

**Fundamentals of Protein Chemistry**  
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**Module - 06**  
**Enzymes and Enzyme Mechanisms**  
**Lecture - 30**  
**Enzyme Mechanisms - III**

In the last class of this module on enzymes and enzyme mechanisms, we will be looking at specific enzyme mechanisms in terms of the types of catalysis possible.

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**CONCEPTS COVERED**

- Covalent catalysis
- Proteases
- Metal ion based catalysis

The slide features a video inset of Prof. Swagata Dasgupta in the bottom right corner. At the bottom of the slide, there are logos for the Indian Institute of Technology, Kharagpur (IIT KGP) and NPTEL (National Programme on Technology Enhanced Learning).

In our previous lecture we looked at acid base catalysis and we also looked at the several enzyme classes and the specific reactions that they catalyze. In this lecture we will focus on covalent catalysis in the example of proteases and metal ion-based catalysis.

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**KEYWORDS**

- Zymogen
- Chymotrypsin, Trypsin
- Binding pocket
- Catalytic triad
- Metal ion catalysis

Here we will look at specific proteins like zymogen, trypsin, chymotrypsin, their binding pockets, what we mean by a catalytic triad and metal ion catalysis.

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**Important aspects of covalent catalysis**

- Covalent bond formed between enzyme and substrate
- More stable the covalent bond formed – more difficult to be decomposed in the final step of a reaction
- The active site contains a reactive group, usually a strong nucleophile that becomes covalently modified temporarily in the catalytic procedure.

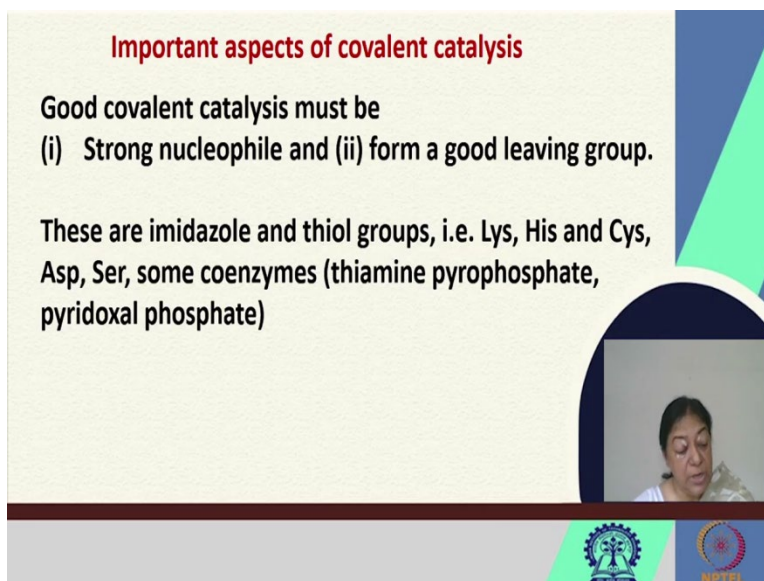
The important aspect of covalent catalysis indicates that there is a covalent bond formed between the enzyme and the substrate as the name implies. The presence of a covalent bond indicates a very strong bond as opposed to the other non covalent interaction types, in terms of where we are looking at acid base catalysis in the sense of the formation of a hydrogen bond or a proton donation or a proton acceptance.

A proton-donor acceptor system or an acid-based system, where we have the histidines, as we saw in the previous lecture, where we do not have any covalent bond formation. So we

understand that the presence of a covalent bond means there is a strong connection between our enzyme and substrate.

The process has to be such that this bond has to be cleaved for the enzyme to restore its original conformation for the active site, so that it can then bind another substrate. The active site in this case is in the enzymes of the examples that undergo covalent catalysis. They have a reactive group that is usually a strong nucleophile, that temporarily becomes covalently modified in the catalytic procedure.

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**Important aspects of covalent catalysis**

Good covalent catalysis must be  
(i) Strong nucleophile and (ii) form a good leaving group.

These are imidazole and thiol groups, i.e. Lys, His and Cys, Asp, Ser, some coenzymes (thiamine pyrophosphate, pyridoxal phosphate)

The important aspects of covalent catalysis, indicate that there has to be a strong nucleophile and it also has to form a good leaving group, because we do not want the bond to be too strong so that it cannot be broken in the catalytic procedure.

In this case also we have imidazole and thiol groups, and specific coenzymes like thiamine pyrophosphate and pyridoxal phosphate.

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### Three stages of Covalent Catalysis

1. Nucleophilic attack of enzyme on substrate
2. Withdrawal of electrons
3. Elimination of catalysts by reversion of step 1 (not shown)

Schiff base (imine)

There are three stages of covalent catalysis. In the first stage [refer to slide] we have a linkage and then we have a covalent formation, then subsequently we have to have a release. There is a nucleophilic attack of the enzyme on the substrate that is going to result in a covalent bond formation. And there is going to be elimination of catalysis by a reversion of step one, which is not shown in this particular indication.

The process here is that we have a covalent bond formation, followed by which there is a catalytic reaction. And there is going to be a cleavage of the covalent bond that was initially formed to bring back our enzyme to a position, where it is able to bind another substrate.

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### Proteases

- Catalyze proteolysis of polypeptide into smaller peptides or amino acids
- Cleaves peptide bonds by hydrolysis - at pH 2 pepsin hydrolyzes proteins to peptides
- Classification of proteases based on the catalytic residue e.g. Serine Protease, Aspartic Protease, Cysteine Protease etc.

The examples of covalent catalysis are mostly shown in proteases. Now proteases as the name implies, catalyze the proteolysis that is the cleavage of polypeptides into smaller peptides or

amino acids. This indicates the cleavage of the peptide bond. This cleavage is possible through several enzymes.

For example at pH 2, pepsin is able to hydrolyze proteins to peptides. Then the classification of these proteases comes from the specific catalytic residue that is involved in the covalent catalysis.

In a specific example of proteases, we have the cleavage of the proteolysis of the peptide bond.

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**Zymogens are inactive enzyme precursors (proenzymes)**

- Proteolytic enzymes are usually made as larger, inactive precursors. The protease zymogens are synthesized in the pancreas and activated in the duodenum.
- Enteropeptidase converts trypsinogen into trypsin, Ser-protease under hormonal control.
- Proelastase, procarboxypeptidase A, B, and phospholipase A2 are all activated by trypsin.

