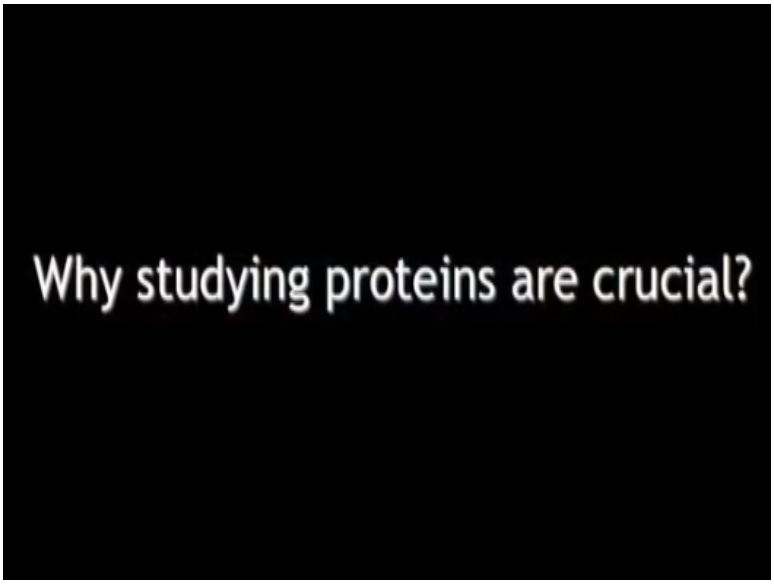
**Bioengineering: An Interface with Biology and Medicine**
**Prof. Sanjeeva Srivastava**
**Department of Biosciences and Bioengineering**
**Indian Institute of Technology- Bombay**

**Lecture – 31**
**Amino Acids & Proteins**

Welcome to MOOC NPTEL course on bioengineering, an interface with biology and medicine. Last week, we studied few basic concepts for cell cycle and development, we also saw many interesting examples, this week we are going to discuss about amino acids, proteins and protein related technology especially, how they have driven the field of proteomics. So, let us start with some very basic fundamental concepts for amino acids and proteins.

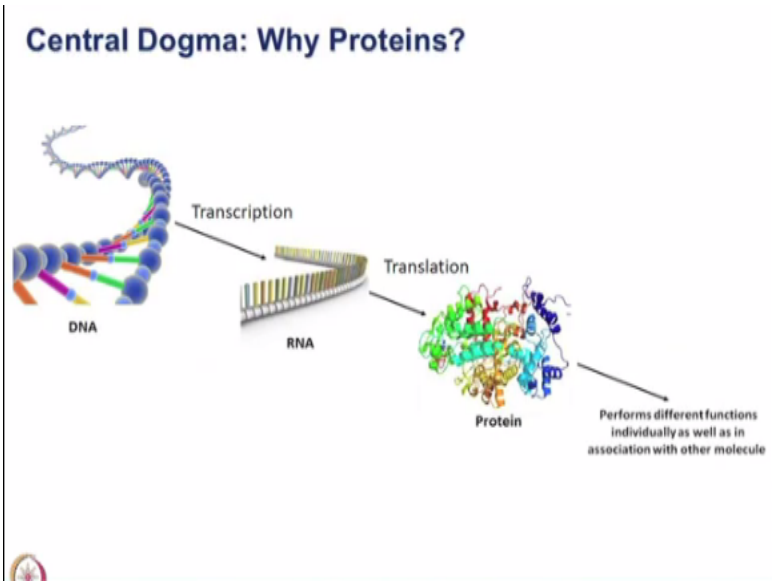
And then, we will slowly build these concepts further and then see how they can be utilized for various new tools and technologies to study proteins in a very high throughput manner.

