

Proteins and Gel-Based Proteomics
Professor Sanjeeva Srivastava
Department of Biosciences and Bioengineering
Indian Institute of Technology, Bombay
Mod 02 Lecture Number 3

(Refer Slide Time: 00:15)

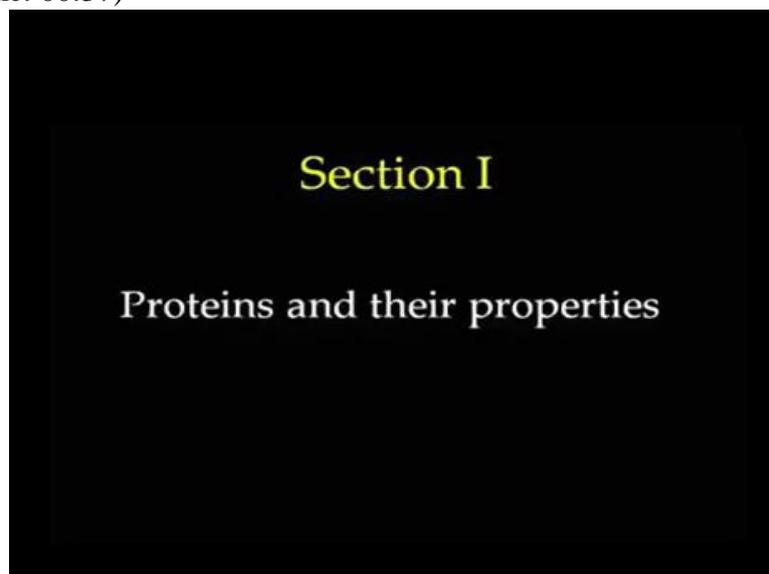


Topics to be discussed today:

- Proteins and their properties
- Different structural levels of proteins
- Proteins and diseases

Let me give you the lecture outline. We will first talk about proteins and its function, and then different levels of protein structures; primary, secondary, tertiary and quaternary.

(Refer Slide Time: 00:37)



Section I

Proteins and their properties

The protein term was derived from the Greek word proteios...

(Refer Slide Time: 00:43)

Proteins

- Derived from Greek "Proteios"
- Linear polymers built of monomers (amino acids)
- Most versatile macromolecules in living systems
- Play key structural and functional roles

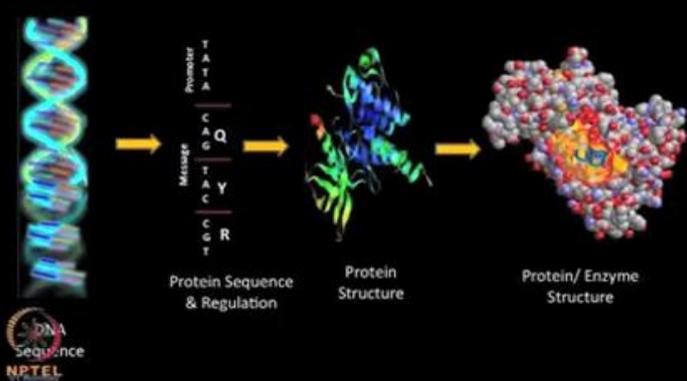


... which means of the first rank or very important. This term was coined by scientist Berzelius in 1833. These are the linear polymers which are built of monomers or amino acid subunits. These are most versatile macromolecules in any living system.

They are crucial for various essential functions of all the biological processes and they play a very critical role both from structural and functional point of view. Therefore studying about proteins is very important.

(Refer Slide Time: 01:25)

Proteins transform 1-D sequences to 3-D functional molecules

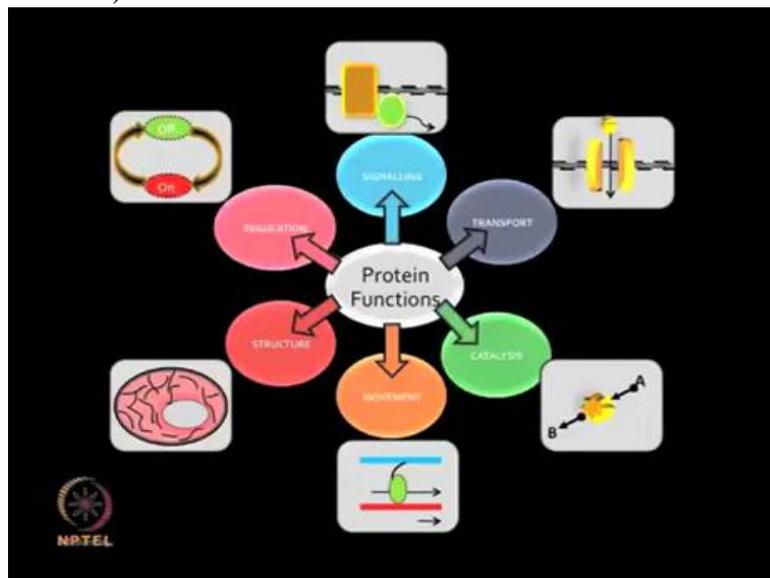


If you look at the central dogma starting from DNA to RNA and protein, the proteins can transform the one dimensional sequence to the three dimensional functional information.

Proteins can play wide range of functional properties because of their different functional groups which can account for various protein functions and its activities.

Protein-protein or protein-other bio-molecular interactions: They are generated because of the chiralistic capability of these proteins which cannot be obtained from the any given individual protein.

(Refer Slide Time: 02:17)



Proteins can perform various types of functions whether it is catalysis, movement, structure, regulation, signaling, transport etc. As you can see in the slide, various types of functions have been shown.

Enzyme catalysis: The enzymes catalyze biochemical reactions by increasing the rate of reactions.

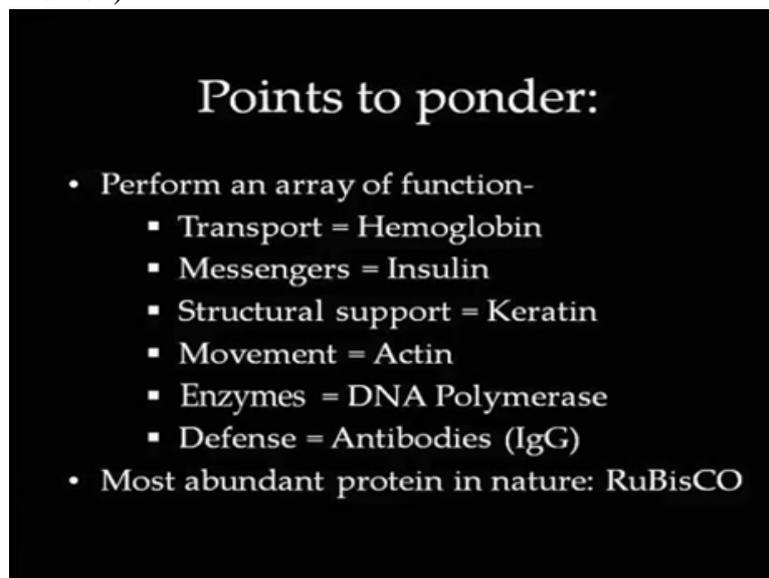
Transport and storage: Proteins can transport small molecules such as Oxygen and iron. Proteins are involved in the movement with muscle contraction.

If you talk about microorganism, in bacteria the chemotaxis; they are responsible for the mechanical strength, for example in the skin and the bones, the Collagen and Keratin, all of these are different examples of mechanical strength.

Proteins are also present as immunoglobulin responsible for the immunity, and antibodies are used for various types of protein-protein and protein-ligand interactions, growth and differentiation, transcription factors, gene expression during growth and development, for example nerve growth factors, hormones such as insulin.

All of these are various examples of proteins and various diverse functions in which they are involved.

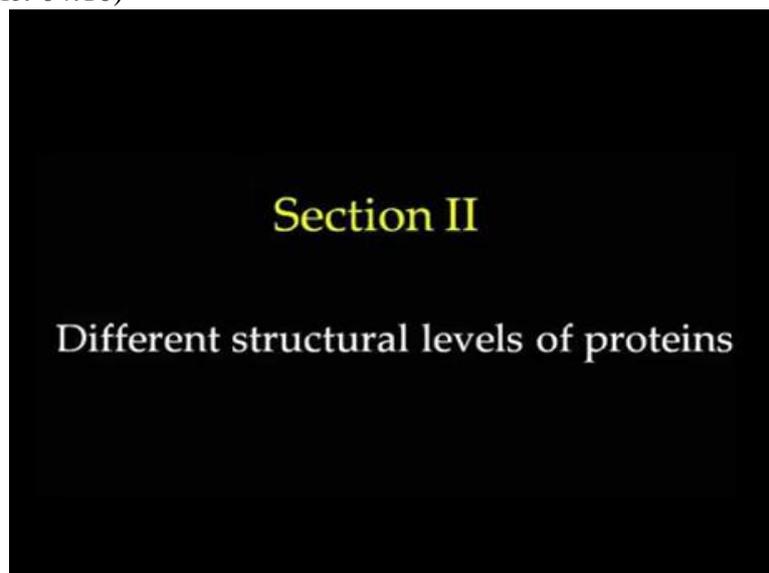
(Refer Slide Time: 04:01)



Points to ponder:

- Perform an array of function-
 - Transport = Hemoglobin
 - Messengers = Insulin
 - Structural support = Keratin
 - Movement = Actin
 - Enzymes = DNA Polymerase
 - Defense = Antibodies (IgG)
- Most abundant protein in nature: RuBisCO

(Refer Slide Time: 04:10)



Section II

Different structural levels of proteins

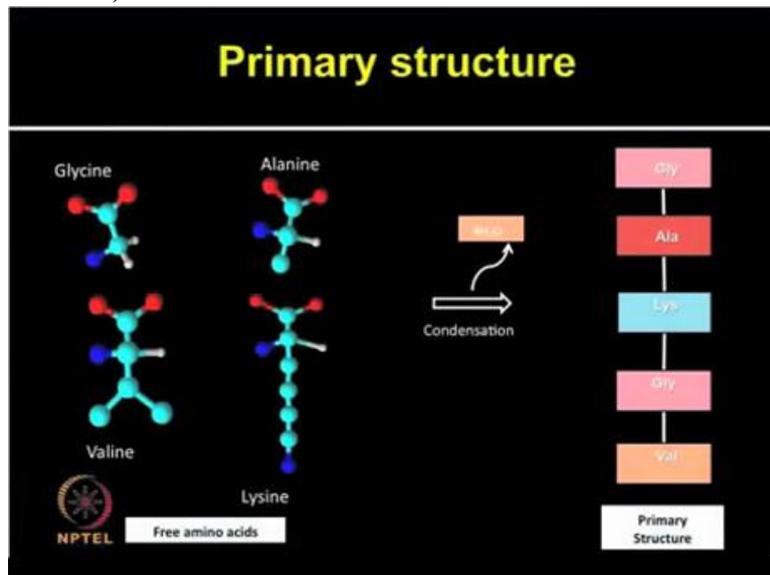
Now let's move on to different structural level of proteins starting with the primary structure.

(Refer Slide Time: 04:20)



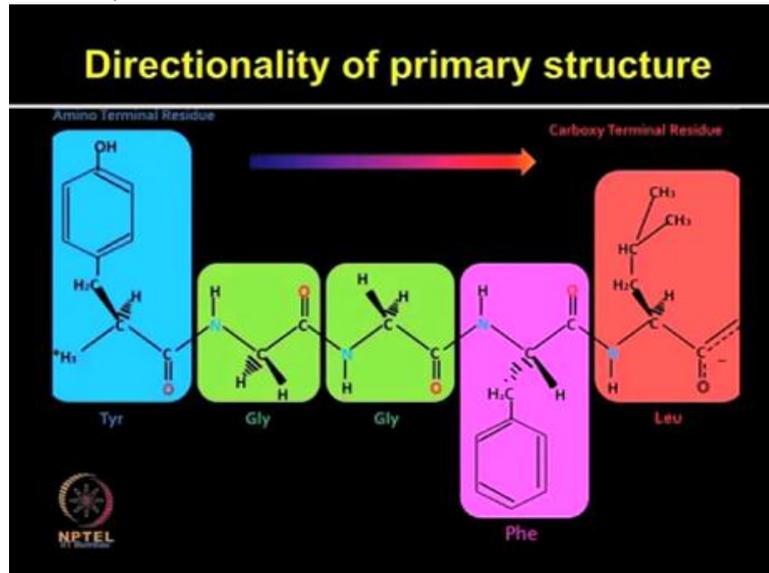
Amino acids constitute basic monomeric unit of proteins and they are joined together by the peptide bonds. These 20 standard amino acids can be arranged in several ways and therefore it can give rise to unique structural and functional properties. Primary structure refers to the sequence of amino acids.

(Refer Slide Time: 04:47)



As you can see, on the left slide, different amino acids can come together and the linear sequence of amino acids constitutes the primary structure with loss of water molecule.

(Refer Slide Time: 05:01)



Now what is the directionality of primary structure? The polypeptide chains have polarity. So one end is alpha amino group and other end is alpha carboxyl group. The amino marks the beginning of any polypeptide chain.

(Refer Slide Time: 05:32)

Amino acid sequence: significance

- Essential for elucidation of its mechanism of action
- Determines 3-D structure of proteins
- Amino acid alteration can produce abnormality
- Sequence tells us an evolutionary history of protein

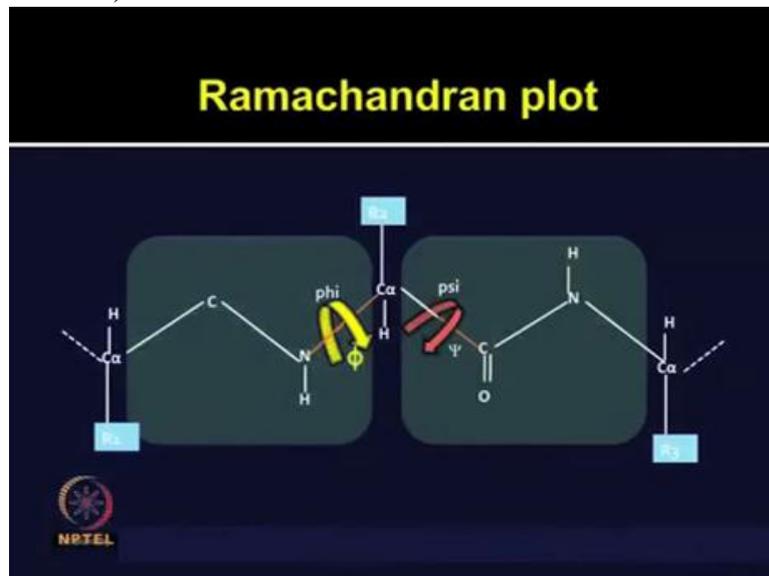
NPTEL

So what is the significance of amino acid sequence? As we discussed, this represents the primary structure. So amino acid sequence is essential for elucidation of its mechanism of action and enzyme's catalytic action can be determined.

It determines three-dimensional structure of the proteins links in the functional three dimensional protein structure and the genetic message obtained from the DNA. The amino acid alterations can produce various types of disease abnormality.

For example cystic fibrosis, change in only one amino acid can give rise to the abnormality and these amino acid sequences can also tell us various types of evolutionary aspect of the protein; so various types of information can be obtained from amino acid sequence.

