs. $1/[S]$
8. Inhibition
 - a. Irreversible: protein modification
 - b. Reversible: Competitive, Uncompetitive, Noncompetitive

F. Active-site identification

- a. Determine mechanism-ordered *versus* random
- b. pH studies;
- c. Protein modification; Irreversible
- d. X-ray crystallography structure; cleft

G. Energetics of Catalysis

- a. The $\Delta\Delta G^\ddagger$ is negative
- b. The $\Delta\Delta G^\ddagger = \Delta\Delta H^\ddagger - T\Delta\Delta S^\ddagger$; bonding effects &

TODAY
 •Reading: Ch5; 157
 Ch12; 413-415

NEXT
 •Reading: Ch5; 157-160
 Ch6; 213-220

•Homework #18

Lecture 17 (10/23/24)

proximity/position effects

- a. Rate dependent on $(kT/h)\text{EXP}(-\Delta G^\ddagger/RT)$
- b. Example of enzyme;
 - I. Proline Racemase
 - II. HIV protease; tetrahedral t.s. seen in two nM inhibitors ($K_i < 1 \text{ nM}$); bioavailability

H. Enzyme Mechanisms**a. Proteases**

1. Introduction; roles and types
 - i. Roles: Serine:
 - ii. Types: based on mechanism; Serine, Thiol, Carboxy (acid), Metallo

b. Serine Proteases

1. Reaction & specificity
2. Activation (zymogens); Ile a-amino pKa impt.
3. Active Site Determination
 - i. esterase activity
 - ii. burst kinetics \Rightarrow two-steps (Ping-pong bi bi)
 - iii. protein modification
 - iv. pH studies
 - v. X-ray crystallography
4. Proposed mechanism
 - i. Catalytic triad (Ser-His-Asp) – highly conserved
 - ii. Mechanism; tetrahedral intermediates and stabilize t.s. with oxy-anion hole
 - iii. Old; charge relay (but Ser-195 does not have the correct pKa)
 - iv. Low-barrier Hydrogen bonds- Role for Asp
5. Specificity
 - i. Chymotrypsin *versus* elastase

c. Other protease mechanisms**I. Enzyme Regulation****a. Introduction****b. Strategies**