The slide features a video inset of a woman speaking, a green and blue geometric design on the right, and logos for a university and NPTEL at the bottom.

We realize that if there are such proteins that have the capability to break a peptide bond, they are actually detrimental in their active form, because of the numerous proteins that are there. Which would mean that these would go about their job of proteolysis.

Nature has devised a method for this, where there are zymogens that are inactive enzyme precursors called proenzymes. That is an actually inactive form of the specific enzyme that has a proteolytic nature or a protease. The proteolytic enzymes are therefore made as larger inactive precursors.

We realize it would not be a good idea to have them as they were, without being inactive. If they were active, they would break the peptide bond. So, the protease zymogens are synthesized in the pancreas and they are activated in the duodenum.

For example enteropeptidase is one such protein that converts the trypsinogen into trypsin. That is the serine protease under hormonal control. Then we have proelastase, procarboxypeptidase, phospholipase, all of these are proenzymes.

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**The activation of trypsinogen to trypsin**

$\text{H}_3\text{N}^+ \text{-Val}^{10} \text{-(Asp)}_4 \text{-Lys}^{15} \text{-Ile}^{16} \text{-Val-..}$   
 Trypsinogen

↓ Enteropeptidase or trypsin

$\text{H}_3\text{N}^+ \text{-Val-(Asp)}_4 \text{-Lys-}$  + **Ile-Val-..**

Cleaves Lys 15 – Ile 16, a trypsin cleavage site,  
 i.e. self activation / autocatalytic

And the way they act has been shown [refer to slide] as an example here in the activation of trypsinogen to trypsin. So we have trypsinogen. There is a cleavage about a specific bond, that will result in the formation of another enzyme that is going to be important for our catalytic process. This can be a self activation or an auto catalytic process.

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**Serine Proteases**

- Synthesized as zymogens in the pancreas, transported to the small intestine and activated by selective proteolysis
- Examples: Chymotrypsin, Trypsin, Elastase, Thrombin, Subtilisin, Plasmin, Tissue plasminogen activator.

Active site Ser

We look at serine proteases where the active site is serine. As we mentioned the terminology of the proteases is based on the type of covalent bond formation that occurs.

So this [refer to slide] is an example of a serine protease, the chymotrypsin molecule they are synthesized as zymogens in the pancreas, then they are transported to the small intestine and activated by selective proteolysis that is going to give rise to the enzyme of action, as we had seen before in the zymogen action.


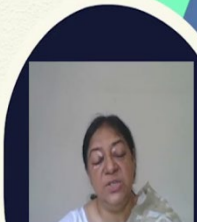
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**Serine Proteases**

**Chymotrypsin:** Selectively cleaves at the carboxyl site of Aromatic Side chains ( Trp, Tyr, Phe) and large hydrophobic side chain (Met)

**Trypsin:** Selectively cleaves at the carboxyl site of Arg and Lys if not followed by Pro

**Elastase:** Selectively cleaves at the carboxyl site of Val and Thr

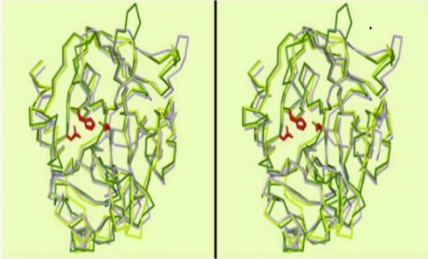


Now the serine proteases, that is the chymotrypsin, as like any other enzyme has substrate specificity. The substrate specificity in terms of chymotrypsin, is that it cleaves selectively at the carboxyl site of aromatic side chains. We have tryptophan, tyrosine and phenylalanine. Chymotrypsin has the capability of cleavage at the carboxyl end of the aromatic residues.


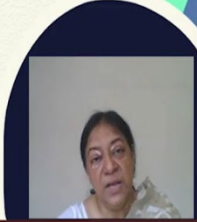
Trypsin selectively cleaves at the carboxyl site of basic amino acid residues; like arginine and lysine, provided it is not followed by a proline because we know that proline is an imino acid and the orientation of the backbone may be in a manner that cannot be bound to the active site of trypsin. Similarly, elastase selectively cleaves at the carboxyl site of small residues. In this case valine and threonine.

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**Chymotrypsin (blue), Trypsin (yellow) and Elastase (green)**



**Backbone conformations and active-site residues (red) are similar in these three enzymes**



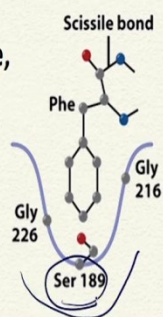
If we look [refer to slide] at the backbone conformations and the active site residues of these three enzymes, we will see chymotrypsin shown in blue, trypsin in yellow and elastase in green and the active site residues in red. As we can see the disposition of the active site residues is the same because their functionality is the same in the cleavage of the peptide bond.

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**Substrate specificities**

X-ray structures suggest the basis for the **different substrate** specificities of chymotrypsin, trypsin and elastase

1. In chymotrypsin, preferred Phe, Trp or Tyr fit into a hydrophobic pocket located near the catalytic groups



**Chymotrypsin**



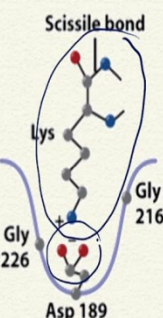
Now to look at substrate specificities. This was established by x-ray structures that established the specificities of the three enzymes that we spoke about. Where we would have chymotrypsin which had a capability of cleavage after the aromatic side chains, which would indicate that it would fit into a specific hydrophobic pocket that is located near the catalytic groups here [refer to slide]. Here is our serine.

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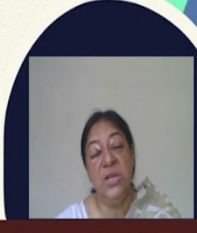
**Specificity pockets of three serine proteases**

2. In trypsin, the Ser 189 of chymotrypsin, which lies at the bottom of the binding pocket is replaced by Asp.

Forms ion pairs with Arg and Lys in substrate.