(Refer Slide Time: 06:25)



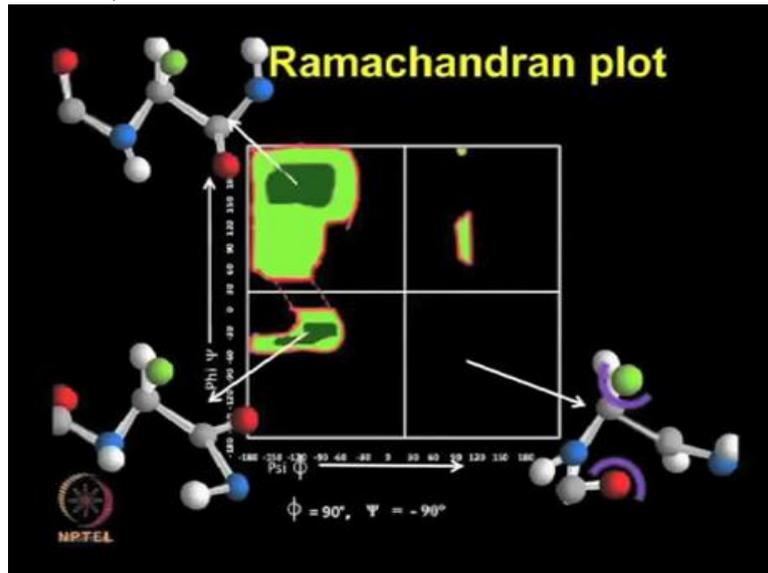
Now let's move on to concept of Ramachandran Plot. Before that it is important to know about the phi and the psi angles. As you can see here in the slide, rotations of two single bonds adjust structure of each amino acid in polypeptides.

The phi angle between the Nitrogen and the alphacarbon atom and the psi angle between alphacarbon and carbonyl carbon; these phi and psi angles determine the path of polypeptide chain. All the combinations of phi and psi angles are not possible.

So the allowed combinations can be viewed on 2D plot which is known as the Ramachandran Plot or Ramachandran diagram.

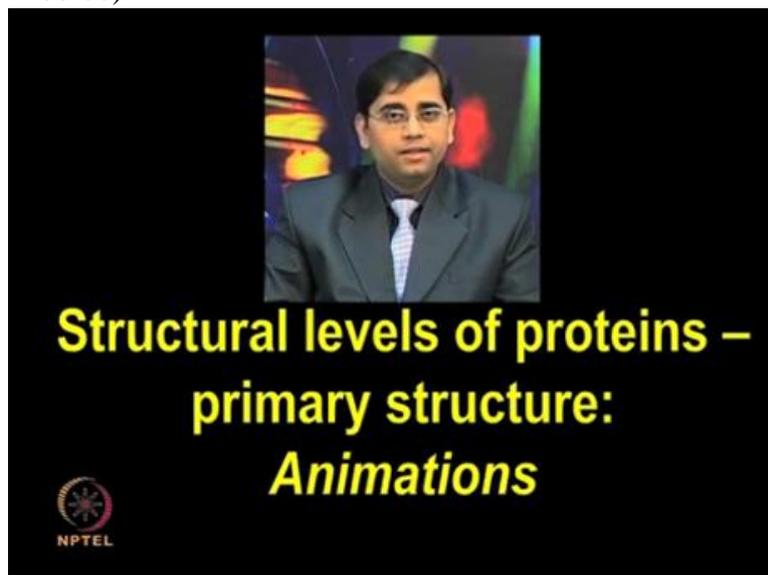
There could be many possibilities of various types of combination but all the combinations are not allowed because of the steric hindrances and collision between the various atoms, therefore steric exclusion can be a powerful governing factor for organizing such plot.

(Refer Slide Time: 07:39)



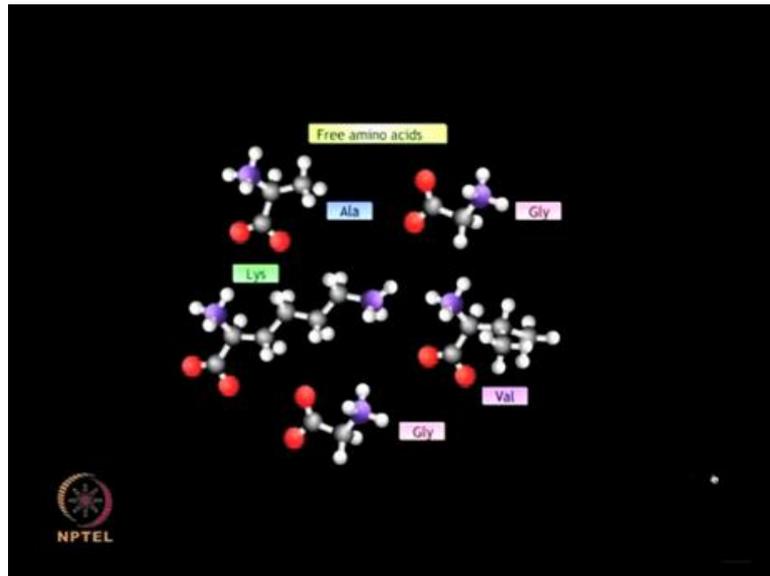
You can see more clearly in this slide, the Ramachandran Plot where most favorable regions are shown in the dark green color and less favored regions are shown in the light green.

(Refer Slide Time: 08:00)



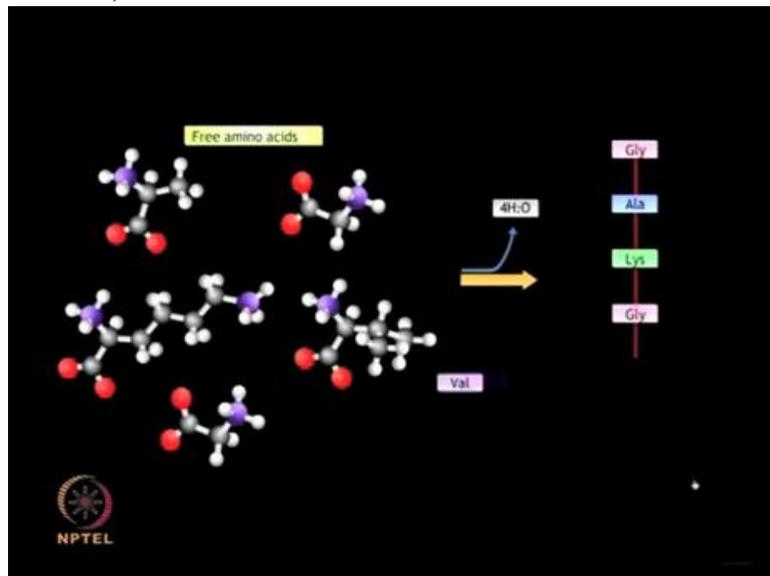
The structure level of proteins, the primary structure; few concepts will be discussed in the following animation.

(Refer Slide Time: 08:08)



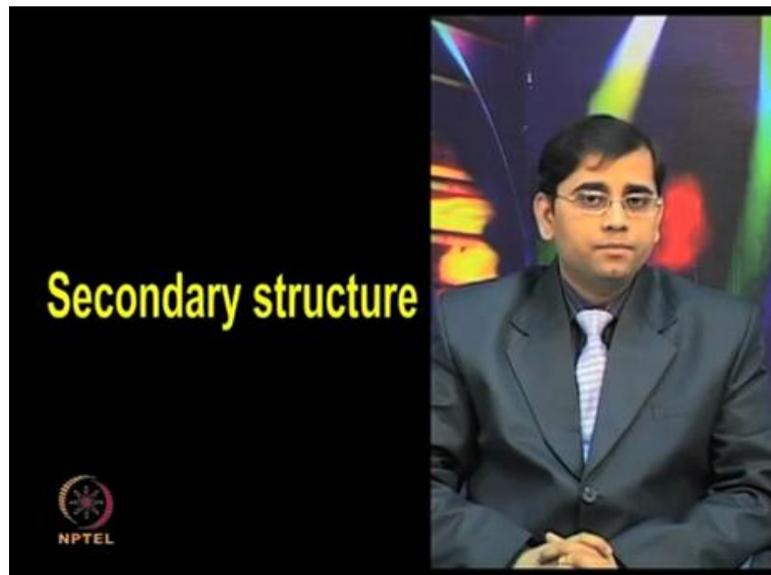
Amino acids are joined together in a head-to-tail arrangement by means of peptide bonds with the release of water molecules.

(Refer Slide Time: 08:28)



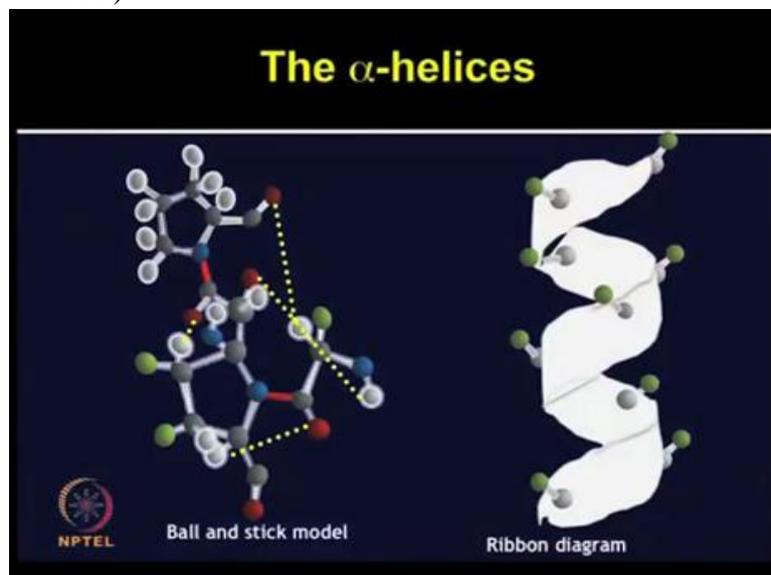
This linear sequence of amino acids constitutes the primary structure.

(Refer Slide Time: 08:31)



Let's now discuss about secondary structure which refers to locally folded regions. The folding of polypeptide or protein chain into regular structures like alpha helices, beta sheets, turns and loops; all this represent the secondary structures.

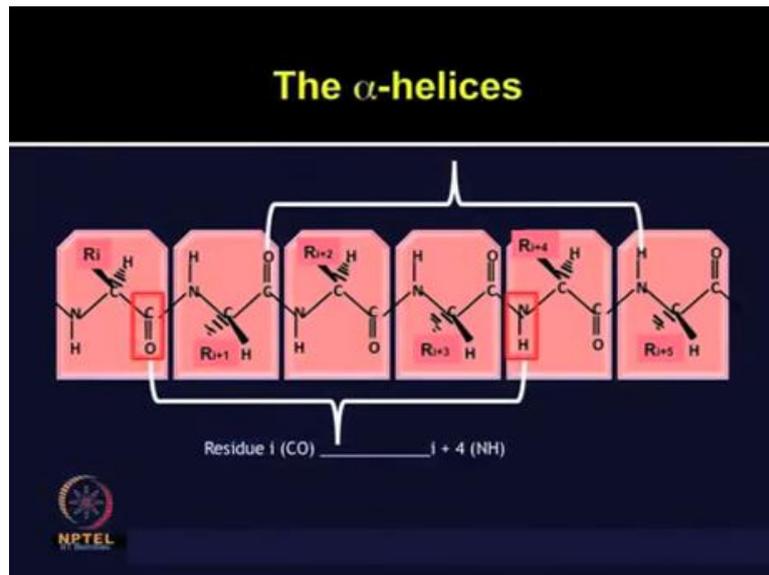
(Refer Slide Time: 08:53)



Let's first start with the alpha helices. Proteins have variable helix content. Alpha helix shows rod-like structure. It has a main chain and a side chain.

The main chain is tightly coiled around helical axis and side chain is extended outward away from the helical axis as you can see in the ribbon diagram on the right side and the ball-and-stick model on the left side. Specific Hydrogen bonds stabilize this helical core.

(Refer Slide Time: 09:32)



Alpha helix can be stabilized by the Hydrogen bond, so the carbonyl group of each amino acid with NH group of amino acid which are 4 residues ahead in the sequence, they form these Hydrogen bonds as you can see in this figure here.

There are special types of alpha helices where 2 alpha helices can wrap up or 3 alpha helices can come together.

(Refer Slide Time: 10:05)

Special type of α -helices

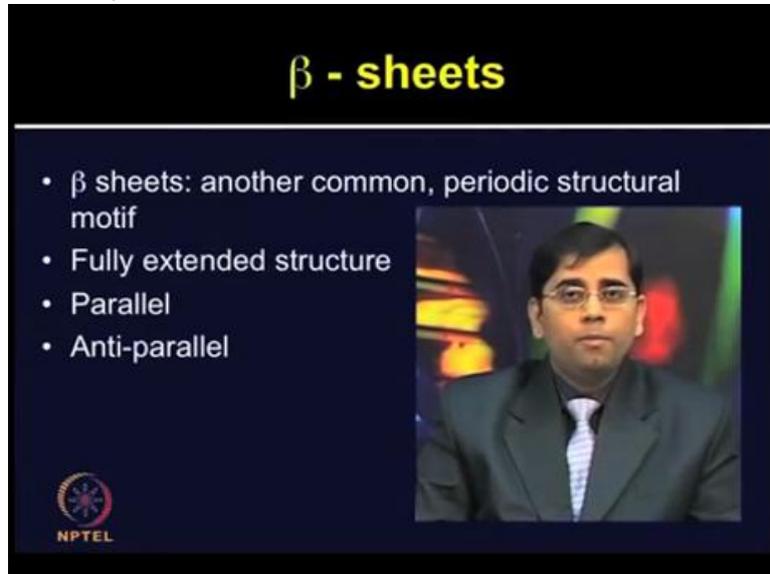
- α -Keratin
 - Two α -helices wrap to form a stable structure
- Collagen
 - It contains 3 helical polypeptide chain

The NPTEL logo is visible in the bottom left corner.

So the first example is alpha Keratin where two alpha helices can wrap to form a stable structure. It is primary component of hair and consists of two helical coils around each other and forms a left-handed super helix which is known as a coiled coil.

Another example is Collagen which is fibrous component of skin, bone etc. It is also most abundant in mammal. It contains 3 helical polypeptide chains.

(Refer Slide Time: 10:46)



β - sheets

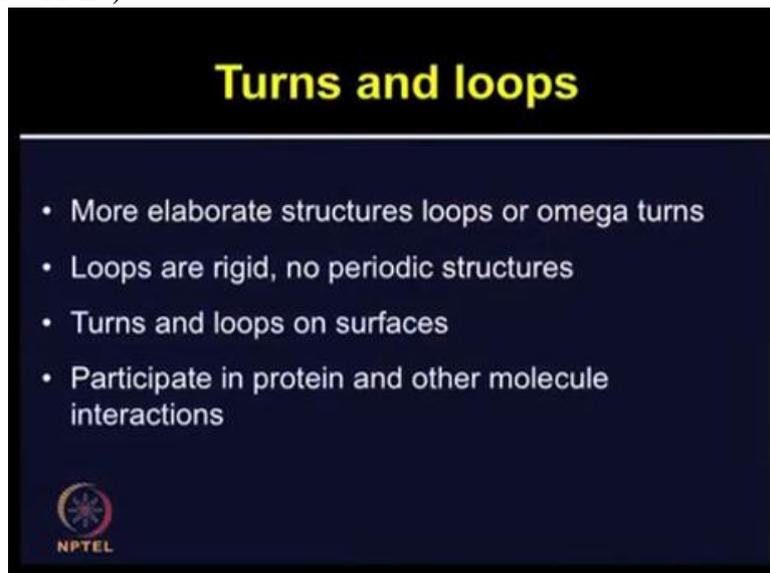
- β sheets: another common, periodic structural motif
- Fully extended structure
- Parallel
- Anti-parallel

NPTEL

The slide features a video inset of a man in a suit and glasses, likely the presenter, positioned to the right of the text. The NPTEL logo is located in the bottom left corner.

