

Covalent Cats - Proteases

4 classes of proteases: Serine, Thiol (Cys), Acid (Aspartyl), & Metal (Zn)

The diagram illustrates the catalytic mechanisms of four classes of proteases:

- a Serine protease:** Shows a catalytic triad (Asp-His-Ser) where the serine residue attacks the carbonyl carbon of the substrate peptide bond.
- b Cysteine protease:** Shows a catalytic dyad (Cys-His) where the cysteine residue attacks the carbonyl carbon.
- c Acid protease:** Shows two aspartate residues (Asp) that facilitate the deprotonation of the substrate, leading to the cleavage of the peptide bond.
- d Metalloprotease:** Shows a zinc ion (Zn²⁺) coordinated to the carbonyl oxygen and the nitrogen of the scissile bond, facilitating the cleavage.

Roles

Function	Protease ex.
Nutrition	trypsin, subtilisin, α -lytic protease
Invasion	matrix metalloproteases
Evasion	IgA protease
Adhesion	ADAM (a disintegrin and metalloproteinase)
Processing	signal peptidase, viral proteases, proteasome
Signalling	caspases, granzymes

The diagram shows a human figure with various physiological processes labeled, each associated with specific proteases:

- Secretion:** signal peptidases
- Adhesion:** P. gingivalis protease
- Immune Response:** T-cell protease
- Blood pressure regulation:** renin
- Development:** matrix protease
- Digestion:** trypsin
- Complement Fixation:** C1 protease
- Reproduction and Fertilization:** acrosome
- Fibrinolysis:** tissue plasminogen activator
- Hormone Processing:** Kex 2
- Pain Sensing:** kallikrein
- Animal Virus Replication:** HIV protease
- Cell fusion:** hemagglutinin
- Immune Response:** tumor invasion, collagenase

Substrate Specificity

Binding pocket is responsible for affinity

The diagram illustrates the binding pockets of three proteases and their specificities:

- Trypsin:** Binds basic amino acids (Asp, Lys, Arg) at the P1 position.
- Chymotrypsin:** Binds aromatic amino acids (Phe, Tyr, Trp) at the P1 position.
- Elastase:** Binds small, non-polar amino acids (Ala, Val, Gly) at the P1 position.

The diagram also shows the scissile bond and the catalytic triad (Ser 195, His 57, Asp 102) for each protease.

Serine Proteases

Ser, His and Asp in active site

The diagram shows the catalytic triad in a serine protease active site, consisting of Ser 195, His 57, and Asp 102. The triad is shown in a 3D representation, with the serine residue attacking the carbonyl carbon of the substrate peptide bond.

Ser Proteases Multiple Mechanism

- Serine not generally an active amino acid for acid/base catalysis
- Catalytic triad of serine, histidine and aspartate responsible for the reactivity of serine in this active site
- Covalent catalysis, Acid/base Catalysis, transition state binding and Proximity mechanisms are used
- Two phase reaction when an ester is used
 - burst phase - E + S initial reactions
 - steady state phase - EP \rightarrow E + P (deacylation)
 - The first step is the covalent bond to the enzyme itself

The diagram illustrates the catalytic mechanism of a serine protease, showing the formation of a covalent intermediate. The serine residue (Ser 195) attacks the carbonyl carbon of the substrate, forming a tetrahedral intermediate. The histidine residue (His 57) acts as a general base, deprotonating the serine. The aspartate residue (Asp 102) stabilizes the histidine. The diagram also shows the oxyanion hole, which stabilizes the negative charge on the oxygen of the leaving group.

Chymotrypsin Mechanism

Nucleophilic attack

The diagram shows the six steps of the chymotrypsin mechanism:

1. Substrate binds. Serine attacks carbonyl.
2. Oxyanion collapses, cleaving peptide bond.
3. The first product leaves.
4. Water binds the enzyme and attacks carbonyl.
5. Oxyanion collapses, cleaving acyl-enzyme bond.
6. The second product is released.

The diagram also shows the catalytic triad (Ser 195, His 57, Asp 102) and the oxyanion hole.

What Factors Influence Enzymatic Activity?