**Trypsin**





In the same way we look at the other chymotrypsin case, where we have the serine replaced by an aspartic acid here. And this trypsin molecule is preferable to basic amino acid residues in the cleavage, after the carboxyl site of the basic amino acid residues. And it has a specific binding pocket understandably an acid, so that there is an electrostatic interaction in the recognition of the substrate.

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**Specificity pockets of three serine proteases**

**3. In elastase, hydrolyzes the nearly indigestible Ala, Gly, and Val-rich protein elastin (connective tissue)**

Pocket contains Val and Thr instead of the two Gly found in trypsin and chymotrypsin -> cleaves substrates with small neutral side chains on the carbonyl side

**Elastase**

In the elastase, there are small hydrophobic molecules that align the active site, that help in the recognition or the binding of the small amino acid residues which are going to be cleaved. So this cleaves substrates with small neutral side amino acids again on the carboxyl.

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**Chymotrypsin**

**Trypsin**

**Elastase**

**Substrate specificities are due to relatively small structural differences in active-site binding cavities**

We have the specific scissile bonds indicate that these [refer to slide] are the high peptide bonds that are going to be broken in these three types of enzymes; the chymotrypsin, the trypsin and the elastase. And the substrate specificities are due to relatively small structural differences as we can see in the active site binding cavities. And we realize the importance of the recognition based on the residues that are present in the active site.

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**Substrate specificities**

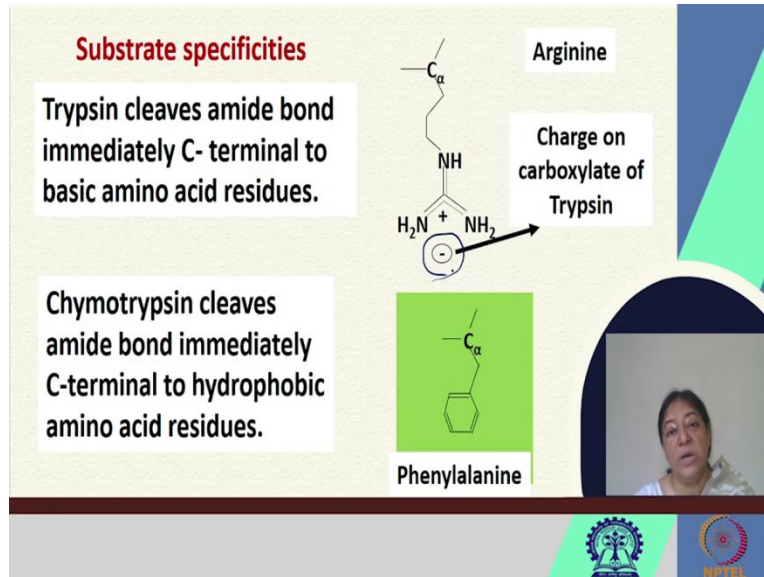
Trypsin cleaves amide bond immediately C- terminal to basic amino acid residues.

Chymotrypsin cleaves amide bond immediately C-terminal to hydrophobic amino acid residues.

Arginine

Charge on carboxylate of Trypsin

Phenylalanine



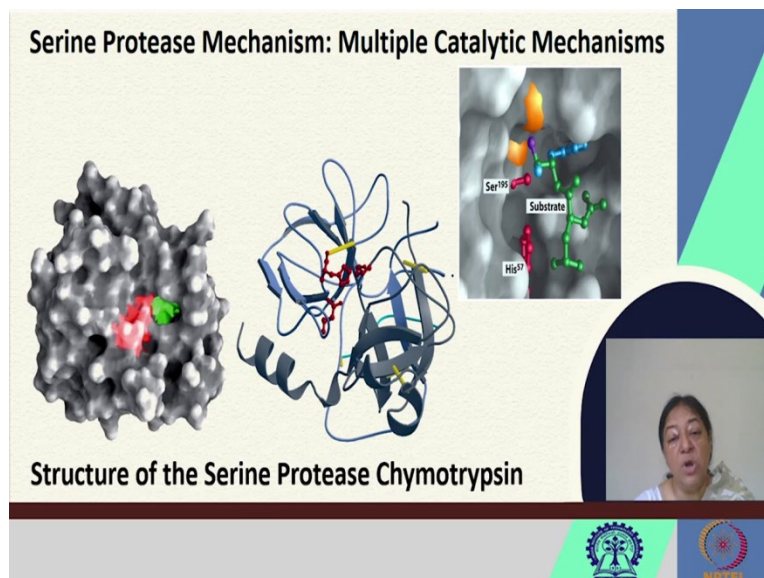
The slide features a light yellow background with a blue and green geometric design on the right. It contains text boxes describing the substrate specificities of trypsin and chymotrypsin. Chemical structures for Arginine and Phenylalanine are shown, along with a diagram of the charge on the carboxylate of Trypsin. A video inset in the bottom right corner shows a woman speaking.

We have trypsin that cleaves at the C-terminal of the basic amino acids. And we know that this charge on the carboxylate comes from the aspartic acid in trypsin and chymotrypsin cleaves the amide bond following hydrophobic amino acids, where we have a hydrophobic pocket that is going to accommodate the substrate.

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**Serine Protease Mechanism: Multiple Catalytic Mechanisms**

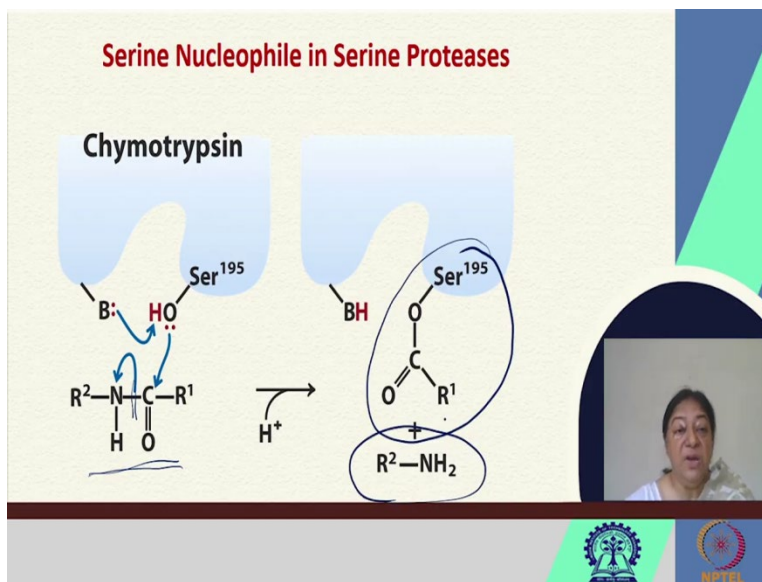
Structure of the Serine Protease Chymotrypsin



The slide features a light yellow background with a blue and green geometric design on the right. It contains a 3D model of the enzyme, a ribbon diagram, and a close-up of the active site showing Ser195 and His57 interacting with a substrate. A video inset in the bottom right corner shows a woman speaking.