Beta sheet is another common periodic structure motif which was discovered by scientist Pauling and Corey. It is fully extended structure unlike the tightly coiled alpha helices. It can be having two directions, the parallel or anti-parallel; parallel when they are running in the same direction and anti-parallel when they are running in opposite directions.

(Refer Slide Time: 11:20)



Turns and loops

- More elaborate structures loops or omega turns
- Loops are rigid, no periodic structures
- Turns and loops on surfaces
- Participate in protein and other molecule interactions

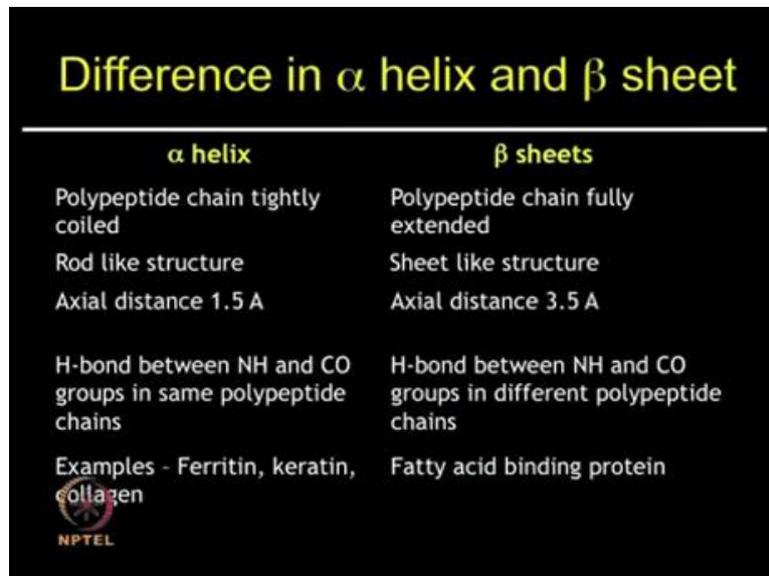
NPTEL

The slide features the NPTEL logo in the bottom left corner.

Another category of secondary structures are turns and loops. These are more elaborate structures, loops or omega turns which also perform chain reversal. Loops are rigid, well-

defined. These are not periodic structures. The turns and loops are present on surface and participate in various important properties of proteins and other biomolecule interactions.

(Refer Slide Time: 11:51)

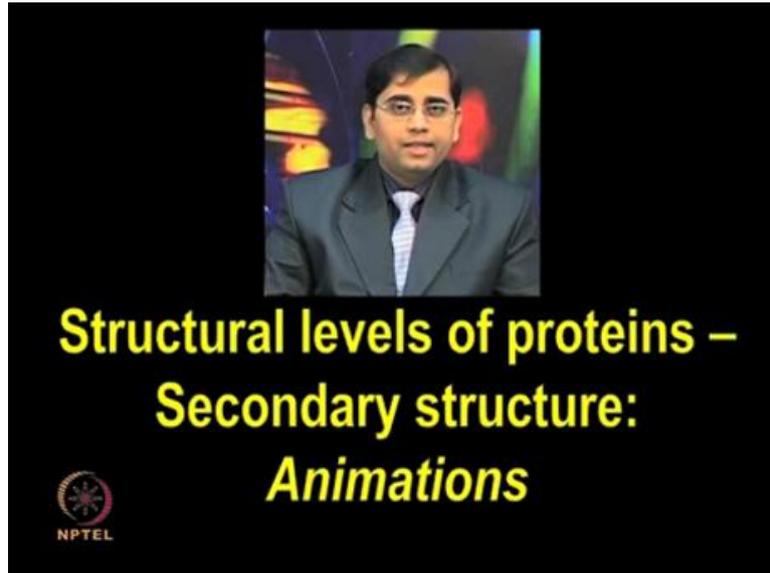


α helix	β sheets
Polypeptide chain tightly coiled	Polypeptide chain fully extended
Rod like structure	Sheet like structure
Axial distance 1.5 A	Axial distance 3.5 A
H-bond between NH and CO groups in same polypeptide chains	H-bond between NH and CO groups in different polypeptide chains
Examples - Ferritin, keratin, collagen	Fatty acid binding protein

The differences in alpha helix and beta sheet are summarized in the slide. The alpha helix polypeptide chain is tightly coiled where as beta sheet, it is fully extended. Alpha helix, rod like structure and beta sheets, sheet like structure.

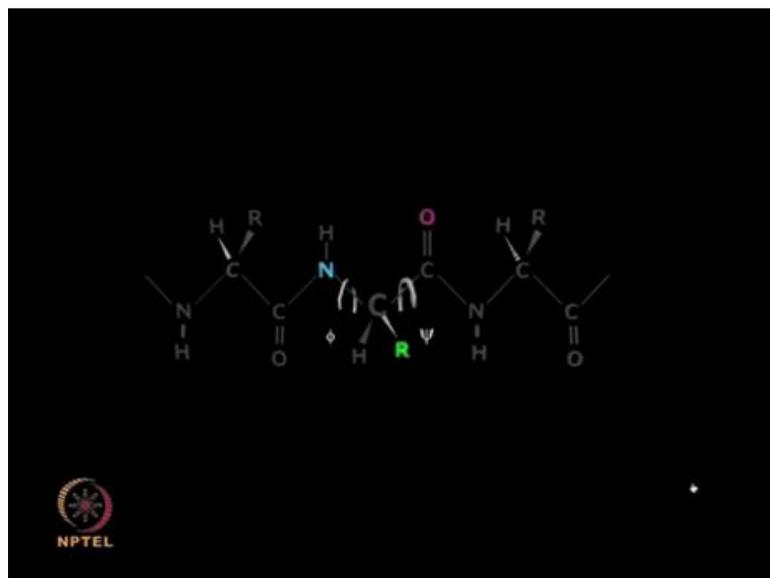
The axial distance between adjacent amino acids is 1.5 Angstrom, where as it is 3.5 Angstrom in beta sheets. In alpha helix, Hydrogen bond between NH and CO groups in same polypeptide chains where as in beta sheet it is in different polypeptide chains. Alpha helix examples include Ferritin, Keratin, Collagen etc; in beta sheet it is fatty acid binding protein.

(Refer Slide Time: 12:40)



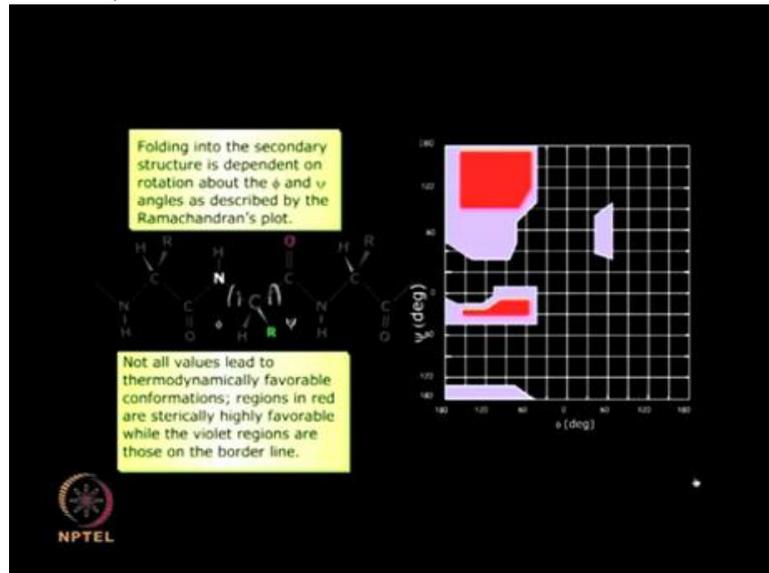
Some of the properties of secondary structures will be described in following animation

(Refer Slide Time: 12:50)



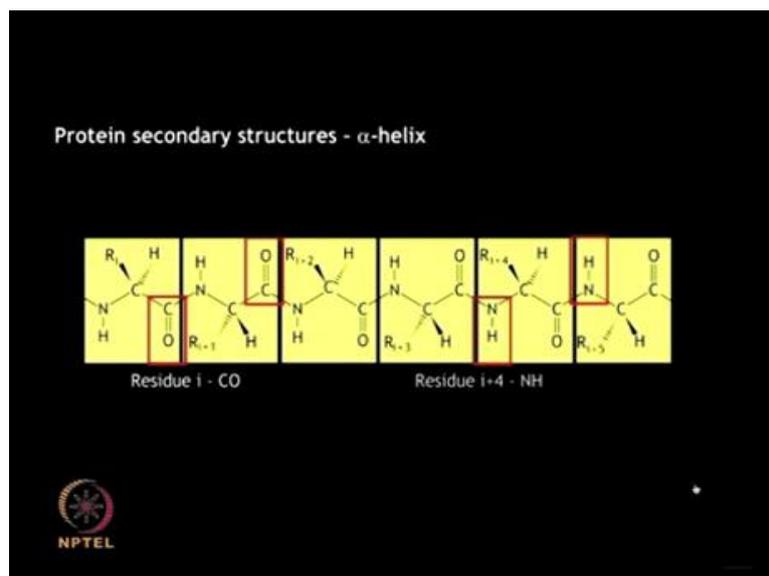
The folding of the primary structure into the secondary is governed by the permissible rotations about the phi and psi angles. Not all values of these angles lead to sterically favorable conformations.

(Refer Slide Time: 13:10)



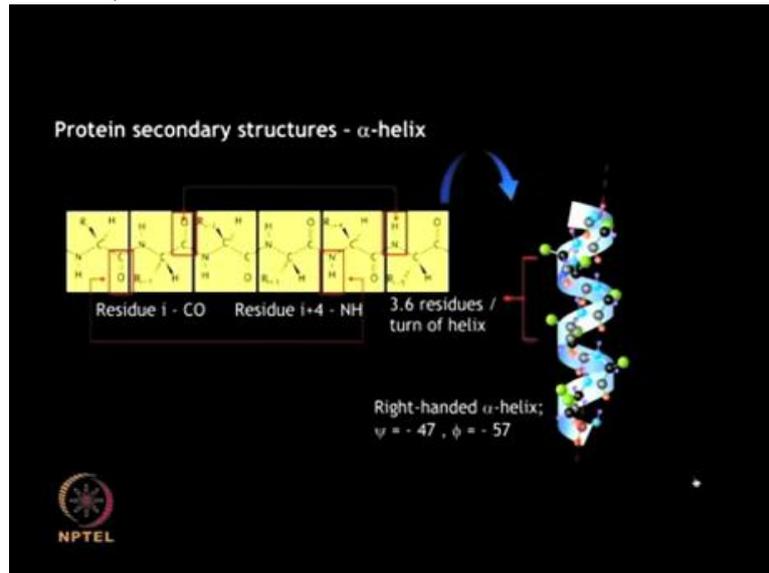
The Ramachandran Plot defines these regions of favorability.

(Refer Slide Time: 13:20)



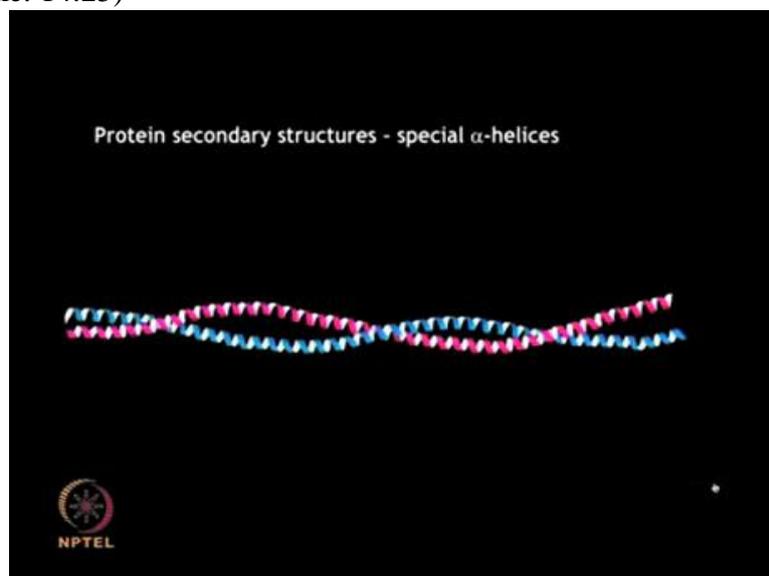
Amino acids along the polypeptide backbone interact through Hydrogen bonds leading to the secondary structures. The alpha helix has intra chain Hydrogen bonds between the Hydrogen of NH and Oxygen of CO in every fourth residue. Most alpha helices are right handed since the conformation is energetically more favorable.

(Refer Slide Time: 14:00)



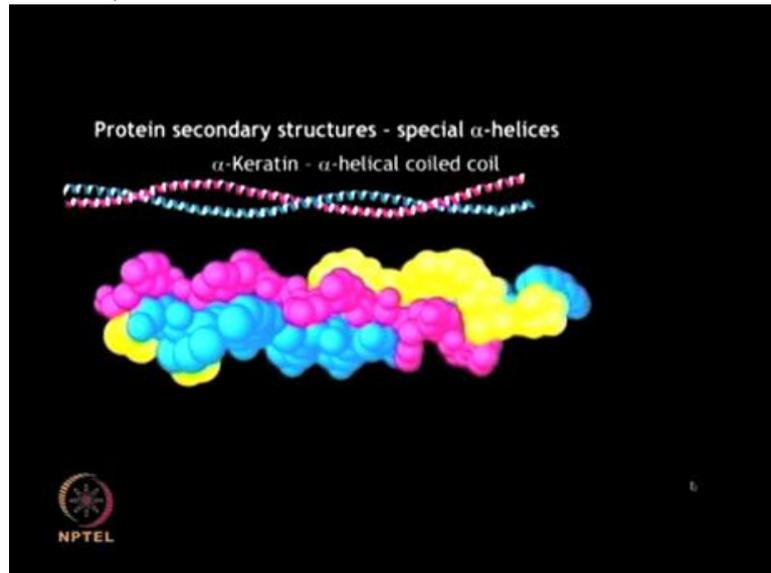
Here you can see more energetically favorable alpha helix structure. The amino acid Proline which has the cyclic side chain does not fit into the regular alpha helix structure and thereby limits flexibility of the backbone. It is commonly referred to as the helix breaker.