Principle means of regulating enzyme activity

- Reversible, non-covalent (allosteric and simple-MM) – typically small molecules
- Reversible, covalent
- Protein-Protein interactions
- Zymogen activation
- Protein expression and degradation
- Availability (both of enzyme and substrate)

Reversible Noncovalent

Simple activation and inhibition by small molecules – substrate, natural regulators of enzymes

MM kinetics K_m , V_{max} – competitive, non competitive...

Substrate inhibition or activation

The availability of substrates and cofactors usually determines how fast the reaction goes
As product accumulates, the apparent rate of the enzymatic reaction will decrease

Reversible Noncovalent: Allosteric

Action at "another site"

Enzymes situated at key steps in metabolic pathways are modulated by allosteric effectors
These effectors are usually produced elsewhere in the pathway

Effectors may be feed-forward activators or feedback inhibitors

Kinetics are sigmoid ("S-shaped")

Allosteric Regulation

Increases or decreases the enzymatic activity by binding at a site other than the active site
Most rapid and most direct form of regulation

Figure 4.23 Allosteric regulation.

Allosteric Regulation Binding Curves

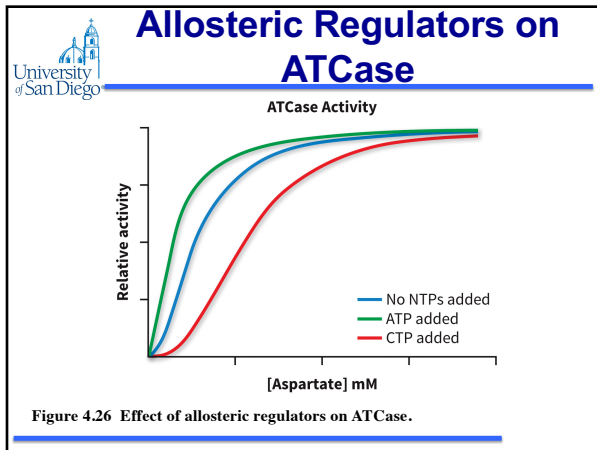
Exhibit sigmoidal activity curves

Figure 4.24 Allosteric enzymes have sigmoidal kinetics.

Aspartate Transcarbamoylase: Allosteric Regulation

The rate-limiting step in pyrimidine biosynthesis

ATCase regulation-An example of feedback control
Regulators are ATP, CTP, and UTP

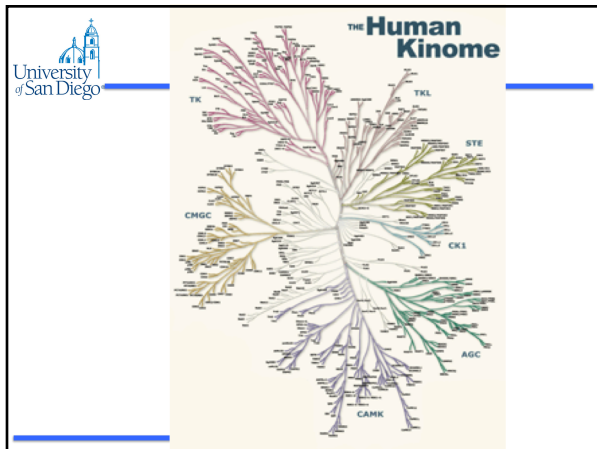


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Reversible Covalent

Examples include: phosphorylation - dephosphorylation, lipid modification.

This method is important because it does not alter the total amount of protein and it is easily reversed depending on cellular needs



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Covalent modification - Protein kinases

Phosphorylation/dephosphorylation

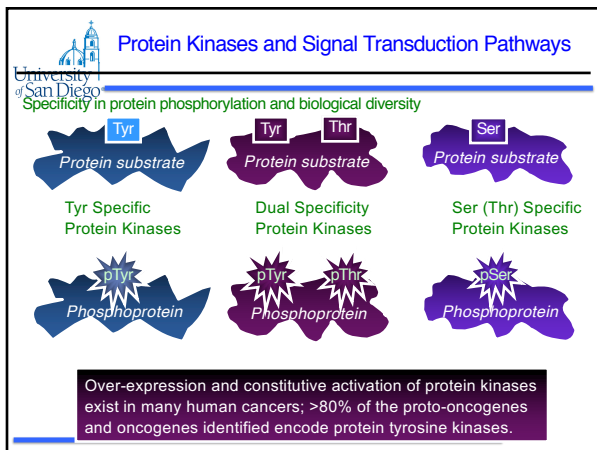
Most common method of reversible modification

- activation and localization

Up one-third of all cellular proteins are phosphorylated (so since there are ~30,000 genes, that would be ~10,000 phosphoproteins/organism, and perhaps a third of that in any given cell type, not including alternatively spliced isoforms).