**(Refer Slide Time: 01:04)**



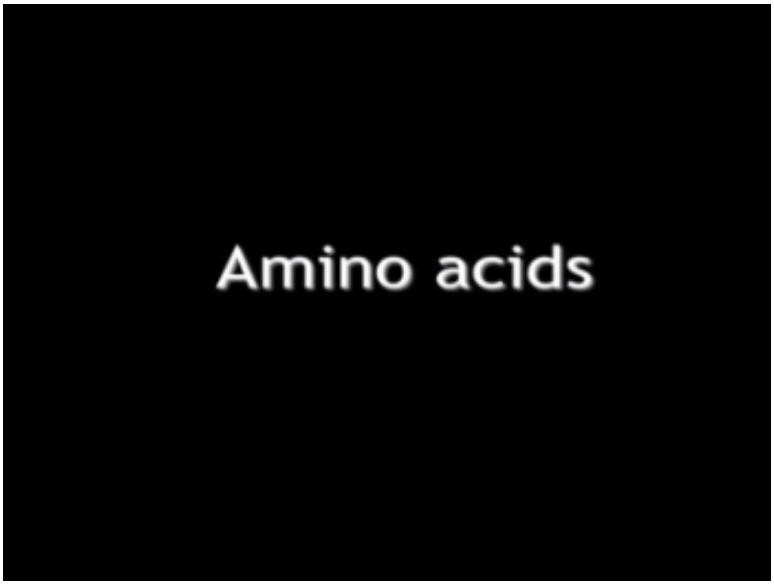

So, first of all, why studying proteins are crucial, proteins perform a range of cellular functions and as a result they are the one which most accurately reflect what is going on inside the human body or physiology, disease results as a part of protein malfunction, so most of the drugs currently either are depending on the protein function or their protein themselves, so therefore studying proteins becomes very crucial.

**(Refer Slide Time: 01:38)**




Again to remind you from the central dogma which we talked in the beginning which reflects that you know starting from DNA to RNA, the process of transcription governs that and then from RNA to protein, it is a translation process and then again protein gets further modified in the post translation modification and, and that kind of you know, gives sort of functionality to the proteins.

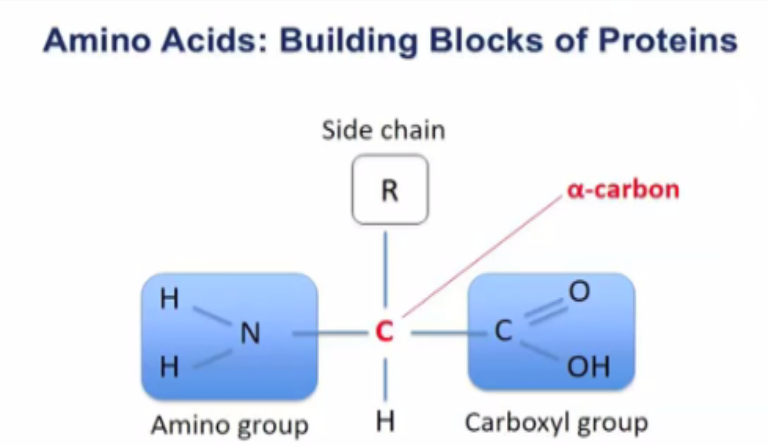
**(Refer Slide Time: 01:57)**




So, what are amino acids; amino acids are building block of proteins, the basic monomeric unit of polypeptides and proteins, there are 20 standard amino acids which are having unique structures and properties that can be combined in multiple ways to make up the wide range of

proteins known to us, each amino acid is specified by 3 letter and single letter code. The amino acids they are linked to each other with peptide bonds.

**(Refer Slide Time: 02:34)**




And they form eventually, the polypeptide proteins, here we have shown a basic amino acid structure with a minor group, carboxyl group and R side chain which keeps changing in different amino acids. Let us briefly start with the broad category of amino acids, starting with aliphatic amino acids, these are large and diverts hydrocarbon side chains which enables them to form the compact structures.

Some examples of these aliphatic amino acids include valine, leucine, isoleucine methionine and prolene, these are large aliphatic side chains and hydrophobic, the water soluble proteins are stabilized by the hydrophobic effects and then therefore, they have a tendency to form the clusters because of the hydrophobic groups.