(Refer Slide Time: 14:25)



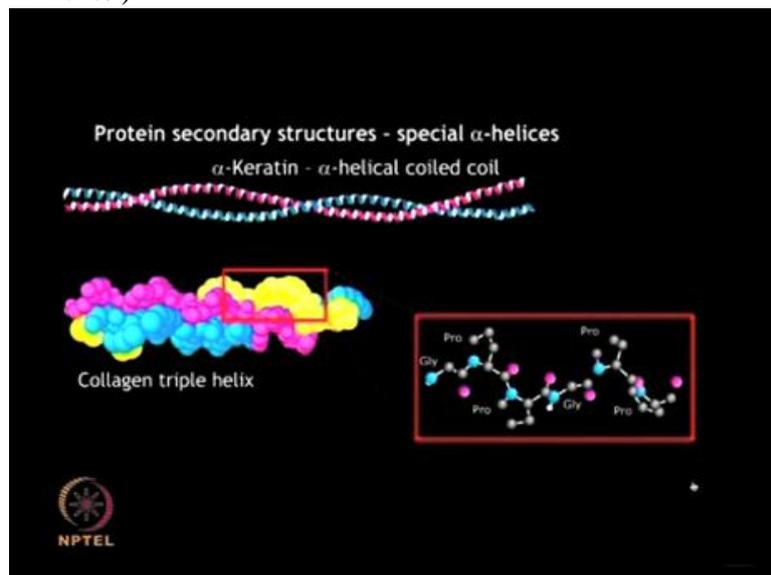
Alpha helices can also wind around each other to form stable structures such that their hydrophobic residues are buried inside while their polar side chains are exposed to the aqueous environment.

(Refer Slide Time: 14:57)



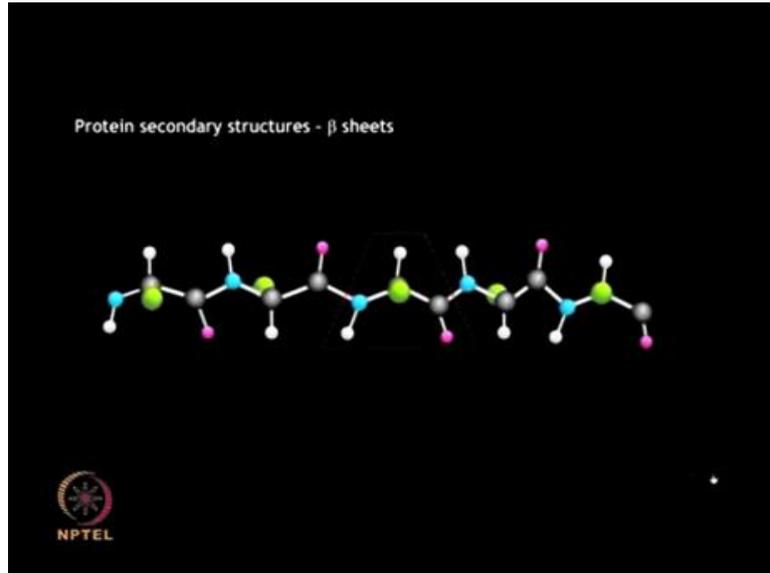
Alpha Keratin, the major protein component of hair consists of two such coiled coils forming a left-handed super helix.

(Refer Slide Time: 15:09)



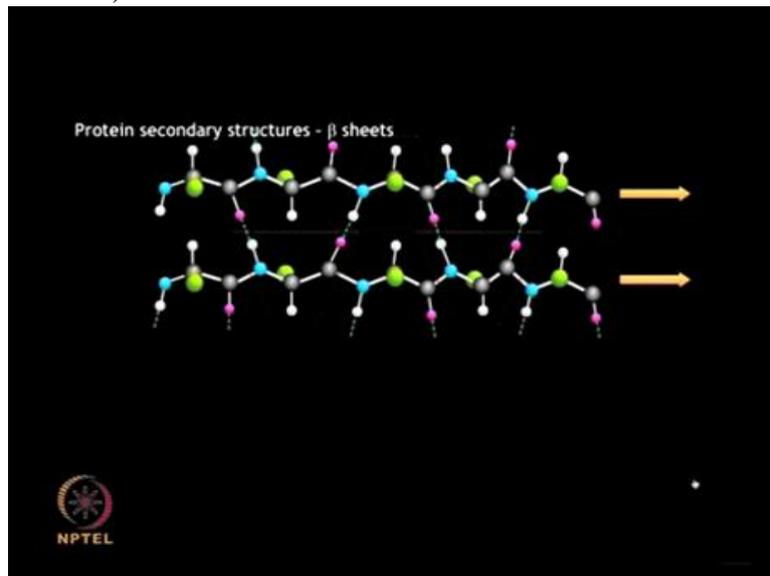
Collagen which is the fibrous component of the skin, muscles etc. consist of 3 such coiled alpha helices. It has a characteristic recurring amino acid sequence of Glycine, Proline, Hydroxyproline with Glycine appearing at every third residue.

(Refer Slide Time: 15:33)



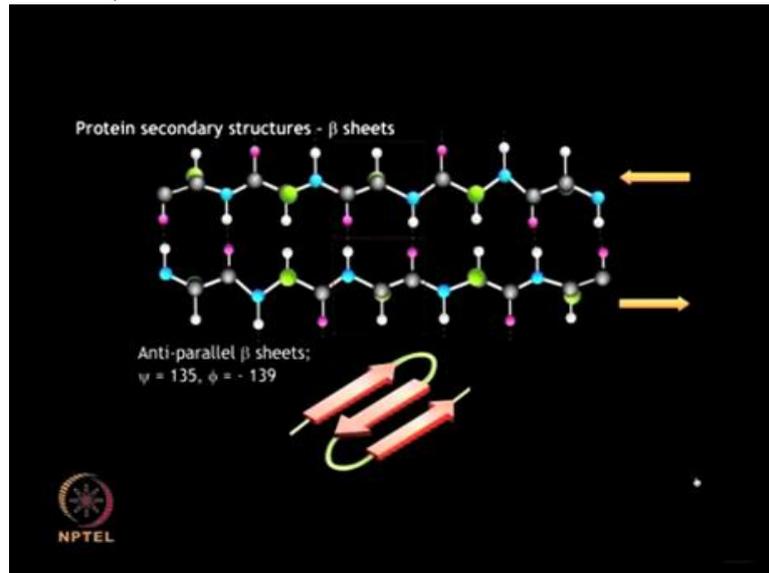
Beta pleated sheets discovered by Pauling and Corey is another common secondary structure with periodic repeating units.

(Refer Slide Time: 15:50)



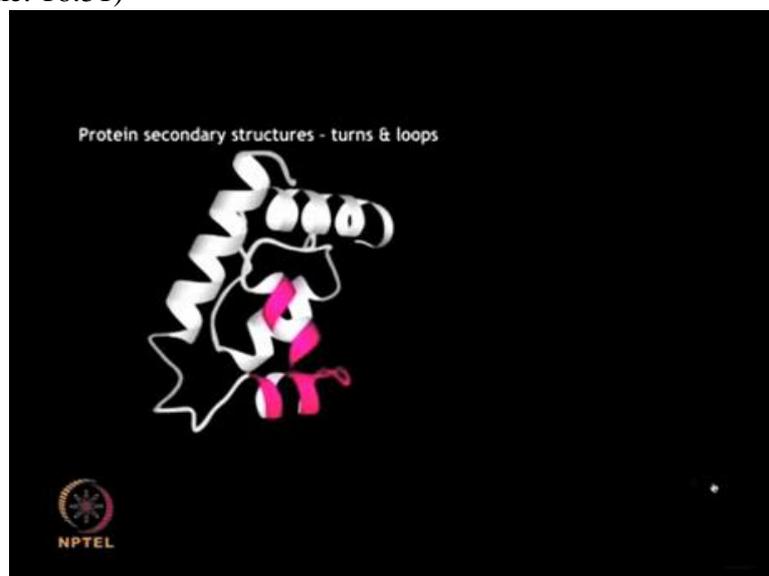
It is composed of 2 or more polypeptide chains with their side chains oriented above and below the plane. It is an extended structure with Hydrogen bonds between the chains stabilizing it.

(Refer Slide Time: 16:21)



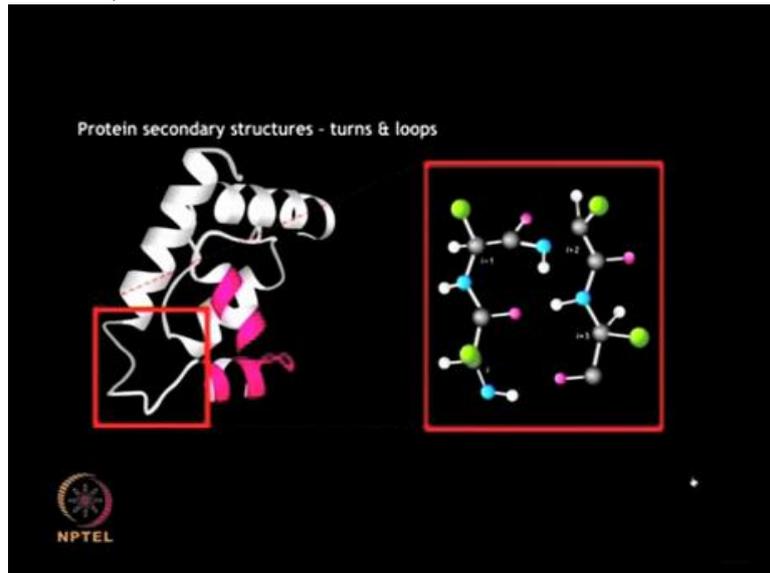
Amino acids in parallel beta sheets which run in the same direction interact with two different amino acids on the adjacent strand through the Hydrogen bonds. Amino acids in anti-parallel strands on the other hand interact with only one amino acid on an adjacent strand.

(Refer Slide Time: 16:51)



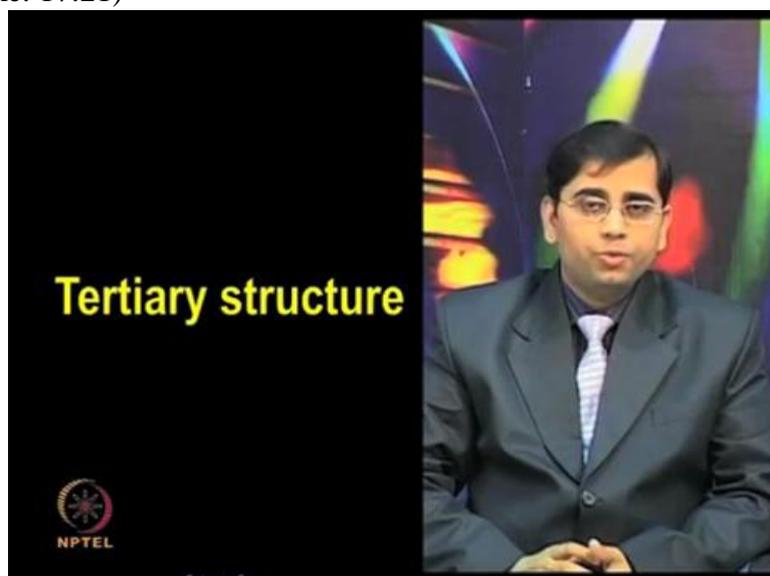
Almost all proteins exhibit a compact, globular structure which is possible only if there are turns or loops between the various regions.

(Refer Slide Time: 17:08)



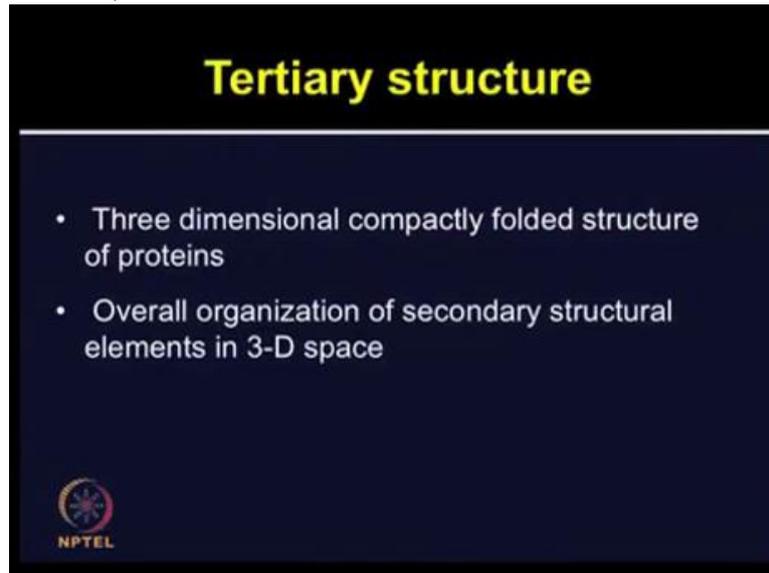
Beta turns which are the most commonly observed turn structures consist of rigid, well-defined structures that usually lie on the surface of the protein molecule and interact with other molecules.

(Refer Slide Time: 17:21)



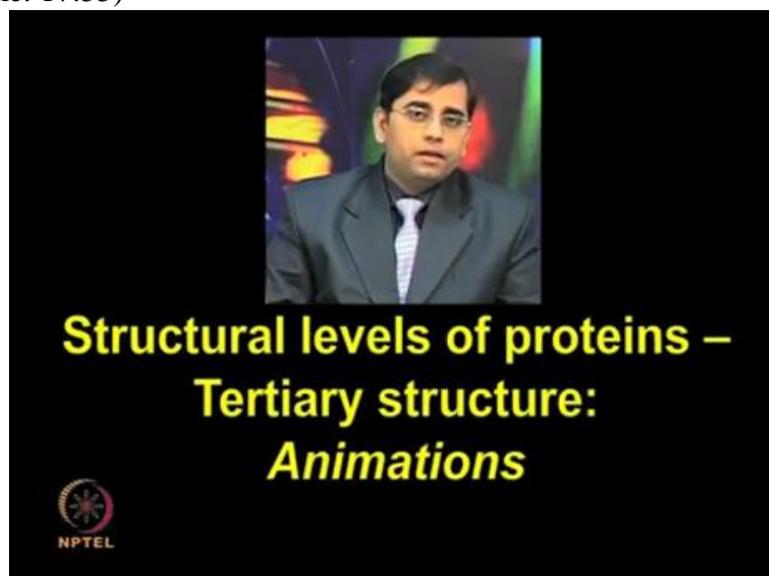
Let's now move on to tertiary structure which refers to overall folded structure. NMR and X-ray crystallography provides detailed three dimensional structures.

(Refer Slide Time: 17:34)



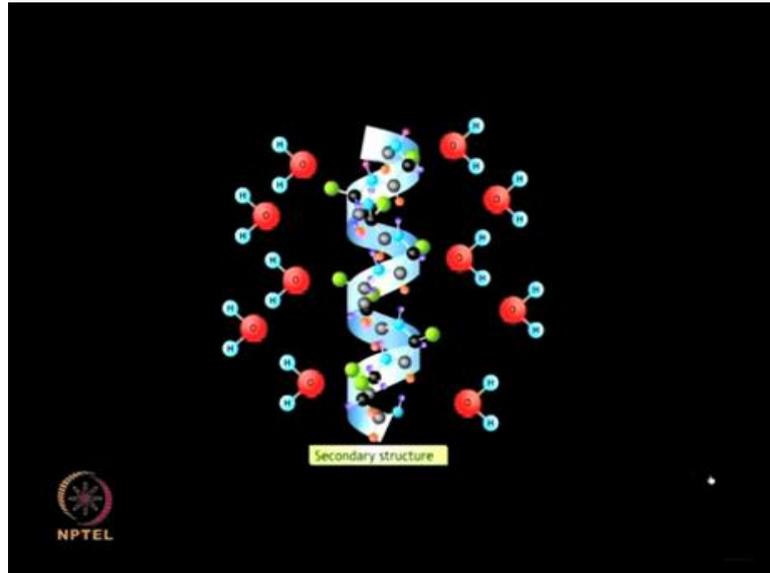
The three dimensional structure is compactly folded structure of proteins and it represents overall organization of secondary structural elements in 3D space. There are numerous interactions which stabilize the tertiary structure of proteins.