Leads to a very fast response to cellular stress, hormonal changes, learning processes transcription regulation

Tony Hunter (Salk Institute) '87 predicted 1001 protein kinases - more like 2000, but what is 999 proteins among friends?



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What Kinds of Covalent Modification Regulate the Activity of Enzymes?

Protein kinases phosphorylate Ser, Thr, and Tyr residues in target proteins

Kinases typically recognize specific amino acid sequences in their targets

In spite of this specificity, all kinases share a common catalytic mechanism based on a conserved core kinase domain of about 260 residues

Kinases are often regulated by **intrasteric control**, in which a regulatory subunit (or domain) has a **pseudosubstrate sequence** that mimics the target sequence, minus the phosphorylatable residue

Covalent modification - Protein kinases

Regulation of protein phosphorylation varies depending on protein

- some turned on or off
- most kinases are regulated
- phosphatases generally not regulated
- can lead to large amplification of original signal

Four general classes of protein kinases, based on substrate (both sequence and amino acid phosphorylated), homology and regulation mechanisms (thousands of kinases)

Protein-Protein Interaction

Based on interface between two proteins

- can cause allosteric regulation but this style of interaction is different than between enzyme subunits

Protein binding can alter structure of second protein – one of the pairs are often regulated by a small molecule or covalent regulation

GTP Binding Proteins as an example

Zymogen Activity

Zymogens are inactive precursors of enzymes. Typically, proteolytic cleavage produces the active enzyme.

Zymogen Activation

Zymogen / proteolytic activation - this is an irreversible mechanism and must have tight control for the activation.

- most digestive enzymes such as trypsin and chymotrypsin
- blood clotting proteins are also commonly activated by this means.

Why is this important?

Irreversible activation by cleavage of one or more peptide bonds. Usually protein is made in one organ and secreted in the inactive form and then made active at a distal site/tissue

- some hormones (insulin)
- digestive enzymes

Protein Concentration

Protein lifetime in cells is not indefinite

- Proteases – regulated activity within cells
- Proteins are usually **tagged** for **selective** destruction in proteolytic complexes called **proteasomes** by covalent attachment of **ubiquitin**, a small, compact protein that is highly conserved.

N-end rule: On average, a protein's **half-life** correlates with its **N-terminal residue**.

- Proteins with N-terminal Met, Ser, Ala, Thr, Val, or Gly have half lives greater than 20 hours.
- Proteins with N-terminal Phe, Leu, Asp, Lys, or Arg have half lives of 3 min or less.

PEST proteins, rich in Pro (P), Glu (E), Ser (S) and Thr (T), are more rapidly degraded than other proteins.

Protein expression – RNA levels influence protein production

Total levels of protein is a balance of both degradation and production

Availability

Availability - there are several means by which the cell controls metabolism this way.

- **altering the physical location of the enzyme with or away from the substrate obviously controls the activity.** Translocation of proteins from one organelle to another is the mode of operation.
- **Sequestering or controlling the enzyme from it's substrate** (glucose-6 phosphate is in the cytosol whereas the enzyme glucose 6 phosphatase is in the inside of the endoplasmic reticulum. The substrate is transported across the ER membrane when the reaction is needed)



Availability

- Turnover - proteins generally have a defined half-life in the cell. Proteins are regularly being made and degraded. Altering either of these processes changes the total concentration of enzyme in the cell available for metabolism. The genetic control or rate of protein expression will play an important role in this regulation.
 - Various pathways can be differentially regulated by the use of Isozymes - Enzymes that catalyze the same reaction but are different kinetic properties and regulation
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