**(Refer Slide Time: 03:22)**

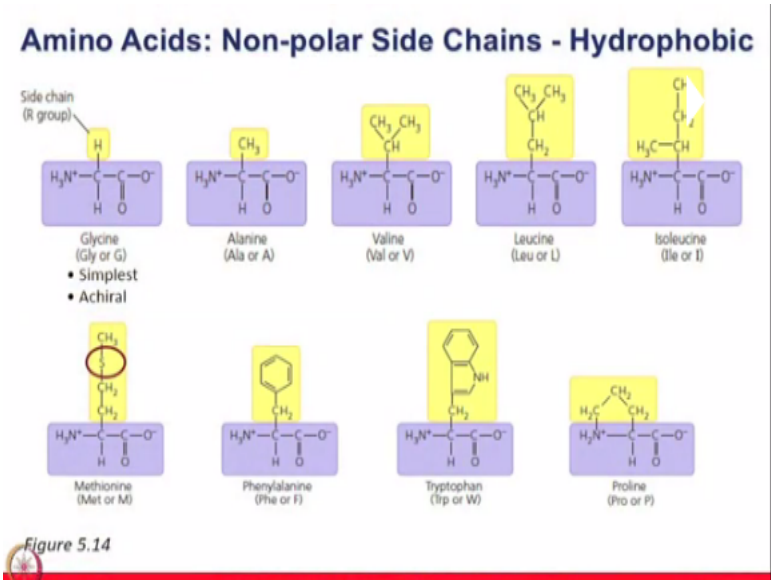
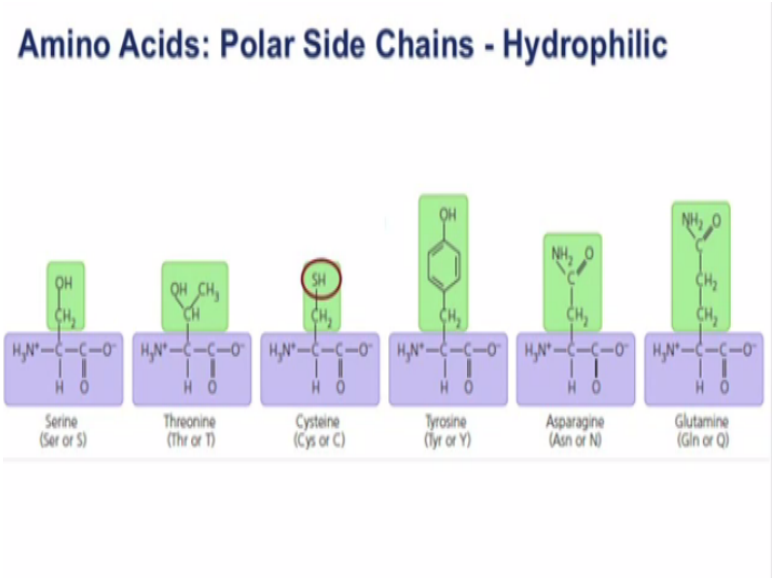


Figure 5.14

Here, I have shown you the structures of these amino acids, which are nonpolar side chains, hydrophobic amino acids, starting from the glycine, the simplest one which is Achiral amino acid and you can see only hydrogenase in the side chain R group and then Alanine is having methyl group CH3, then we have valine when we have CH3 CH3 and CH group then, we have further methyl groups being added in leucine and the isoform of that which is isoleucine.

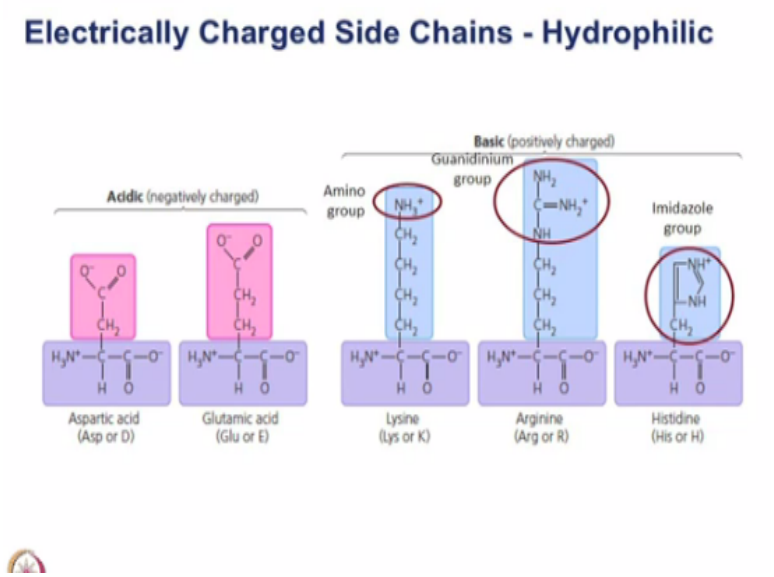
Then, we have methionine which is a cell for containing amino acid includes thioether group, then we have phenyl alanine with the phenyl group, tryptophan rings which is characteristic of tryptophan amino acid and then, we have proline, which is not having any free amino group and they have a ring structure which provides some sort of conformational restriction and that gives some sort of uniqueness to a amino acid protein.