(Refer Slide Time: 17:55)



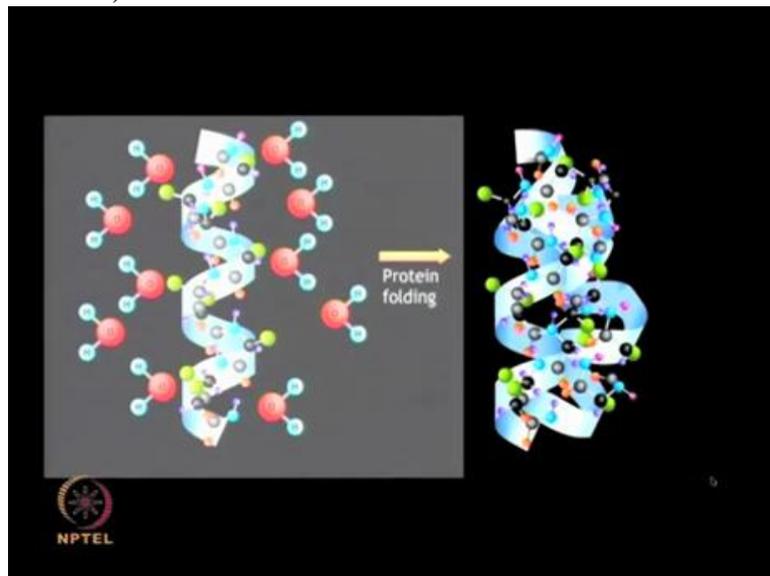
We will take Myoglobin as an example and describe some of the properties of tertiary structure in following animation.

(Refer Slide Time: 18:26)



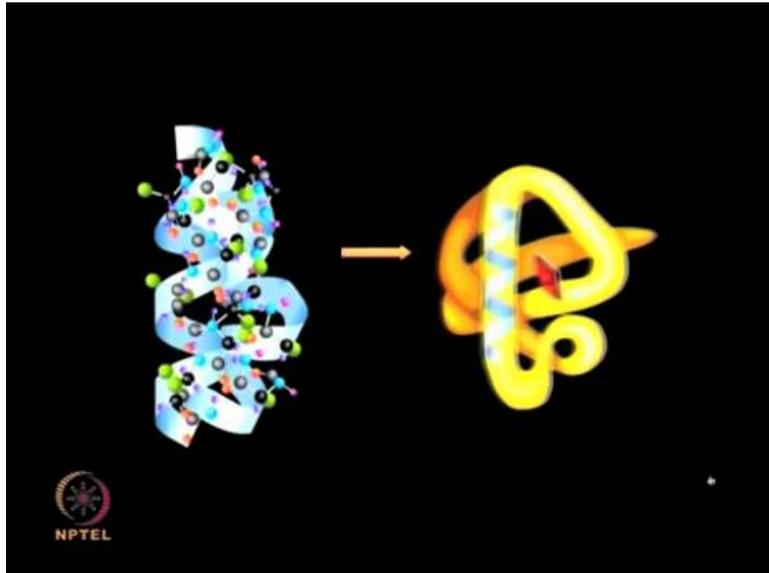
Amino acids located far apart on the polypeptide chain interact with each other by means of Hydrogen bonds, electrostatic interactions, disulfide bridges etc.

(Refer Slide Time: 18:35)



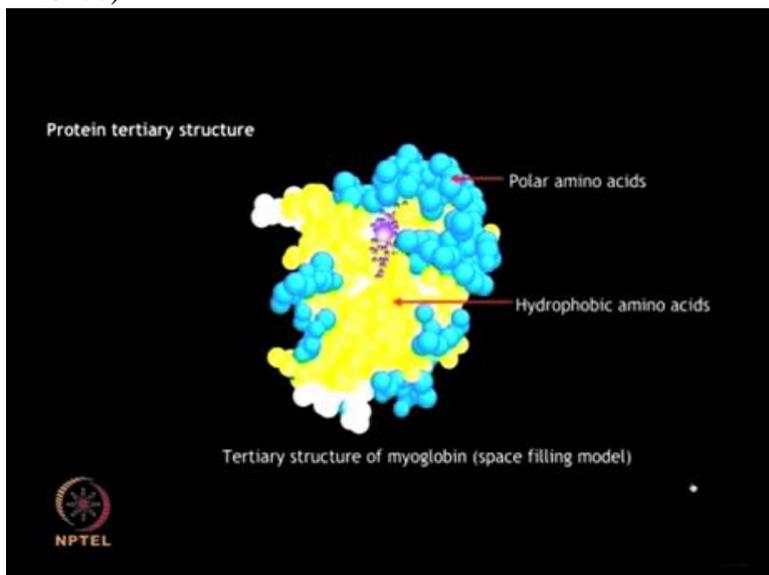
... which allow the protein to fold three dimensionally in the space giving rise to the tertiary structure.

(Refer Slide Time: 18:39)



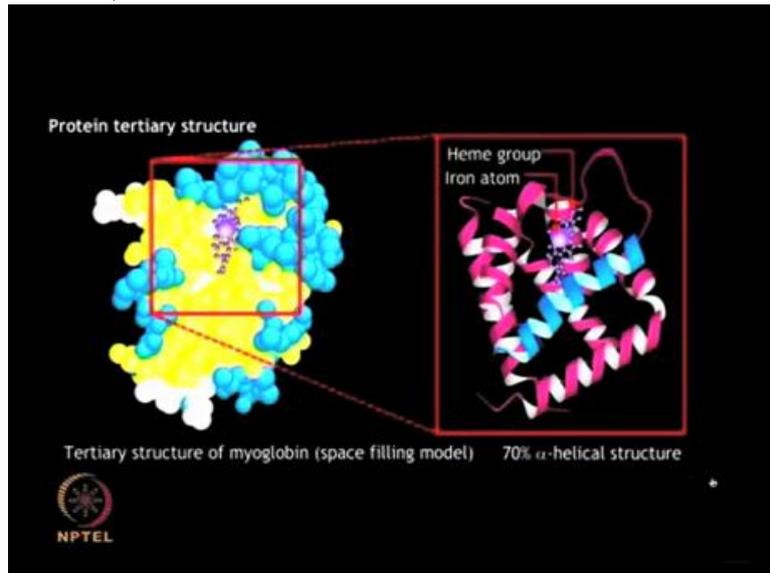
Protein folding takes place such that the hydrophobic residues are buried inside the structure while polar residues remain in contact with the surroundings.

(Refer Slide Time: 19:00)



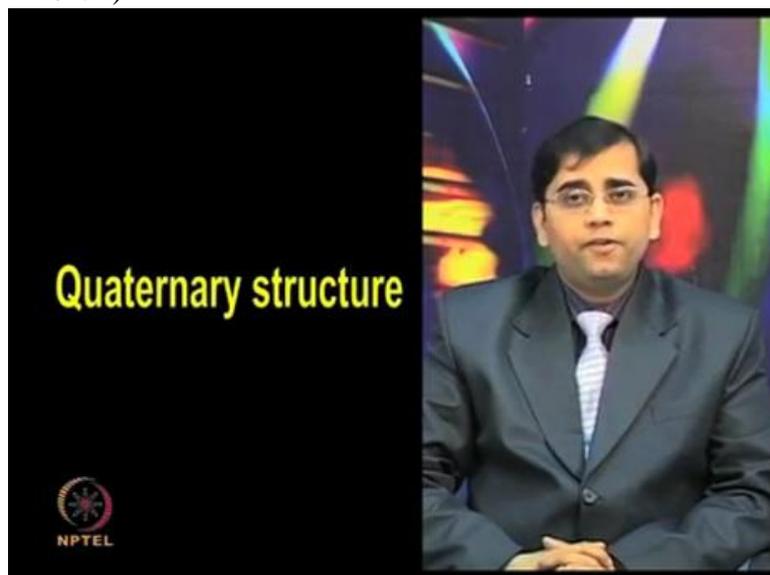
The tertiary structure of Myoglobin determined by John Kendrew clearly revealed that the nature of amino acid side chains dictate their location in the tertiary structure. The hydrophobic residues are found buried inside the structure while the polar amino acids are present in the surface.

(Refer Slide Time: 19:36)



70% of main chain of Myoglobin is folded into alpha helices with the rest being present in the form of turns and loops which are essential to provide it a compact structure.

(Refer Slide Time: 19:54)



What is quaternary structure? It refers to interaction between individual protein sub-units in a multi-subunit complex.

(Refer Slide Time: 20:04)

Quaternary structures

- Final level of protein structure
- Spatial arrangement of subunits and their interactions
- Polypeptide chains assemble to form multisubunit structure

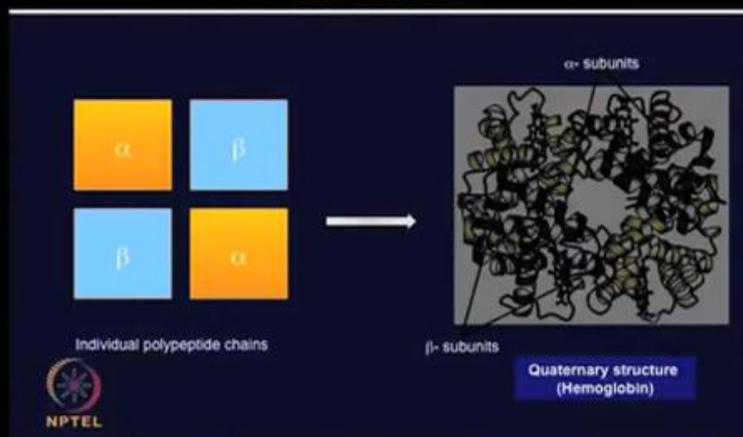


So, quaternary structures represent final level of protein structures which is special arrangement of subunits and their interactions. The polypeptide chains assemble to form multi-subunit structure and each polypeptide chain is known as subunit.

The different examples such are DNA binding, co-protein of bacteriophage lambda which is representing simplest quaternary structure, then we have classical example of Hemoglobin.

(Refer Slide Time: 20:39)

Hemoglobin: tetramer quaternary structure

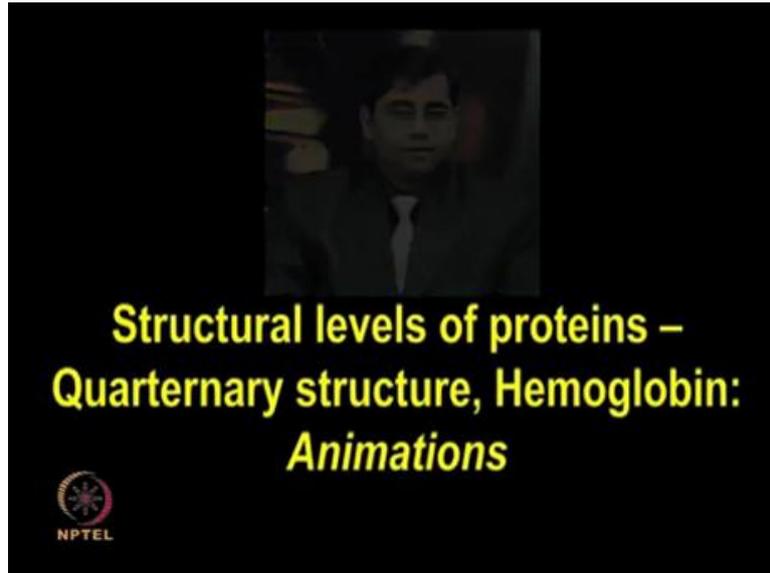


Individual polypeptide chains α -subunits
 β -subunits Quaternary structure (Hemoglobin)



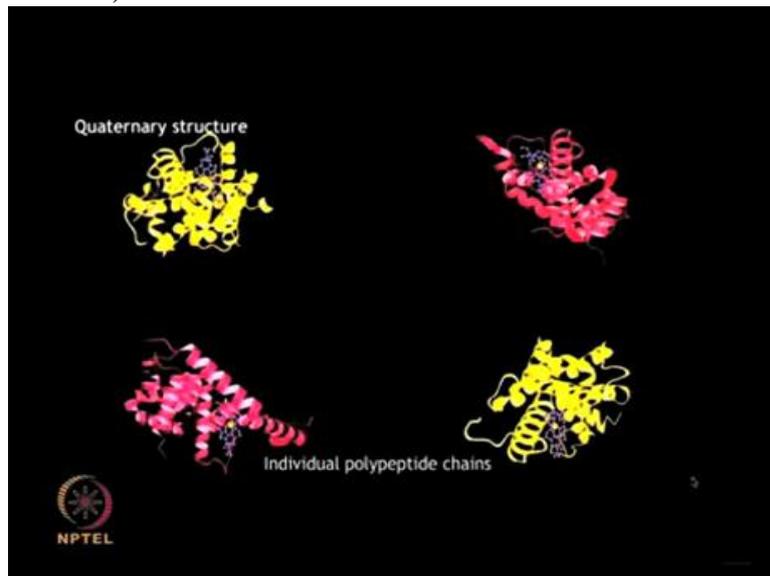
Let's look at Hemoglobin, the tetramer quaternary structure. It has 2 alpha subunits and 2 beta subunits. The individual polypeptide chains, they come together and form quaternary structure.

(Refer Slide Time: 20:58)



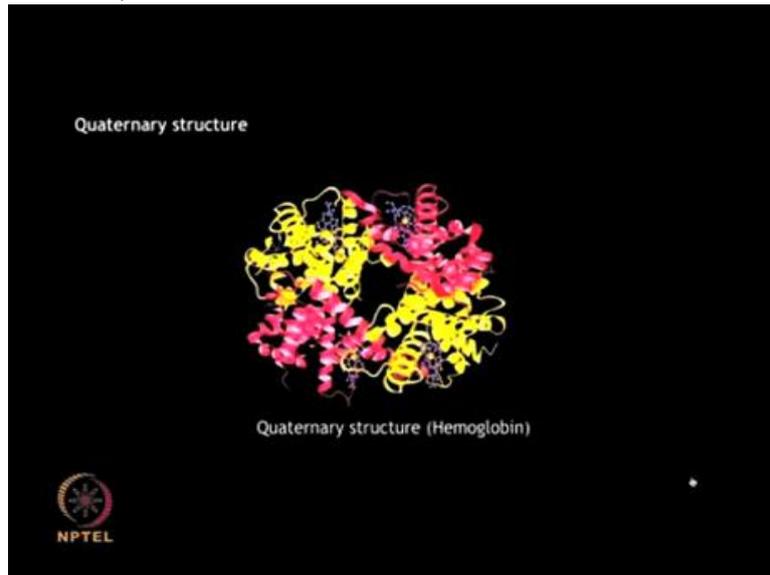
Properties of quaternary structures and some details about Hemoglobin and comparison of Myoglobin and Hemoglobin will be discussed with following animation.