- a. Gene Regulation
- b. Covalent Modification
- c. Allosteric Control

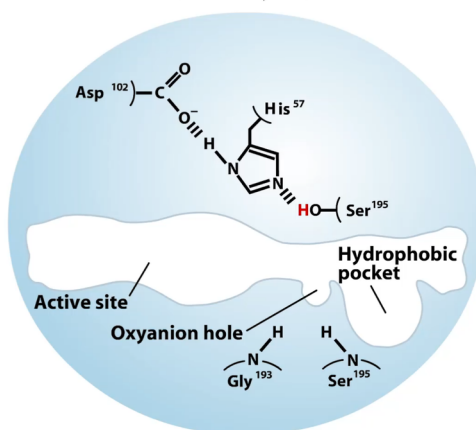
c. Covalent Modification

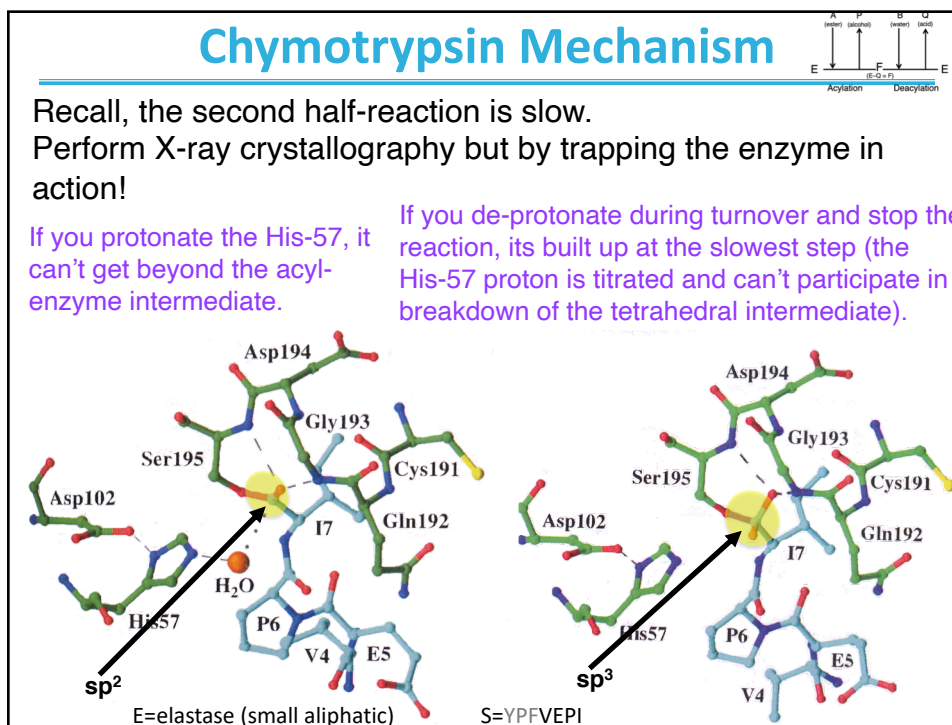
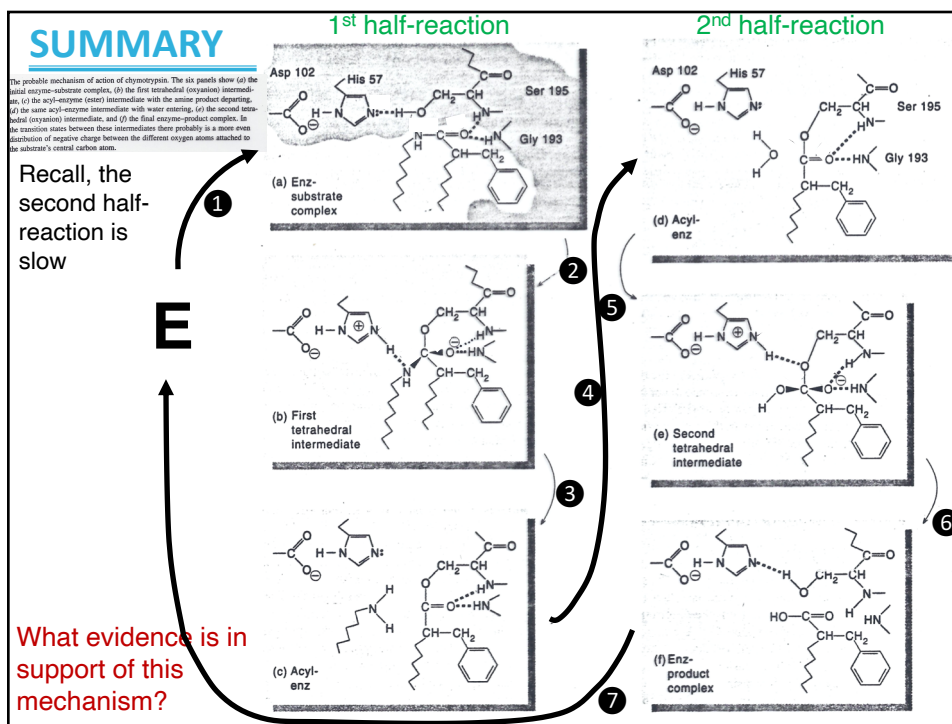
1. Proteolysis
2. Protein modification
 - i. Phosphorylation
 - a) Kinases
 - b) Phosphatase

Chymotrypsin Mechanism

Animation

Chymotrypsin
(free enzyme)





• Enzyme mechanism and binding energy

Chymotrypsin Mechanism

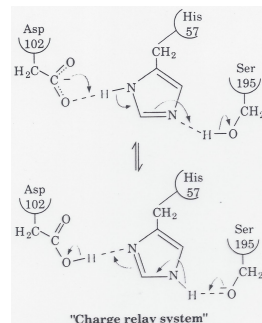
The “catalytic triad”

Asp102 – His57 – Ser195

The catalytic triad is found in all Serine Protease and Serine Esterases (e.g., acetylcholinesterase)

How does this work?