**(Refer Slide Time: 04:31)**




Now, let us look at the polar side chain based amino acids which are hydrophilic in nature for example, serine; serine is having a CH2OH group, it resembles like Alanine but having unique a hydroxyl group; OH group, then we have Throenine which resembles with valine but it also has the hydroxyl group, so it an additional asymmetric center, then we have a cysteine amino acid which is having sulfhydryl or thiol groups.

**(Refer Slide Time: 05:01)**

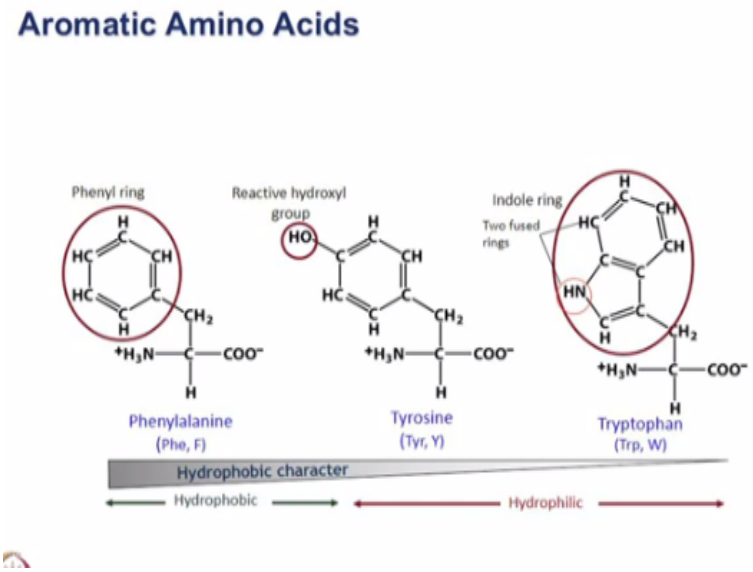



Then tyrosine amino acid, asparagine and glutamine which has these CH2 CNH2O bond, then coming to electrically charged side chain or hydrophilic amino acids, we have Aspartic acid and glutamic acid, which are acidic and having negatively charged groups, then we have a lysine

arginine and histidine which are having the positive charge and these are basic amino acids, they are again characterized with in the case of lysine with amino group.

In case of arginine, with the guanidinium group and case of histidine having one imidazole group, so I am going to talk about some of these amino acid structures in some more detail in the animation.

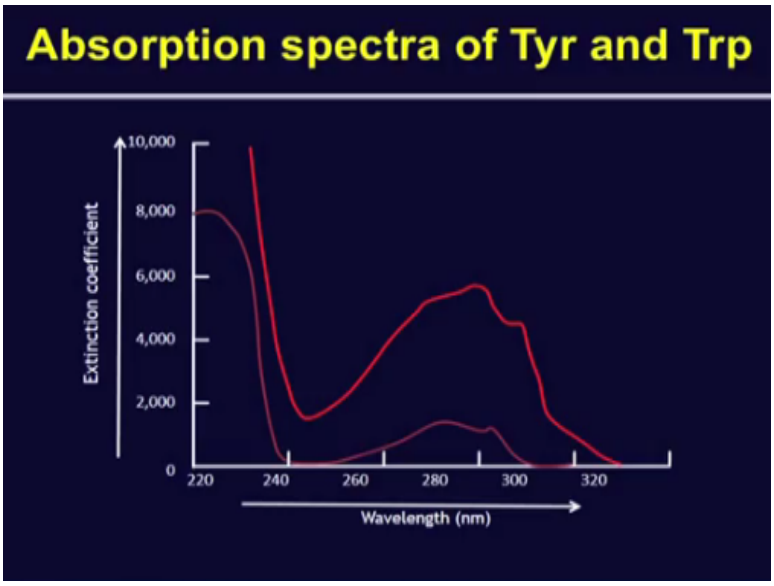
**(Refer Slide Time: 05:40)**




But for the time being let us you know, focus on aromatic amino acids looking at these 3; phenylalanine, tyrosine and tryptophan, the phenylalanine has a phenyl ring as you can see in the structure, tyrosine having a reactive hydroxyl group and then tryptophan is having indole ring which are you know, 2 fused rings are there with NH. So, now these kinds of properties of these aromatic amino acids, they give them the hydrophobic characteristics like especially in case of the phenylalanine.