(Refer Slide Time: 21:17)



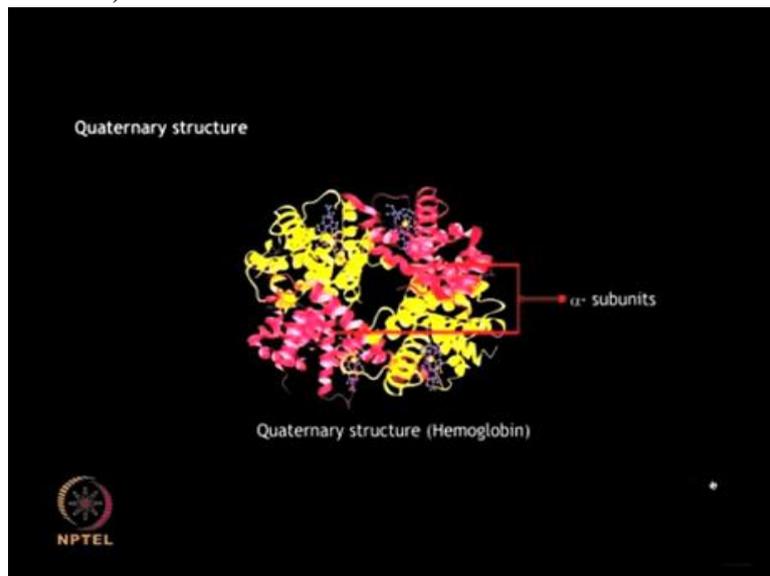
Different subunits or polypeptide chains interact with one another

(Refer Slide Time: 21:31)

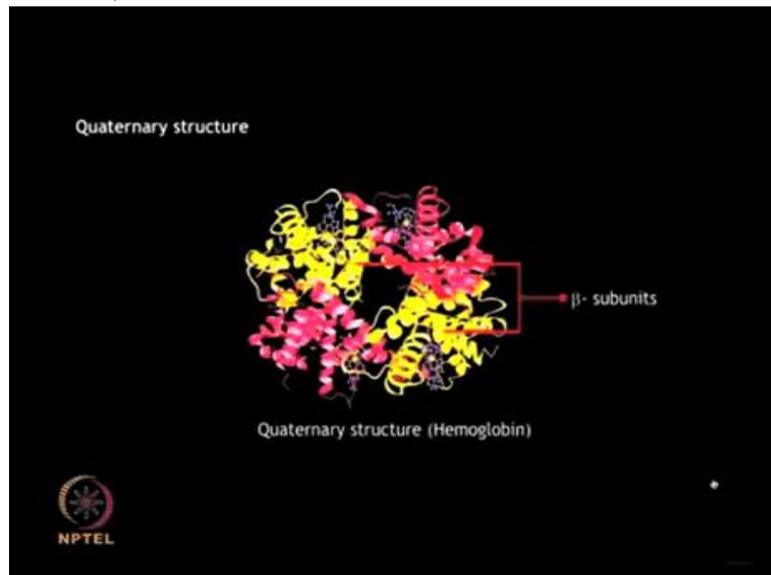


... and are held together by means of ionic, electrostatic, Vander Waal's etc interactions. Such multi-subunit proteins are having a quaternary structure...

(Refer Slide Time: 21:42)

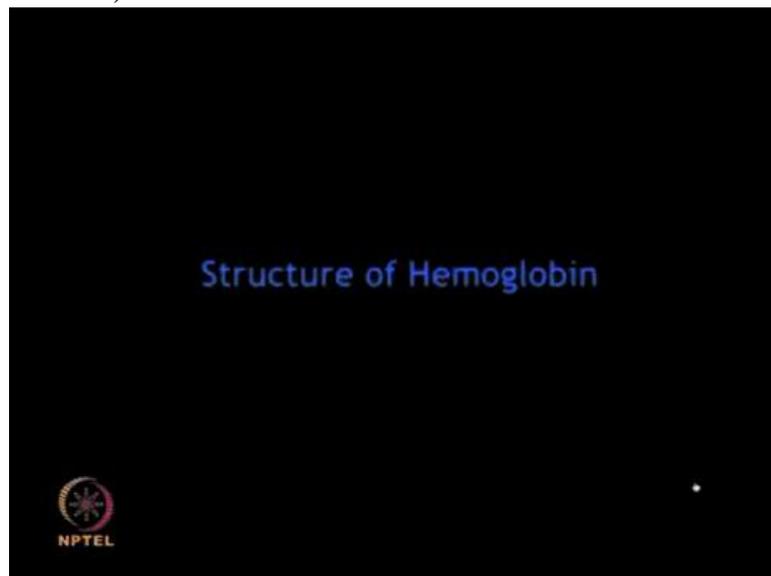


(Refer Slide Time: 21:45)

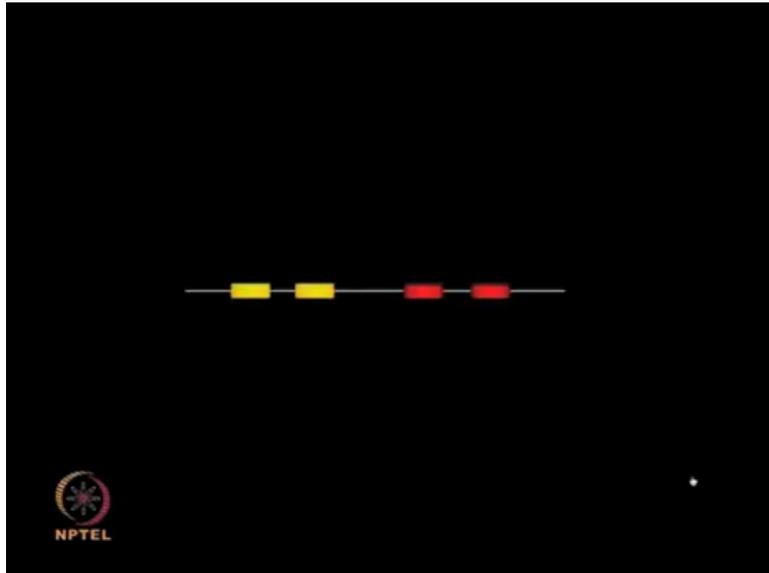


... which is the final level of protein structure.

(Refer Slide Time: 21:47)

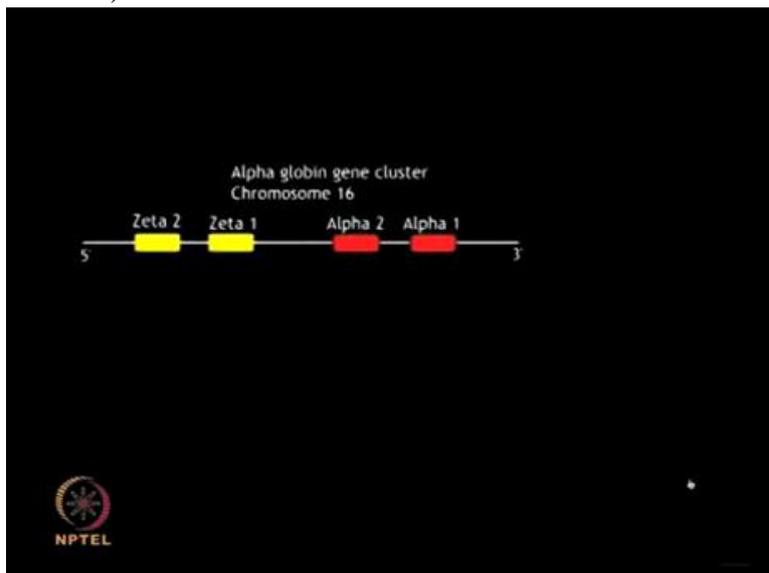


(Refer Slide Time: 21:53)



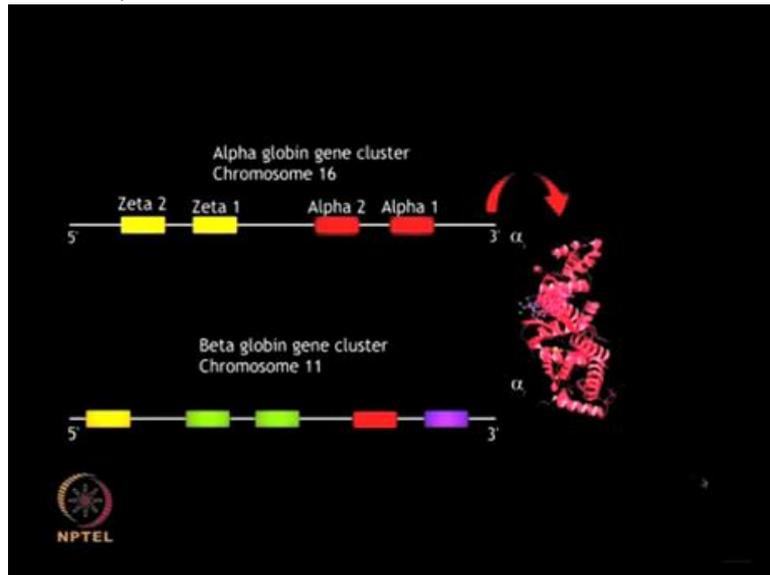
Hemoglobin is hetero tetramer composed of 2 alpha and 2 beta chains.

(Refer Slide Time: 22:11)



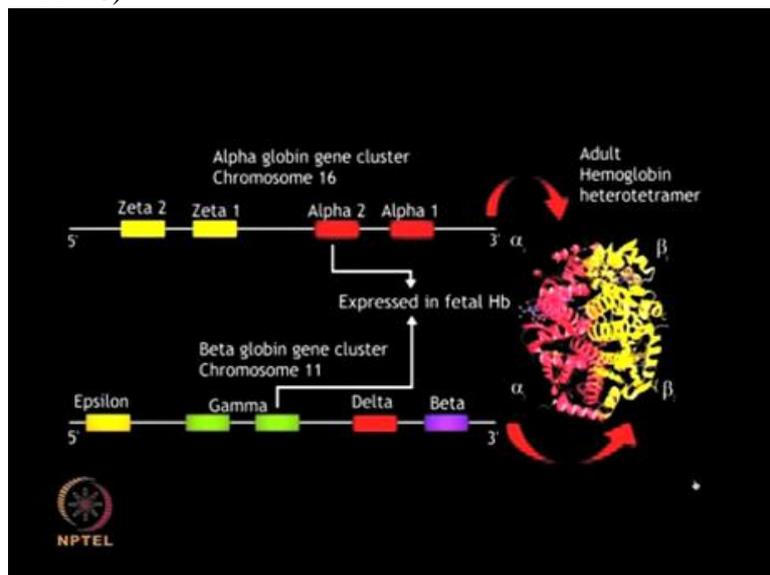
The alpha globin gene locus resides on chromosome 16 with each gene contributing to the synthesis of alpha globin chain.

(Refer Slide Time: 22:16)



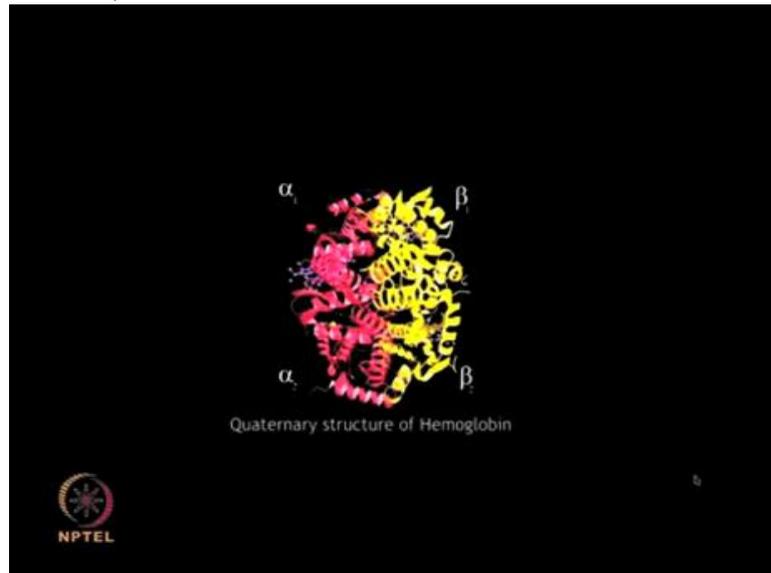
The beta globin gene locus resides on chromosome 11 and consists of all genes that are expressed...

(Refer Slide Time: 22:18)



... from the time of embryonic development of Hemoglobin to that of adult beta globin gene. The globin chains are synthesized by ribosomes in the Cytosol.

(Refer Slide Time: 23:02)



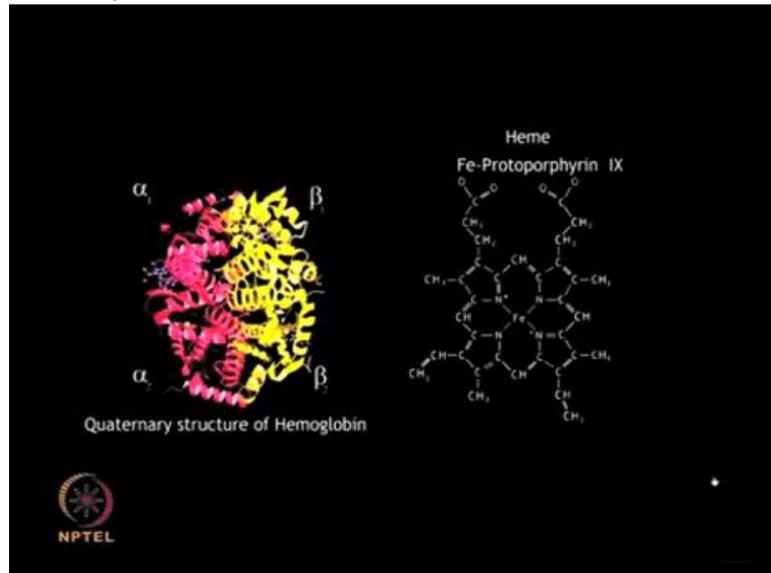
Every subunit of Hemoglobin is bound to the prosthetic group known as Heme.

(Refer Slide Time: 23:06)



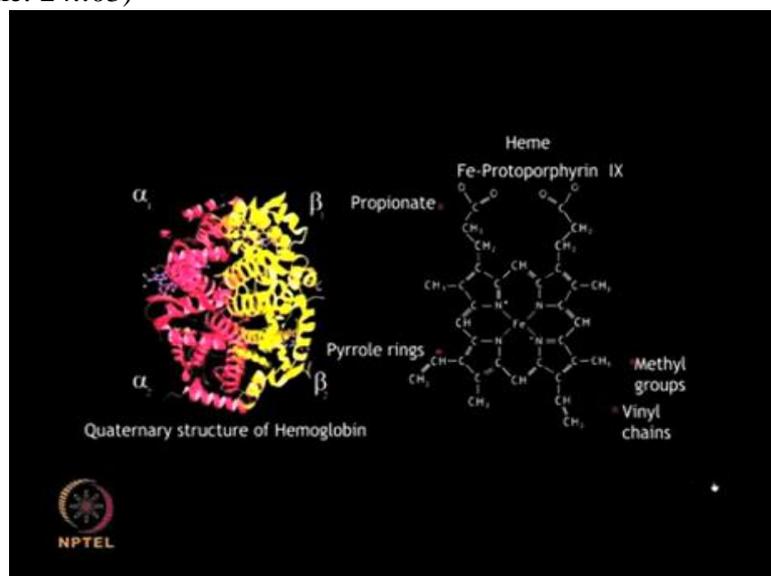
This consists of a central iron atom....

(Refer Slide Time: 23:16)



... in its ferrous state surrounded by a complex organic ring structure known as protoporphynin. The Heme group is essential for the Oxygen binding property of Hemoglobin.