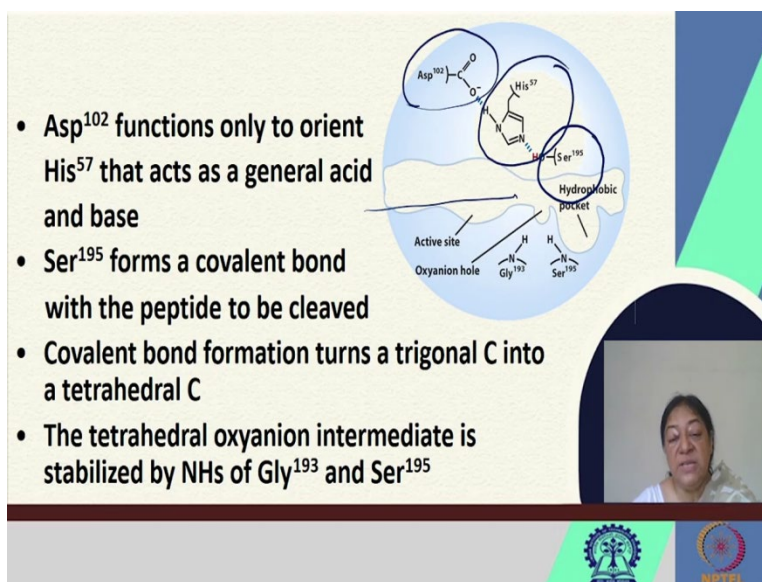
We will just be briefly looking at the serine protease mechanism, where we have the active site structures as we looked at and we know that we are going to have a covalent linkage that is going to be brought about by the serine.

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Ser<sup>195</sup> is the nucleophile and we have a covalent linkage formed which is important in the breakage. So, here [refer to slide] is our peptide bond that is going to be cleaved and here we have the R<sup>2</sup> being lost initially, the R<sup>1</sup> still connected which will subsequently be released.

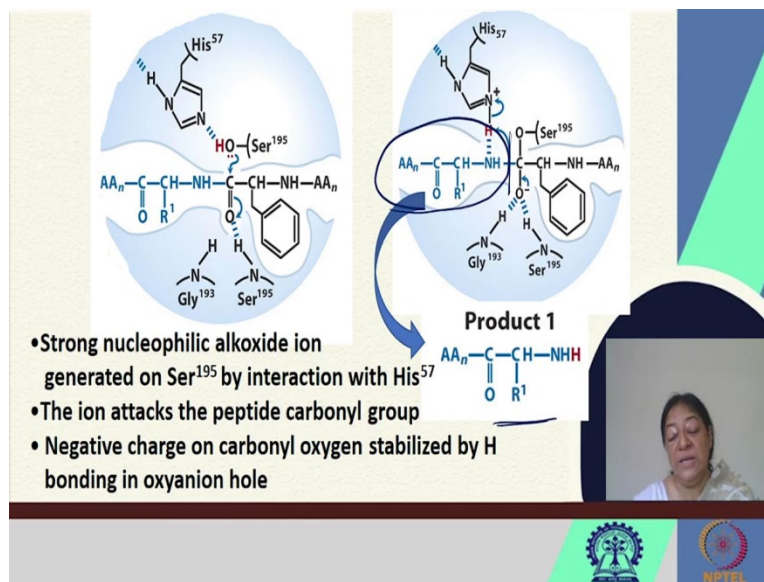
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We have conditions here, where we have the catalytic triad, where the Asp<sup>102</sup> acts to orient the His<sup>57</sup>, that acts as a general acid and base.

The Ser<sup>195</sup> is the one that forms the covalent linkage and in the formation of the covalent linkage, we have the active site and we have these orientations of the active site residues possible, where we have a stabilization of our molecule.

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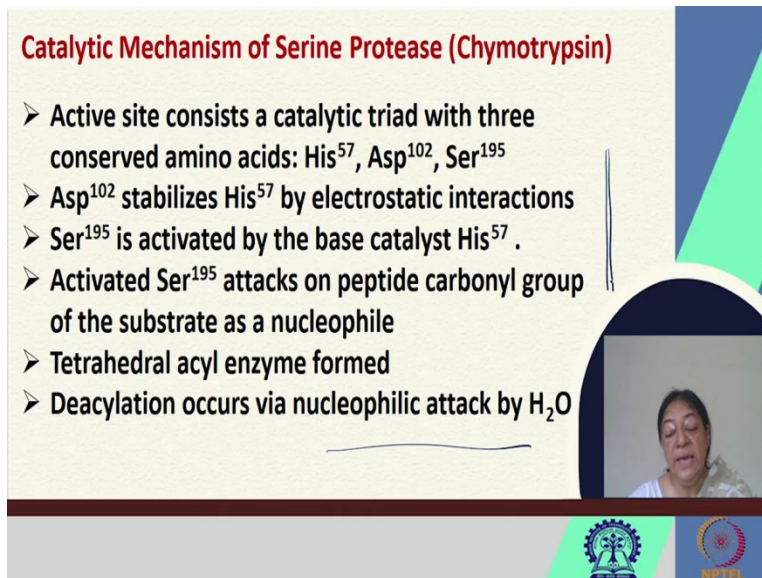
Without going into too much detail, but just to understand the beauty of the breakage and the recognition of how the molecule is able to enter the active site. There is a covalent bond formation and then we have the cleavage of our peptide bonds. So we have an initial product form, this [refer to slide] is our product form where we have the cleavage around this.