Whereas, the tyrosine and tryptophan they are more hydrophilic because of the presence of OH and NH group, these aromatic amino acids are also being utilized for you know, measuring the concentrations in the protein and people look into the absorption spectra of tyrosine and tryptophan.

**(Refer Slide Time: 06:32)**




So, I shown here on the slide, the tryptophan and tyrosine aromatic rings they strongly absorb at the UV light and the light absorption is a characteristic which can be used for the protein estimation.

**(Refer Slide Time: 06:48)**

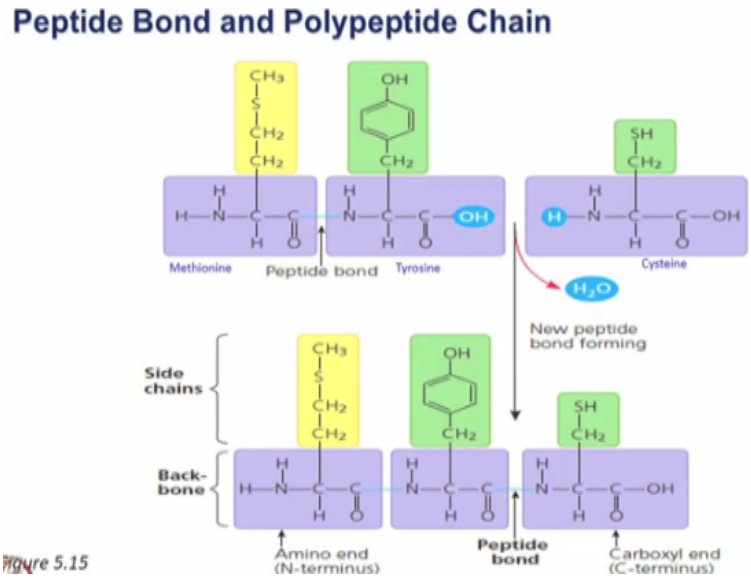


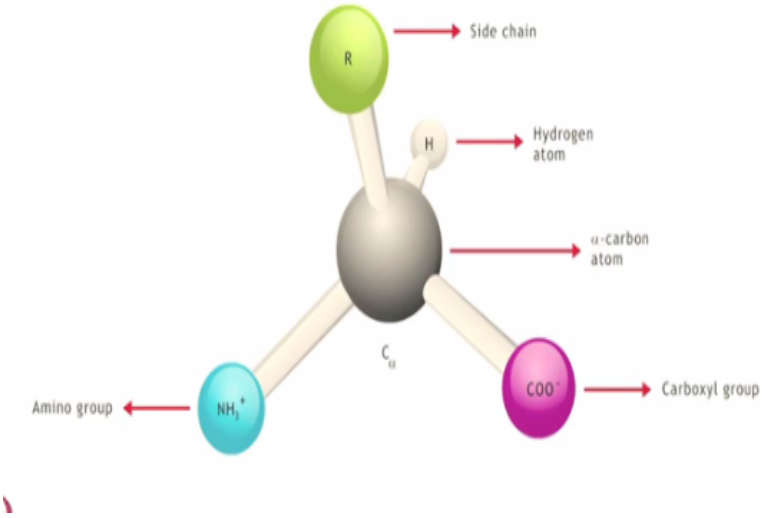

Figure 5.15

So, as I mentioned that you know these amino acids they come together to, to form peptide bonds and the peptide bond is formed during the process of linking together these amino acids with the carboxyl group of one amino acid being linked to the amino group of another amino acid with the loss of a water molecule.