(Refer Slide Time: 24::03)



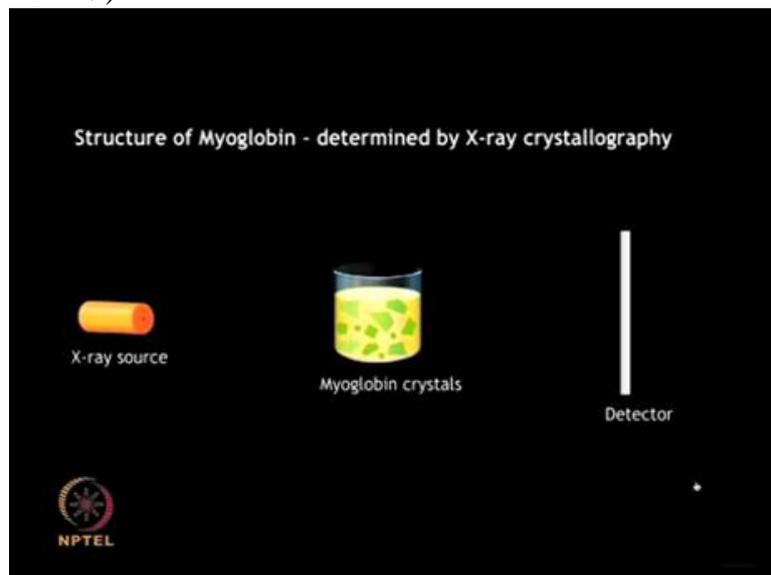
The iron atom forms 6 coordinate bonds, 4 of which are to the Nitrogen atom of Porphyrin ring, 1 to Histidine side chain in the globin subunit and the other being the binding side for Oxygen.

(Refer Slide Time:24:09)



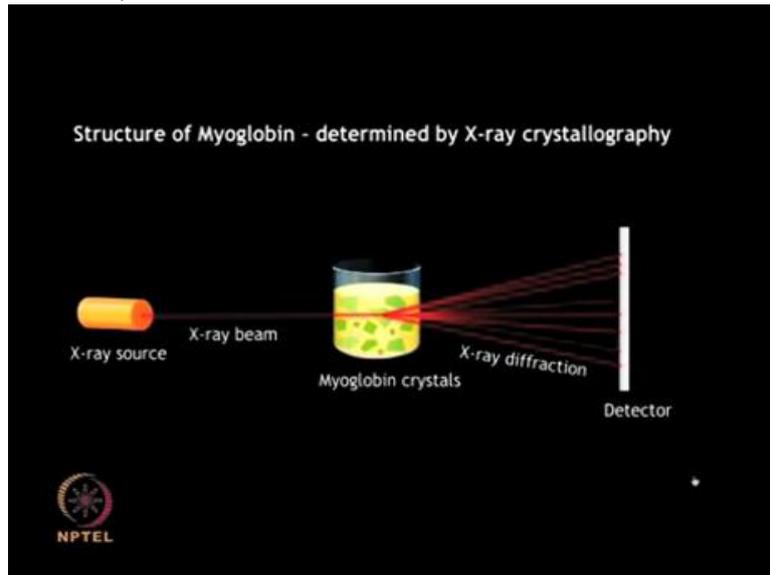
X-ray crystallography is a very useful visualization technique that facilitates the determination of the three-dimensional coordinates of atoms in a protein.

(Refer Slide Time:24:19)



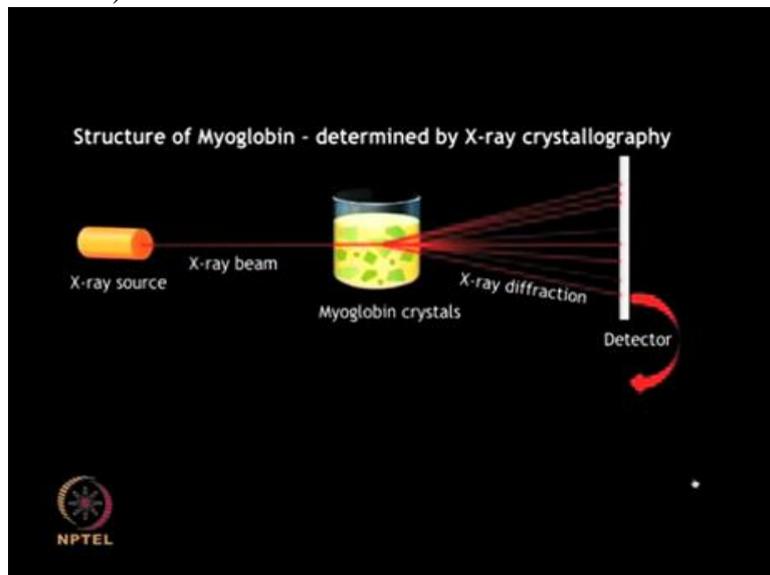
Myoglobin was the first protein whose structure was determined by X-ray Crystallographic studies.

(Refer Slide Time: 25:02)



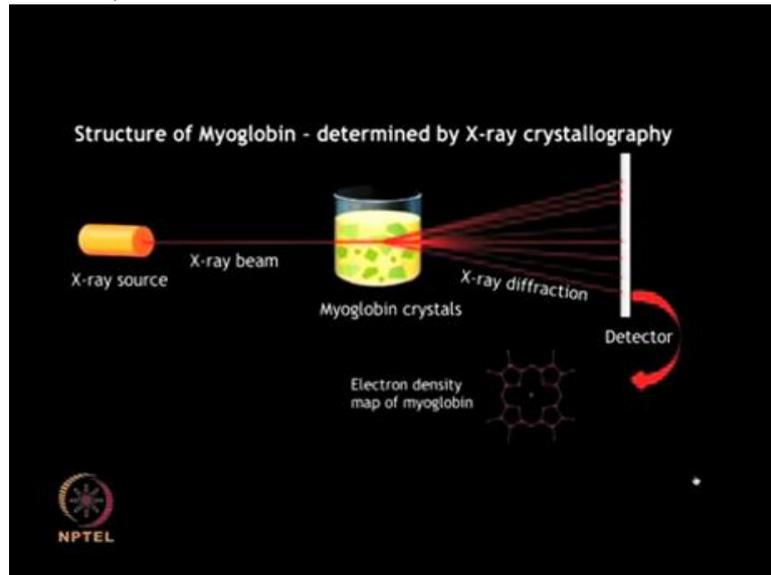
When the beam of X-ray was passed through the crystals of Myoglobin some part of the beam was found to pass straight through while the others were scattered in different directions.

(Refer Slide Time: 25:07)



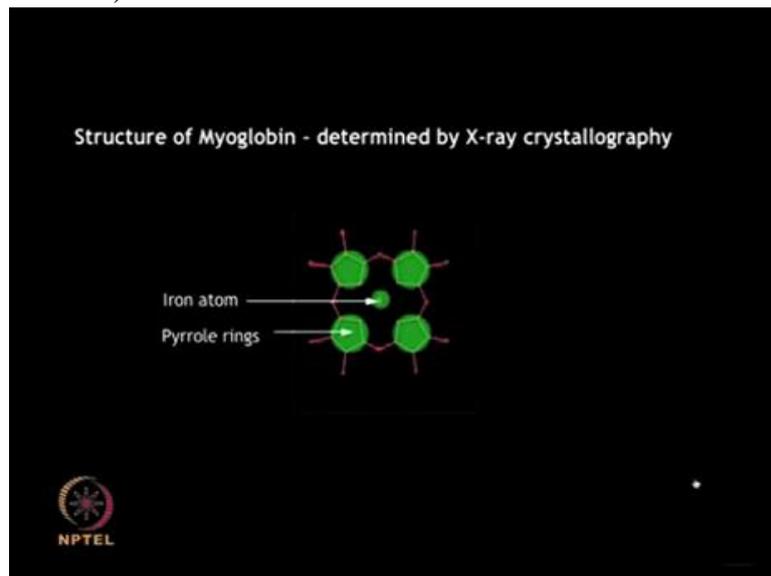
These scattered beams were detected by means of an X-ray film.

(Refer Slide Time: 25:14)



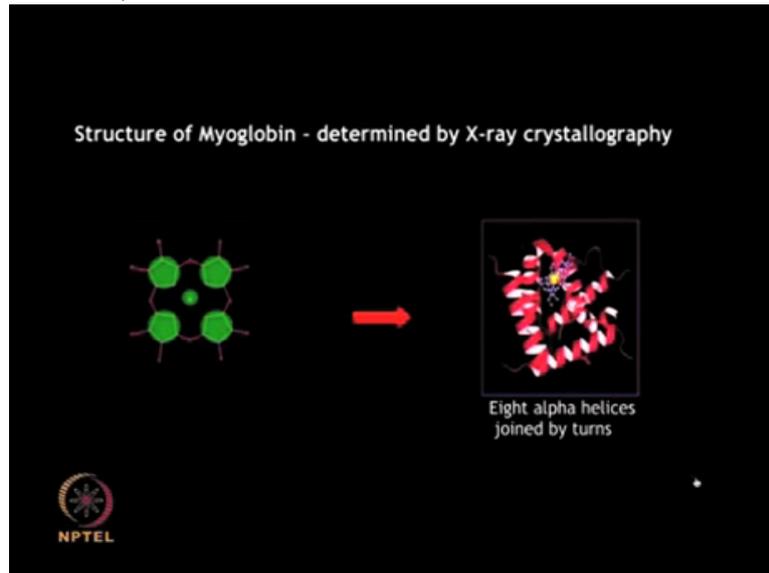
After the spot intensity calculations, it provided an electron density map of the protein.

(Refer Slide Time: 25:24)



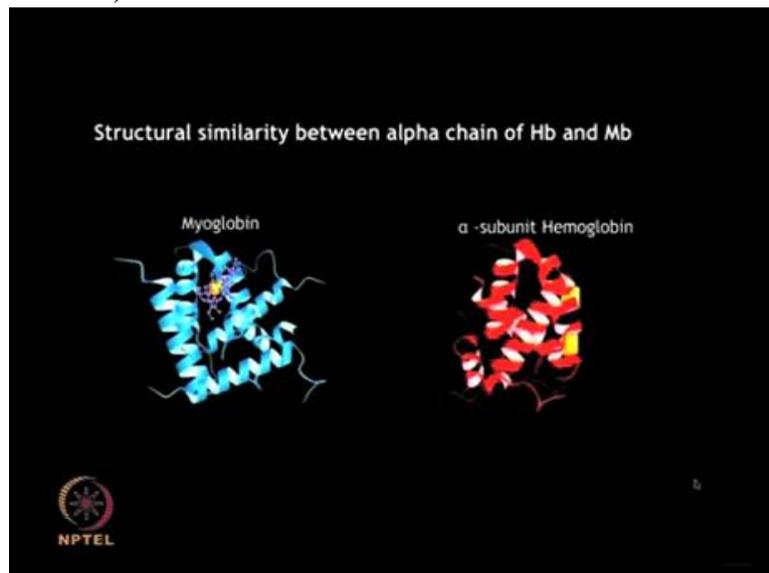
The protein was found to consist of a single polypeptide chain having ...

(Refer Slide Time: 25:46)



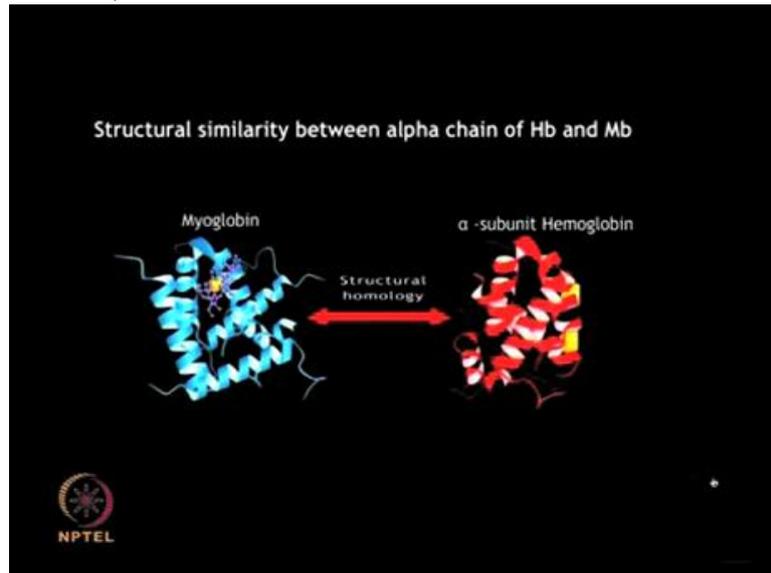
...8 alpha helices along with a Heme group in the center similar to the Hemoglobin.

(Refer Slide Time: 26:01)



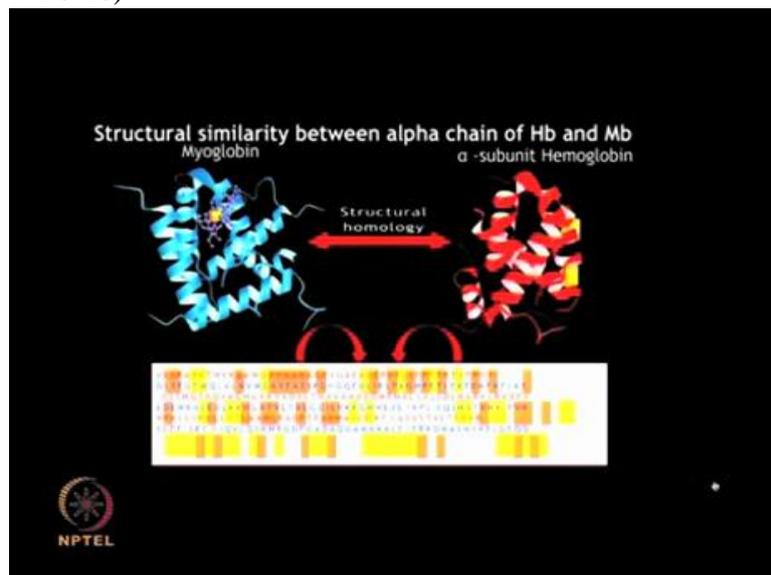
Myoglobin found largely in muscle tissues has been found to be structurally similar to the alpha subunit of Hemoglobin.

(Refer Slide Time: 26:16)



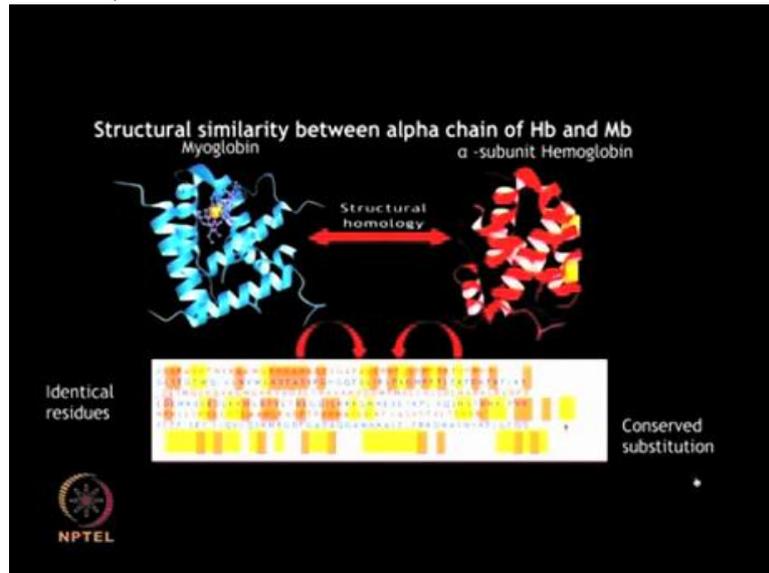
The alpha helix arrangement of both proteins has been found to be the same with the recurring structures being known as globin fold.