We realize that there is a catalytic triad. The catalytic triad, the importance of orientation, the importance of connection and the importance of acid base catalysis. And in this case of covalent catalysis a formation of a covalent linkage, which subsequently breaks to bring back our original enzyme, which is usually brought about by a hydrolysis or an attack by water.

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### Catalytic Mechanism of Serine Protease (Chymotrypsin)

- Active site consists a catalytic triad with three conserved amino acids: His<sup>57</sup>, Asp<sup>102</sup>, Ser<sup>195</sup>
- Asp<sup>102</sup> stabilizes His<sup>57</sup> by electrostatic interactions
- Ser<sup>195</sup> is activated by the base catalyst His<sup>57</sup>.
- Activated Ser<sup>195</sup> attacks on peptide carbonyl group of the substrate as a nucleophile
- Tetrahedral acyl enzyme formed
- Deacylation occurs via nucleophilic attack by H<sub>2</sub>O



The active site in this example of a serine protease chymotrypsin; The catalytic triad has His<sup>57</sup> Asp<sup>102</sup> and Ser<sup>195</sup>, each with their own roles to play in this catalytic reaction.

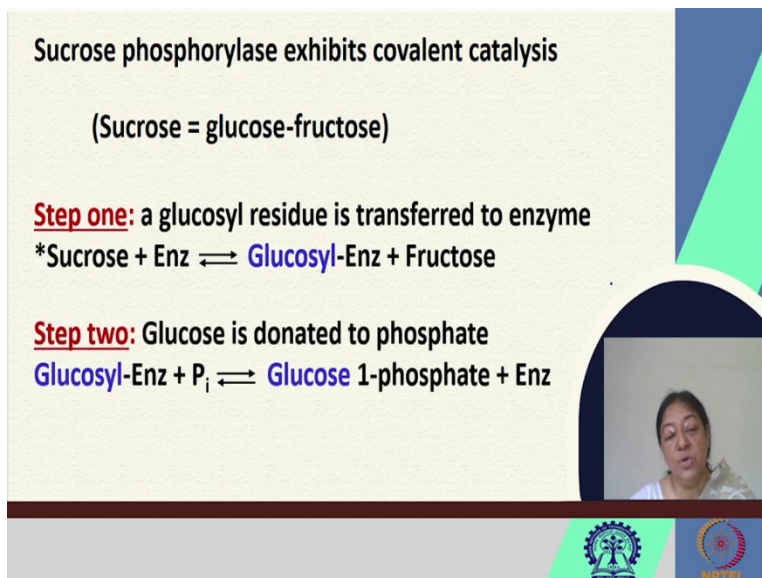
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### Sucrose phosphorylase exhibits covalent catalysis

(Sucrose = glucose-fructose)

**Step one:** a glucosyl residue is transferred to enzyme  
 \*Sucrose + Enz  $\rightleftharpoons$  Glucosyl-Enz + Fructose

**Step two:** Glucose is donated to phosphate  
 Glucosyl-Enz + P<sub>i</sub>  $\rightleftharpoons$  Glucose 1-phosphate + Enz



There are other examples of covalent catalysis, where we have sucrose that is a combination of glucose and fructose, where we have a glucosyl residue that is transferred to the enzyme, followed by the glucose donated to the phosphate and the formation of the product.

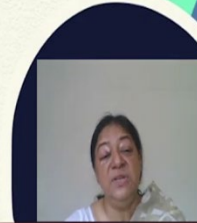
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### Papain: a proteolytic enzyme

The mechanism by which papain breaks peptide bonds involves the use of a catalytic dyad with a deprotonated cysteine.

A covalent acyl-enzyme intermediate is formed that frees the amino terminus of the peptide

Enzyme is deacylated by a water molecule that releases the carboxy terminal of the peptide.



Another example is papain. This is also a proteolytic enzyme and here it uses a catalytic dyad with a deprotonated cysteine. In this case also, as in a covalent catalysis, we have a covalent acyl-enzyme intermediate formed, that frees the amino terminus. We have to realize that in a proteolytic system, we are cleaving the peptide bond; these are proteases, proteolytic enzymes that are cleaving the peptide bond.

So, there are the generation of a new amino terminus for the cleaved peptide and a new carboxyl terminus. So, the enzyme is then deacetylated by a water molecule that releases the carboxy terminal of the peptide.

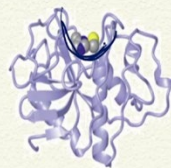
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### Papain: a proteolytic enzyme

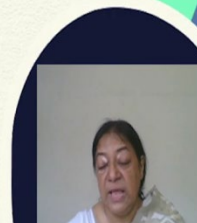
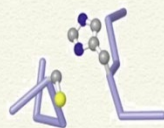
Activity of papain depends upon ionizable residues: His-159 and Cys-25

(a) Ribbon model  
(b) Active site residues (N blue, S yellow)

(a)

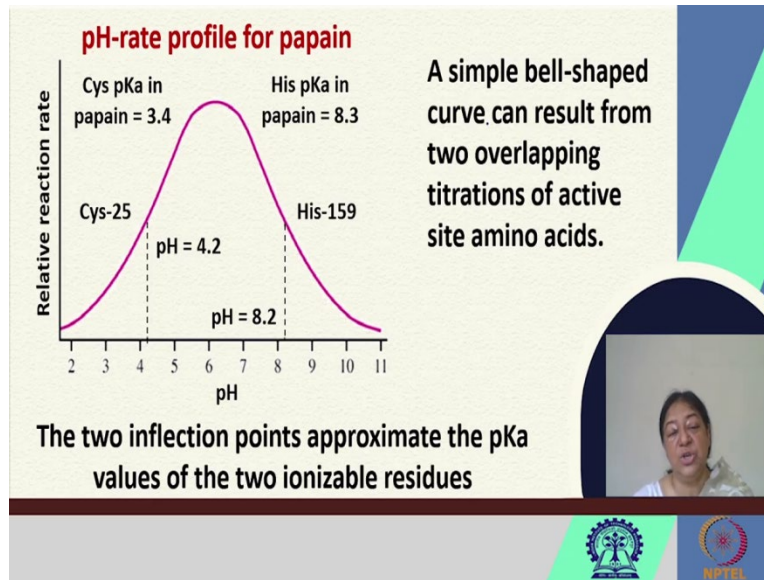


(b)



If we look at this again, we have ionizable residues histidine and cysteine. There is a specific picture [refer to slide] as in the orientation, where we have an active site cleft that can bind the enzyme and the substrate.