For this to work, all pK_a values should be similar. In other words, pK_a value of Asp slightly higher than that of Ser



Asp102 – His57 – Ser195

pK_a values as amino acids are: 3.5 6.0 15.0

The measured pK_a values are: 7.0 7.0(12.0)* 15.0

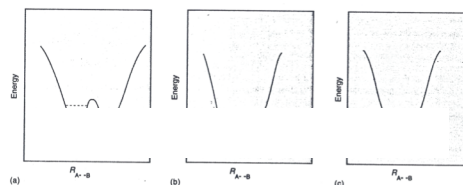
*only transiently

• Enzyme mechanism and binding energy

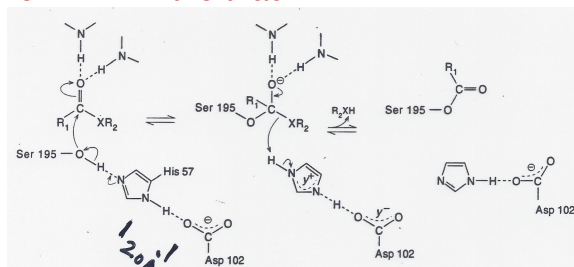
Chymotrypsin Mechanism

Low-barrier H-bond in the Transition State?

What is a Low-Barrier H-bond?



Where is the LBHB in the triad?



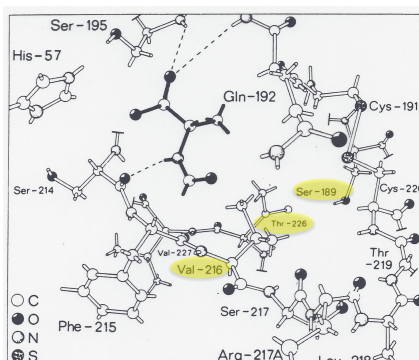
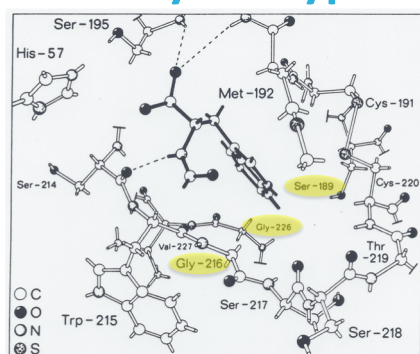
2.8 Å
2.0 Å
1.5 Å

What is significant about LBHBs is that they are 4-5x stronger than normal 2.8 Å H-bonds (~20 kcal/mole)

Enzymes

Substrate Specificity

Chymotrypsin vs. Elastase

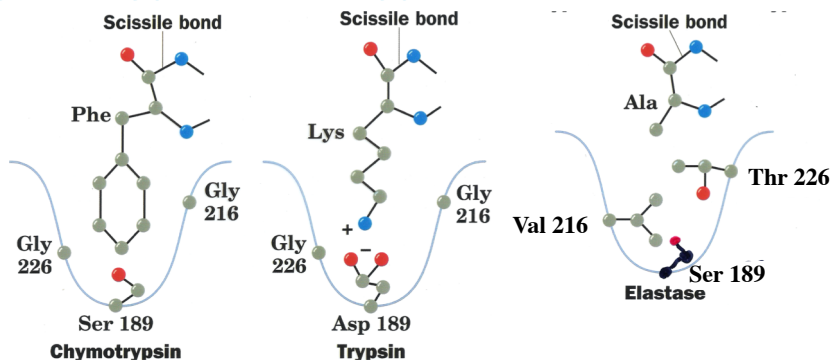


Trypsin is much like Chymotrypsin except for a Asp-189 instead of Ser-189.

Enzymes

Substrate Specificity

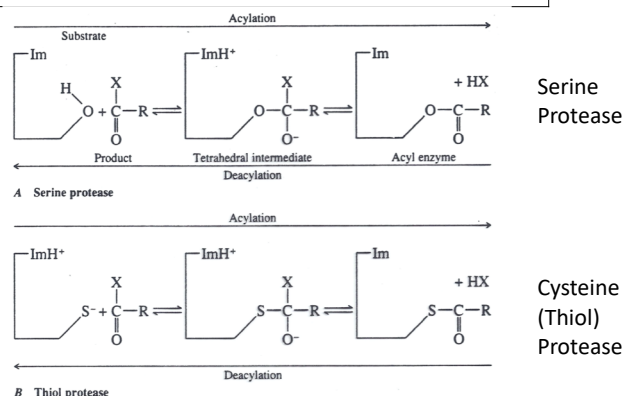
Chymotrypsin vs. Trypsin vs. Elastase



Enzymes

Class of Protease	Examples
Serine	Trypsin, Chymotrypsin, Elastase
Thiol	Papain, Cathepsin B, Caspases
Acid	HIV protease, Pepsin, Cathepsin D, Renin, Chymosin
Metal	Carboxypeptidase A, Thermolysin

Very similar with acylation/deacylation half-reactions



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