**(Refer Slide Time: 07:04)**

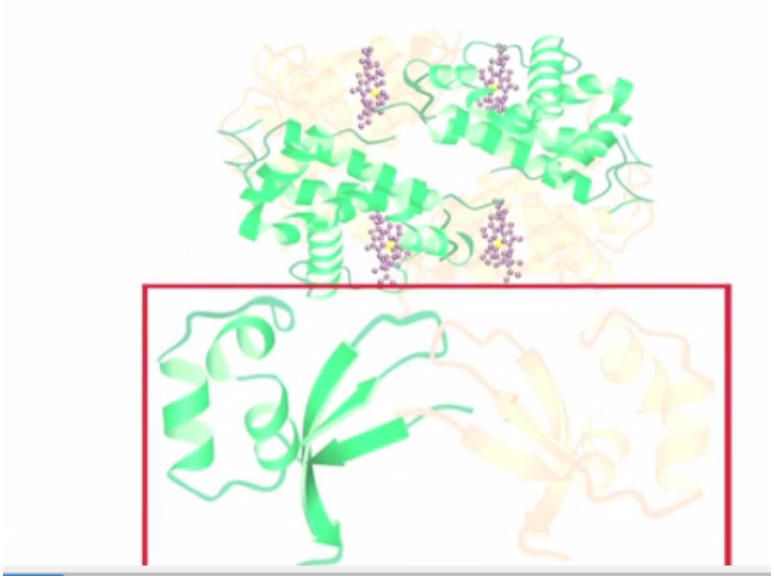

Let us now review some of these concepts in an animation.

**(Refer Slide Time: 07:09)**



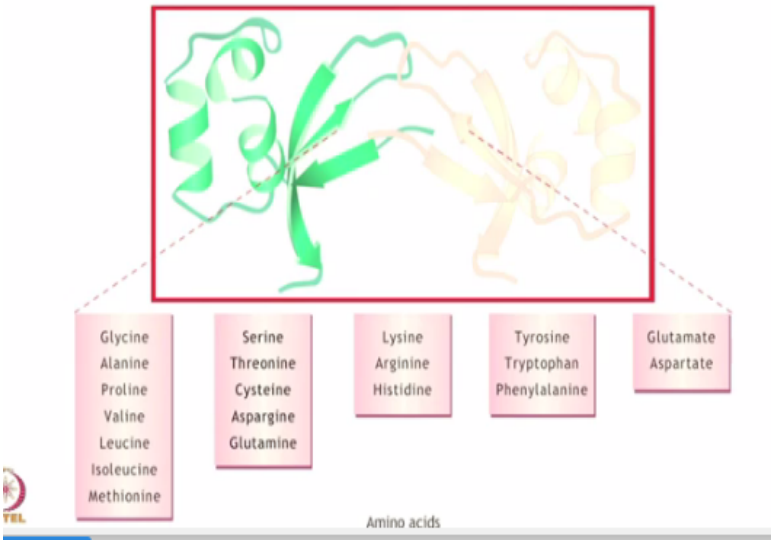

Amino acids are the building blocks or monomers that make up proteins; they consist of a central alpha carbon atom bonded covalently to an amino group, a carboxyl group, a hydrogen atom and a variable side chain also called the R group.

**(Refer Slide Time: 07:33)**



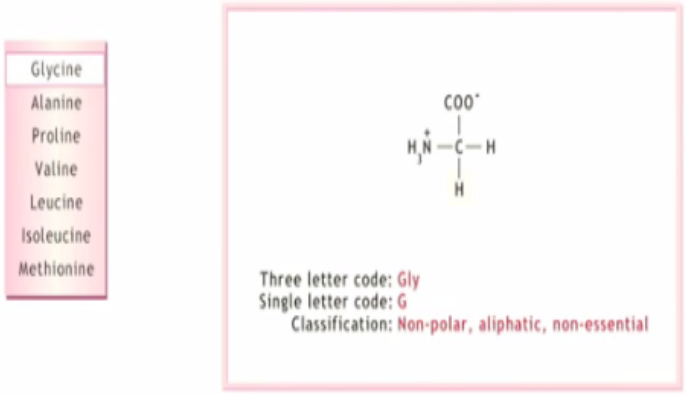
Amino acids are the basic monomeric constituents of proteins found in varying amounts depending upon the type of protein; they are classified based on the properties of their side chains or R groups which vary in size, structure and charge.