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If we look at the titrations of these curves of the two overlapping titrations of the pH rate profile for papain, it is interesting to note that we have two Cys<sup>25</sup> and His<sup>159</sup> and the pKa changes to such a degree that allows the specific catalytic reaction tell us that these two ionizable residues are involved in this particular catalytic process, the catalytic reaction of this protein.

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**Metal cation catalysis:**

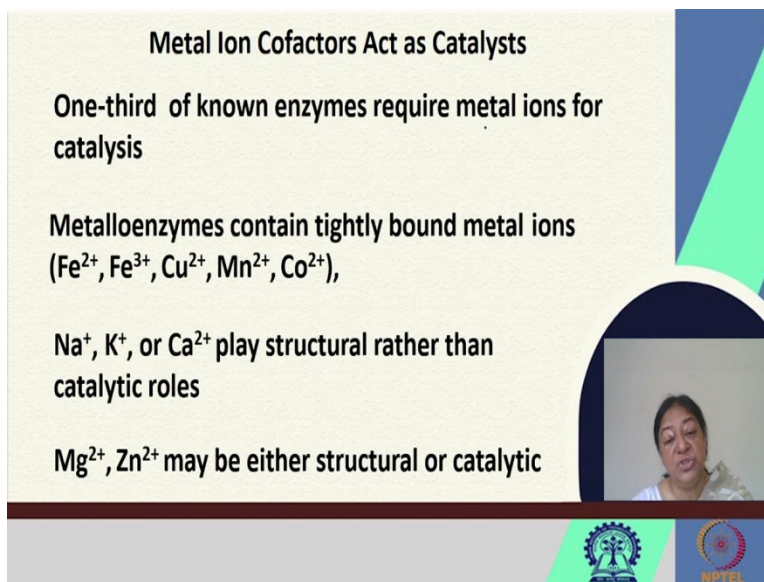
Catalytic metals in enzymes:

- Zinc (Zn<sup>2+</sup>)
- Copper (Cu<sup>2+</sup>/Cu<sup>+</sup>)
- Magnesium (Mg<sup>2+</sup>)
- Manganese (Mn<sup>2+</sup>/Mn<sup>3+</sup>)
- Iron (Fe<sup>3+</sup>/Fe<sup>2+</sup>)
- Cobalt (Co<sup>2+</sup>/Co<sup>3+</sup>)
- Molybdenum (Mo<sup>3+</sup>/Mo<sup>4+</sup>/Mo<sup>6+</sup>)
- Vanadium (V<sup>5+</sup>)
- Tungsten (W<sup>4+</sup>/W<sup>6+</sup>)

Logos for IIT Bombay and NPTEL are visible at the bottom.

In our next examples we will be looking at metal cation catalysis. In the catalytic metals in enzymes there are zinc, copper, magnesium, manganese, iron and a whole list of such metals are present.

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**Metal Ion Cofactors Act as Catalysts**

**One-third of known enzymes require metal ions for catalysis**

**Metalloenzymes contain tightly bound metal ions ( $\text{Fe}^{2+}$ ,  $\text{Fe}^{3+}$ ,  $\text{Cu}^{2+}$ ,  $\text{Mn}^{2+}$ ,  $\text{Co}^{2+}$ ),**

**$\text{Na}^+$ ,  $\text{K}^+$ , or  $\text{Ca}^{2+}$  play structural rather than catalytic roles**

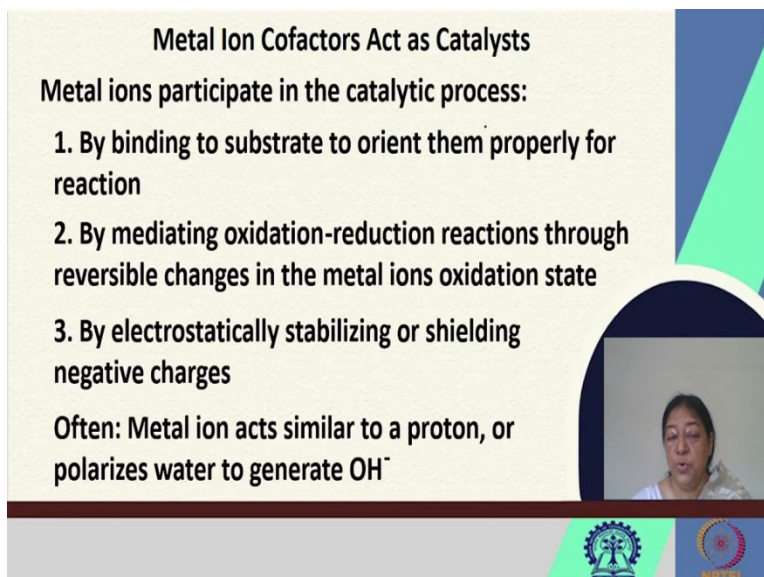
**$\text{Mg}^{2+}$ ,  $\text{Zn}^{2+}$  may be either structural or catalytic**

The slide features a video inset of a woman in the bottom right corner. At the bottom, there are logos for IIT Bombay and NPTEL.

These metal ion cofactors act as catalysts. They have more than one third of known enzymes require metal ions for catalysis.

The metalloenzymes contain tightly bound metal ions. And the smaller ones where we have sodium, potassium and calcium, they play structural roles rather than catalytic roles. And we have  $\text{Mg}^{2+}$  and  $\text{Zn}^{2+}$  that may be structural or catalytic in the roles that they play.

