## Slide :Enzymes 3

Dr. Name Nayef Karadsheh •
Sections: . $4,2,5,6$
$\square$ Slide $\square$ Sheet

Medical Committee The University of Jordan


General Strategies of Enzyme Catalo:

- Proximity and Orientation
- Transition state Stabilization
- Acid -base Catalysis
- Nucleophilic Catalysis
- Electrophilic Catalysis
- Covalent Catalysis

Chymotrypsin:-
Employs

Proteins with A common Catalytic Mechamism:

- Protecilytic en 2 ymes are classified by their catalytic mechanism
- Serine proteases
- Aspartate proterses
- metalloproteases
- endopeptidases
- exopepticlases

Aspartic protease familly
e.g. pepsin, lysosomal cathepsin, HIl puthense


## B. The active site of chymotrypsin

Chymotrypsin is a proteolytic enzyme secrated into the simail intestine by the pancreas in the form of an inactive precursor or zymogen called chymotrypsinogen. Chymotrypsinogen, which has a single polypeptide chain of 245 residues and five intrachain disulfide tross-links contributed by five cystine residues, is activated by the action of trypsin, another proteolytic enzyme in the intestine. Trypsin removes two dipeptides from positions $14-15$ and 147-148 of chymotrypsinogen" by hydrolysis to yield active chymotrypsin, which thus has thrae polypeptide chains, covalently connected by two disulfide cross-links, one between chains A and B ard the other between chains B and C,
as sbown in Figure 1. Chymotrypsin requires for activity histidine residue 57 and aspertic acid residue 102 in chain B, as well as serine residue 195 in chain C. Although they are far apart in the sequence, and one is actually in a different chain from the others, these three residues lie very close together in the three-dirnensional structure of the enzyme molecule. This is shown in the scale drawing of the backbone of the chymotrypsin molecule (Figure 2), as deduced from the x-ray diffraction pattern of crystalline chymotrypsin by David M. Blow and his colleagues of the University of Cambridge. In this drawing tha R groups of only the three specific residues at the active site are shown.


I Ansaty

Proteolysis in the absence of chymotrypsin:

A
$\cdots$


B
Unstable tetra hedtral any
anion infer mediate. transition state
complex"

C



Serine Proteases: family onzymes uses serin residue. in catalytic site to. hydrolyze peptide bonds. e.g. trypsin,
chymotrypsin and: thrombin

- Rave a catalytic triad of ser. His and Asp.
- form covalent-agy enzyme intermediate.

Steps in the cleavage of a peptide bond by chymotrypsin:-
mformational mange
His activates ser for nucleophillic attack

leavage of peptide bond
-CH:
First tetrahedral
(b) intermediate


Acyl-
(c) enzyme


Water attacks the carborylearbon


Second bey groin cefintifin/ cithencerter

(e) intermediate (e) intermediate
Acid entugris Greater ina
dey vincent bond

$\square$ C. Brown Communications, inc., Dubuque, Iowa. All Rights Reserved.

## Energy cliagram for the

 reaction catalyzed by> Second enzyme-stabilized CHYMOTRYPSIN

,


Mechanism of Enzyme Action


(a)


(b)
3. Catalytic effect (acid-base catalysis)
4. Energy effect: lower the energy barrier by inducing straci in bonds

(c)