(Refer Slide Time: 26:26)



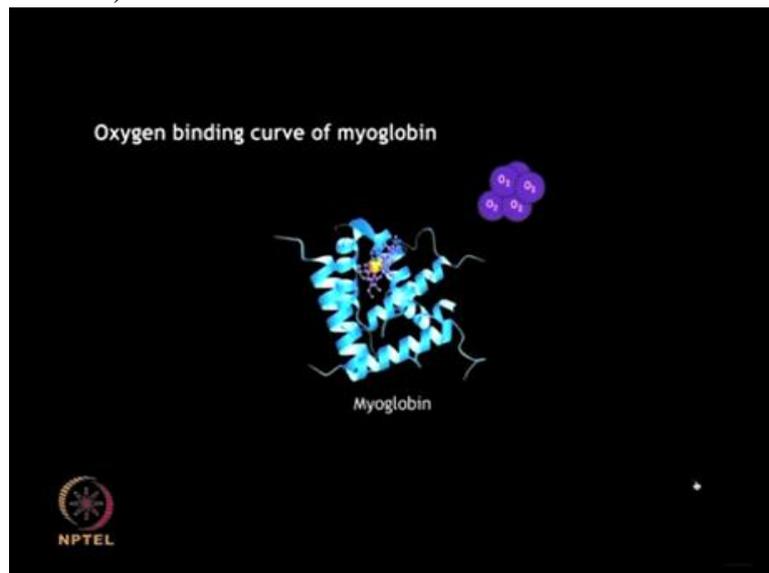
The Hemoglobin chain having 141 amino acids and Myoglobin having 153 residues have also been found to have very high sequence homology.

(Refer Slide Time: 26:52)



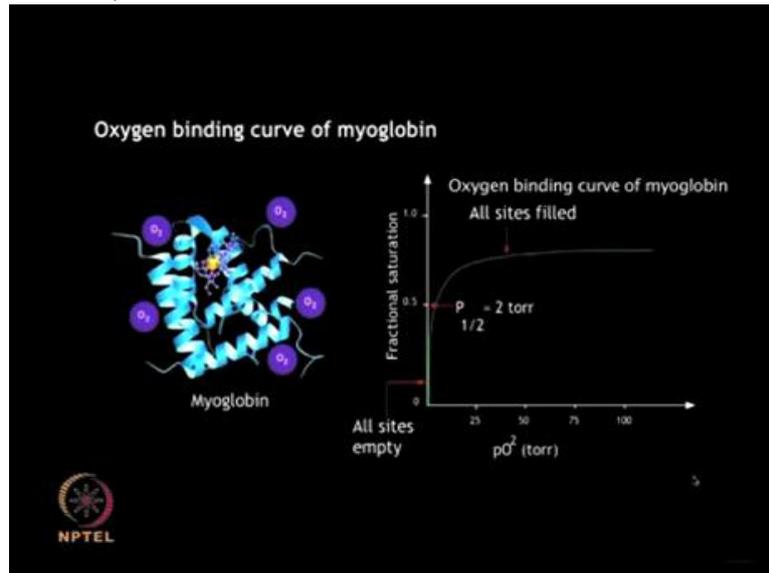
Despite the similarities their Oxygen binding capacities are different.

(Refer Slide Time: 27:01)



Myoglobin functions largely as an Oxygen binding protein that stores a reserve supply of Oxygen in muscle tissues while Hemoglobin serves to transport Oxygen.

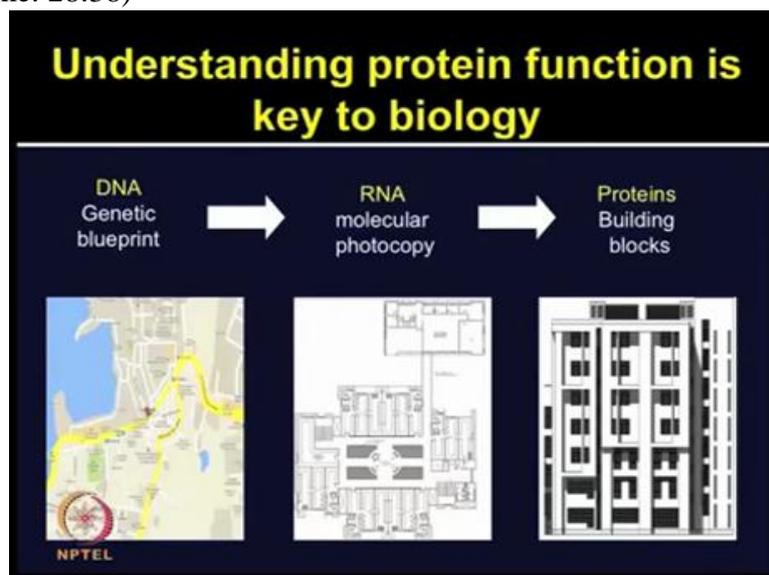
(Refer Slide Time: 27:36)



Myoglobin binds strongly to the Oxygen and acts as Oxygen storage protein rather than a transporter. It shows 50% saturation at a pressure as low as 2 Torr and gets saturated even under low Oxygen pressure condition that prevails in the muscle.

Myoglobin can use only 7% of the Oxygen carrying capacity as opposed to Hemoglobin which can utilize nearly 90% of the Oxygen carrying capacity. Unlike Hemoglobin which has a sigmoidal Oxygen binding curve, Myoglobin has a hyperbolic curve which indicates that it binds to Oxygen irrespective of the surrounding partial pressure of oxygen in the tissue.

(Refer Slide Time: 28:38)



After discussing various properties of amino acids and different level of structural proteins; primary, secondary, tertiary and quaternary, now let's just touch upon why understanding protein function is key to the biology.

So diseases result as ...due to the protein malfunction. Therefore all the current drugs, they are either targeting the protein function or they are proteins themselves which demonstrates the significance of studying about proteins. Let me describe you the slide where I have shown the various bio-molecules of central dogma; DNA, RNA and protein.

For example if you look at the map here where IIT is located in Powai area, so it is like DNA which is the genetic blueprint. It contains only information. Now if you want to make a building in this area, it is...you have to define that area which is like RNA molecule which is a molecular photocopy and it is used on the site of construction by the contractors.

Now proteins are like the building which you want to create on that site. These are the building blocks or building materials. They are bricks and mortars of engines of biology. So it shows you how various types of biomolecules have their significance but it is the protein which ultimately defines the function.

(Refer Slide Time: 30:40)

Points to ponder:

- Primary structure: Sequence of amino acids
- Secondary structure: Local folding of polypeptide chain
- Tertiary structure: Overall folding of polypeptide chain
- Quaternary structure: Interactions among different subunits

(Refer Slide Time: 31:47)

Sickle cell anemia

Sequence in normal hemoglobin (HbA)

Nucleotide	CTG	ACT	CCG	GAG	GAG	AAG	TCT
Amino acid	Leu	Thr	Pro	Glu	Glu	Lys	Ser

Normal red blood cells (HbA)

Sickled red blood cells (HbS)

NPTEL

Replacement of the Glutamin residue by Valine creates a sticky hydrophobic contact point at position 6 of the beta chain. These sticky spots cause deoxy Hemoglobin S molecules to associate abnormally with each other leading to the clumping of the cells.

(Refer Slide Time: 032:12)

Sickle cell anemia

Sequence in normal hemoglobin (HbA)

Nucleotide	CTG	ACT	CCG	GAG	GAG	AAG	TCT
Amino acid	Leu	Thr	Pro	Glu	Glu	Lys	Ser

Sequence in mutant hemoglobin (HbS)

Nucleotide	CTG	ACT	CCG	GAG	GTG	AAG	TCT
Amino acid	Leu	Thr	Pro	Glu	Val	Lys	Ser

Normal red blood cells (HbA)

Sickled red blood cells (HbS)

NPTEL

Their Oxygen carrying capacity is greatly reduced and these patients require frequent transfusions.

(Refer Slide Time: 32:20)



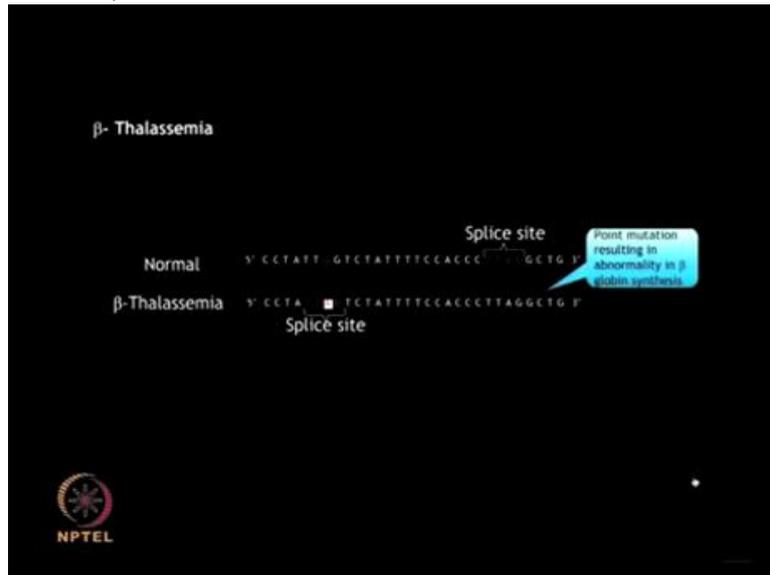
Thalassemia is the result of abnormalities in Hemoglobin synthesis. Deficiency in beta globin synthesis results in beta Thalassemia. Mutation of a single base from G to A in intron of beta globin G generates a new splice site.

(Refer Slide Time: 32:58)



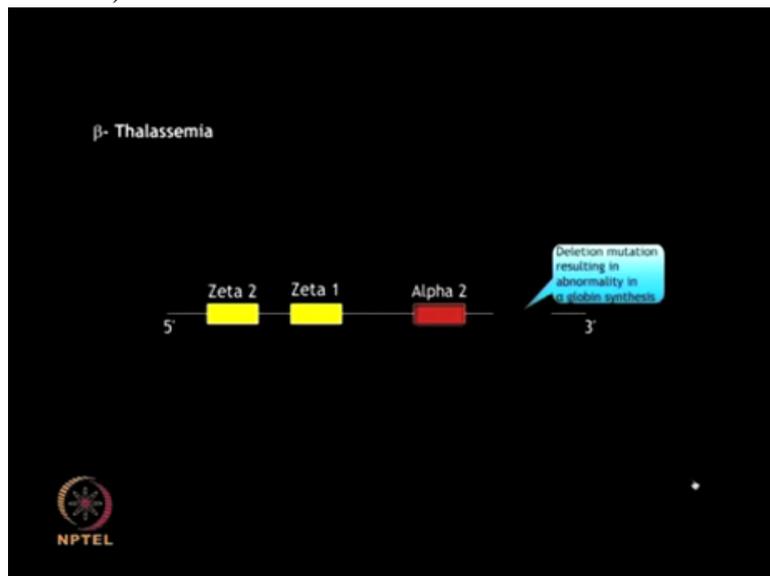
The resulting m-RNA contains a stop codon further upstream and leads to premature translation termination...

(Refer Slide Time: 33:07)



... thereby producing aberrant protein.

(Refer Slide Time: 33:23)

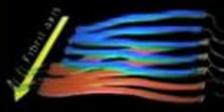


Deficiencies in alpha globin synthesis due to inactivation of one or all the 4 alpha globin genes results in the alpha Thalassemia.

(Refer Slide Time: 33:30)

Parkinson & Alzheimer disease

Cause	Clinical manifestation
The structure of certain normal cellular proteins which are normally rich in alpha helical regions are believed to be converted into beta strand conformations which can further link with each other to form beta sheets aggregates known as amyloids. These amyloid plaques, found in the brain of patients with these diseases, are essentially made up of a single polypeptide chain known as Aβ.	Neurodegenerative, tremors, stiffness, memory loss, confusion, dementia.



Go Back



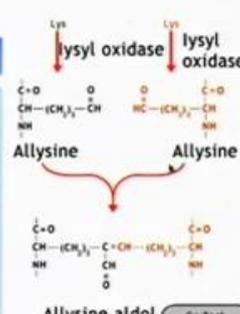
Parkinson's and Alzheimer's disease: The structure of certain normal cellular proteins which are normally rich in alpha helical regions are believed to be converted into beta strand conformations which can further link with each other to form beta sheet aggregates known as amyloids.

These amyloid plaques are found in the brains of the patients with these diseases are essentially made up of a single polypeptide chain. The clinical manifestations include neurodegenerative tremors, stiffness, memory loss, confusion, dementia etc.

(Refer Slide Time: 34:20)

Lathyrism

Cause	Clinical manifestation
Regular ingestion of seeds from sweet pea <i>Lathyrus odoratus</i> leads to disruption of cross-linking in the muscle protein, collagen. Collagen is an important structural protein having a triple helical structure. The cross-links formed are due to the oxidation of some lysine residues by the enzyme lysyl oxidase. β-aminopropionitrile, present in abundance in sweet pea, deactivates this enzyme by binding to its active site.	Reduced cross-linking causing increased fragility of the collagen fibres.



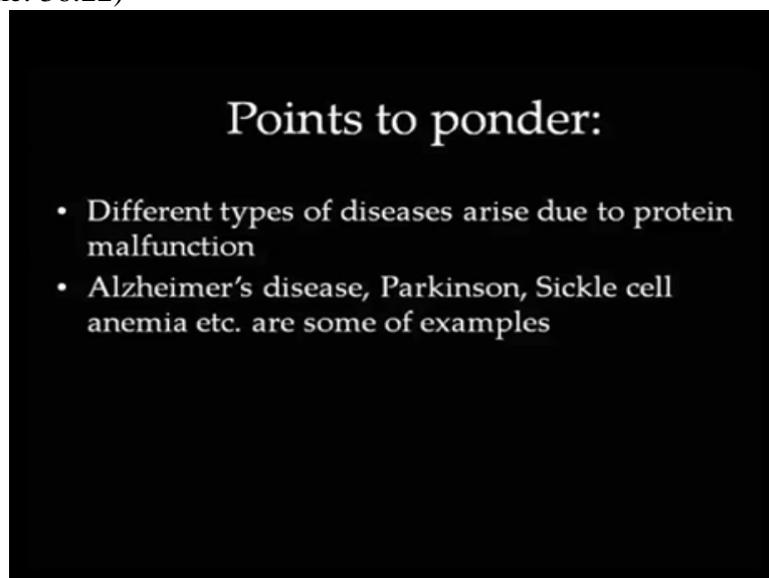
Go Back



Lathyrism, cause is regular ingestion of seeds from sweet pea *Lathyrus odoratus* which leads to disruption of cross-linking in the muscle protein Collagen. Collagen is an important structure protein having a triple helical structure.

The cross-links formed are due to the oxidation of some Lysine residues by the enzyme Lysyl oxidase. Beta aminopropionitrile present in abundance in sweet pea deactivates this enzyme by binding to its active site. The clinical manifestation includes reduced cross-linking causing increased fragility of the Collagen fibers.

(Refer Slide Time: 36:22)



In summary today we talked about proteins and its function. We have talked about different levels of protein structures; primary, secondary, tertiary and quaternary.

We discussed in little more detail about Myoglobin and Hemoglobin, the model proteins and then briefly we touched upon significance of studying proteins and its malfunction may result into various diseases. We will continue our discussion on basic concepts of proteins in the next class. Thank you.