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**Metal Ion Cofactors Act as Catalysts**

**Metal ions participate in the catalytic process:**

- 1. By binding to substrate to orient them properly for reaction**
- 2. By mediating oxidation-reduction reactions through reversible changes in the metal ions oxidation state**
- 3. By electrostatically stabilizing or shielding negative charges**

**Often: Metal ion acts similar to a proton, or polarizes water to generate  $\text{OH}^-$**

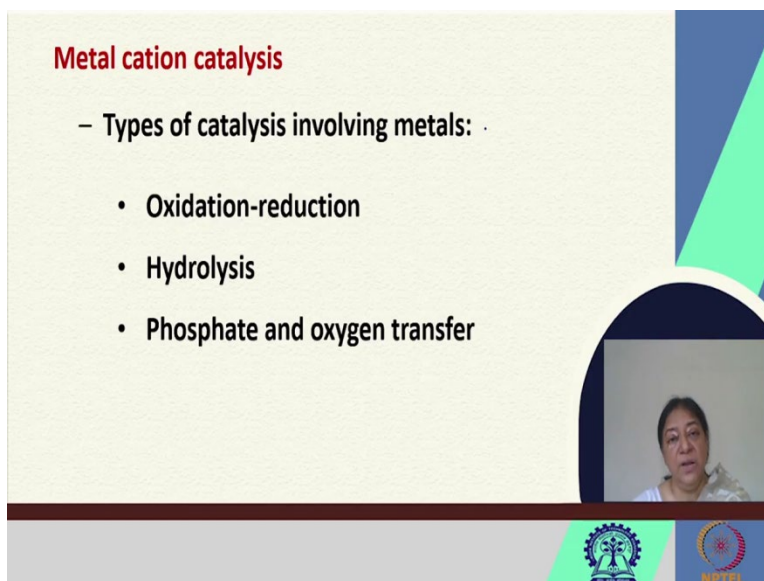
The slide features a video inset of a woman in the bottom right corner. At the bottom, there are logos for IIT Bombay and NPTEL.



The way they participate in the catalytic process is, they can bind to the substrate in order to orient them properly, so that they can participate in the catalytic reaction or they can mediate the oxidation-reduction reactions, through reversible changes in the metal ion oxidation states. As there is iron there can be a reversible change in the oxidation states, that will facilitate the specific oxidation reduction reactions.

It can also electrostatically stabilize or shield the negative charges, being positive in nature and often the metal ion can also act like a proton that polarizes the water to generate  $\text{OH}^-$ .

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**Metal cation catalysis**

– Types of catalysis involving metals:

- Oxidation-reduction
- Hydrolysis
- Phosphate and oxygen transfer



The slide features a video inset of a woman in the bottom right corner and two logos at the bottom: a blue gear logo on the left and a red and blue circular logo on the right.

We will be looking at some examples. So the types of catalysis that involve metals are oxidation-reduction reactions, hydrolysis and phosphate and oxygen transfer.

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**Specific roles of catalytic metals:**

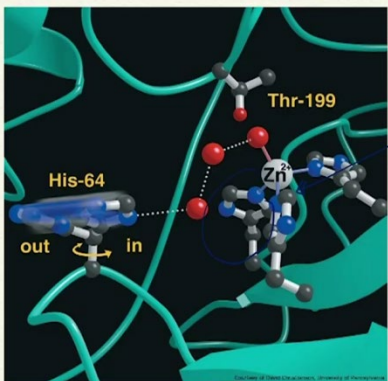
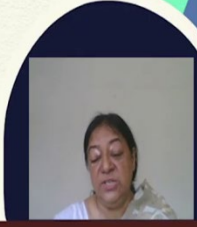

- Electron transport
- Electrostatic stabilization of negatively charged species
- Activation of substrates, coenzymes, and water molecules for catalysis by electronic bond polarization

In the examples we have, electronic transport possible, electrostatic stabilization, activation of the substrates, coenzymes and water molecules for a reaction; a catalytic reaction that is going to involve a metal.

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**Example of Metal Ion Catalysis: Carbonic Anhydrase**  
 Carbonic anhydrase catalysis :  $\text{CO}_2 + \text{H}_2\text{O} \rightleftharpoons \text{HCO}_3^- + \text{H}^+$

The example that we will be looking at is carbonic anhydrase, where a catalysis occurs in the formation of the bicarbonate ion. This [refer to slide] is the catalytic site of the enzyme active site, where we see the zinc ion in a specific location because of the role that it has to play and the coordination for the zinc ion, is with histidine residues; which we will see in a moment.

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**Metal cation catalysis:**

– Metal-induced water deprotonation in *carbonic anhydrase*

Carbonic anhydrase catalyzes the reaction:  $\text{CO}_2 + \text{H}_2\text{O} \rightarrow \text{HCO}_3^- + \text{H}^+$

NPTEL

In the metal ion catalysis therefore, that occurs in the overall reaction in the catalysis, where we have the formation of the bicarbonate ion from the carbon dioxide; involves a metal induced water deprotonation using the zinc, which is the metal that is present in the active site of carbonic anhydrase.

This [refer to slide] is the location of the zinc in the carbonic anhydrase and these are the histidine residues that are involved in its catalytic activity.

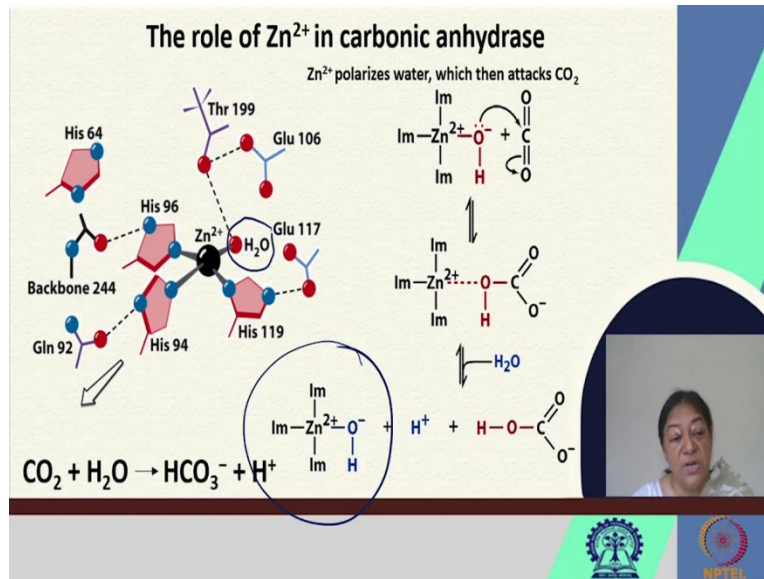
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**Metal-induced water deprotonation in *carbonic anhydrase***

NPTEL

So, this [refer to slide] is the overall example of the catalytic cycle. These are the histidine residues that are involved in the coordination of the zinc. We have this zinc activated, we have the carbon dioxide come into the picture and the bicarbonate being released.

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If we look [refer to slide] at the enzyme action; the role zinc plays in carbonic anhydrase. The three histidine molecules that hold it together in the linkage and it polarizes the water molecule.

The water molecule that is attached here is polarized by the zinc, that then attacks the carbon dioxide, which subsequently is linked to the  $Zn^{2+}$  in a manner, which is then hydrolyzed to form the bicarbonate ion and we have our imidazole connected to  $Zn^{2+}$ . So, this is the overall reaction that occurs.

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**Enolase**

Glycolysis converts glucose into two 3-carbon molecules called pyruvate.

The energy released during glycolysis is used to make ATP.

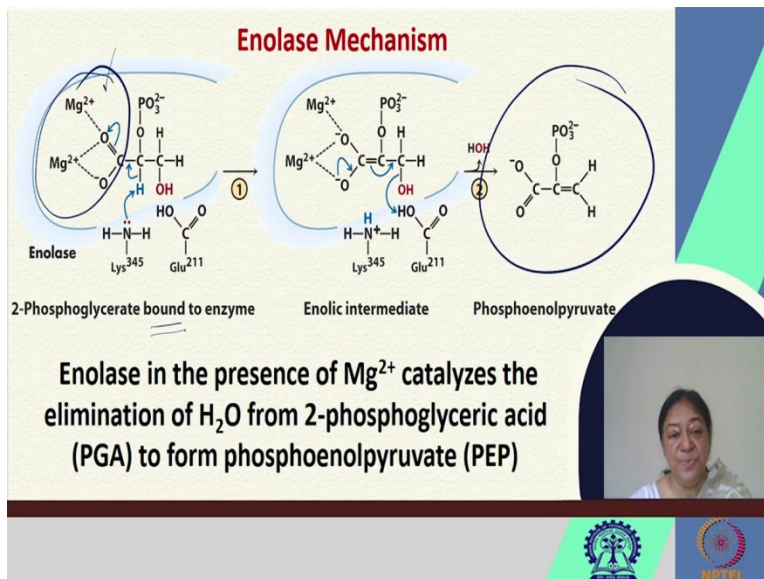
Enolase is an enzyme that catalyzes a reaction of glycolysis.

The metal ion works by binding to the enzyme at the active site to produce a conformational change.

Another example that we will look at is enolase. We know glycolysis converts glucose into two 3-carbon molecules that are called pyruvate and the energy released during glycolysis is used to make ATP.

Enolase is an enzyme that catalyzes a specific reaction of glycolysis and the metal ion works by binding to the enzyme at the active site, as we would expect in a metal catalysis to produce a specific conformational change.

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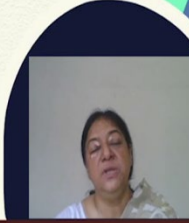


What happens in this case, is the enolate in the presence of magnesium now, catalyzes the elimination of water from 2-phosphoglyceric acid molecules. So, we have 2-phosphoglyceric acid molecules bound to the enzyme. In an example where we have the metal, in this case  $Mg^{2+}$ , that catalyzes the elimination of the water, in the event forming phosphoenolpyruvate which we know is important in our glycolysis reaction.

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**Catalytic Mechanisms**

- Acid-base catalysis
- Covalent catalysis
- Metal ion catalysis
- Electrostatic catalysis
- Proximity and orientation effects





We have looked at acid-base catalysis, we have looked at covalent catalysis in the formation of a covalent bond and subsequent cleavage in our proteases in the proteolytic enzymes, that involve the cleavage of the peptide bond.

Then the metal ion catalysis, where we looked at several examples and had an idea of which metals are actually involved in the catalysis and the roles that they can play. The electrostatic catalysis that involves the electrostatic interactions, in mostly all the cases where we have an interaction between the specific residues involved in catalytic reactions and the type of residues. We also looked at the proximity and the orientation effects.

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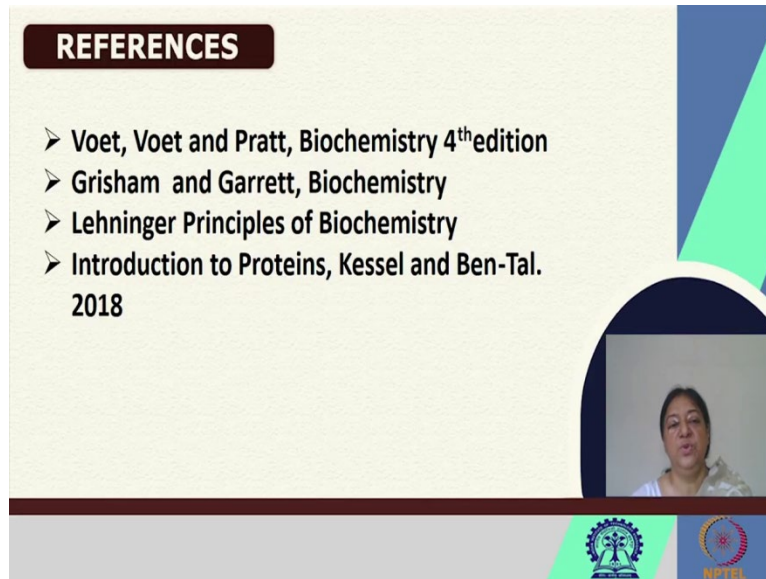
**END OF MODULE 6**

**ENZYMES AND ENZYME MECHANISMS**



This is the end of module 6, enzymes and enzyme mechanisms

(Refer Slide Time: 25:09)



**REFERENCES**

- Voet, Voet and Pratt, Biochemistry 4<sup>th</sup> edition
- Grisham and Garrett, Biochemistry
- Lehninger Principles of Biochemistry
- Introduction to Proteins, Kessel and Ben-Tal. 2018

The slide features a light beige background with a dark blue header containing the word 'REFERENCES' in white. A list of four references is presented with blue arrowheads. On the right side, there is a vertical decorative element with blue and green geometric shapes. At the bottom right, a circular video inset shows a woman with dark hair wearing a patterned top. The bottom of the slide has a dark blue footer with two logos: the Indian Institute of Technology (IIT) logo on the left and the NPTEL logo on the right.

The books that we have followed have been specified in the specific lectures.