**(Refer Slide Time: 07:58)**



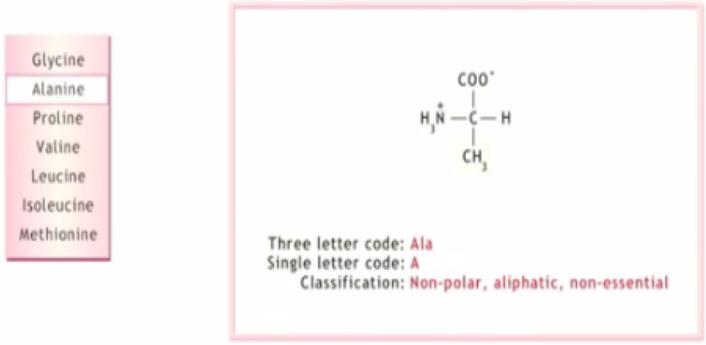

The polarity of the side chains is one of the main bases for classification.

**(Refer Slide Time: 08:04)**



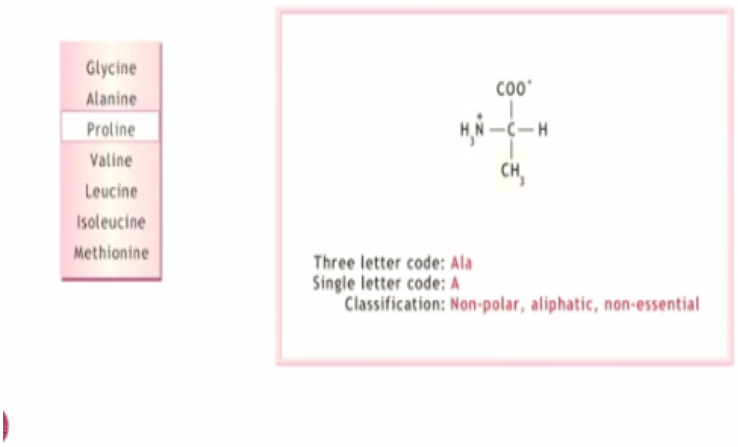

Amino acids having nonpolar aliphatic side chains include glycine.

**(Refer Slide Time: 08:12)**



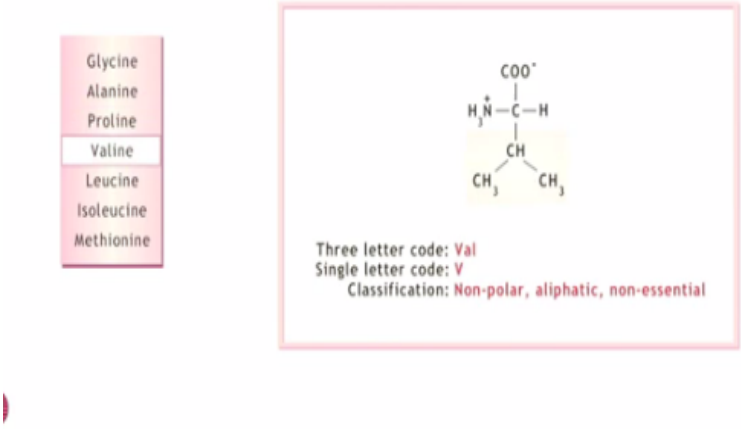

Alanine.

**(Refer Slide Time: 08:14)**



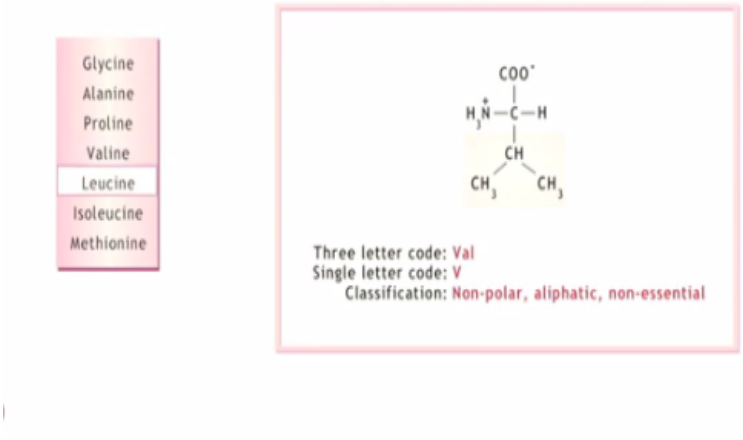

Proline.

**(Refer Slide Time: 08:15)**



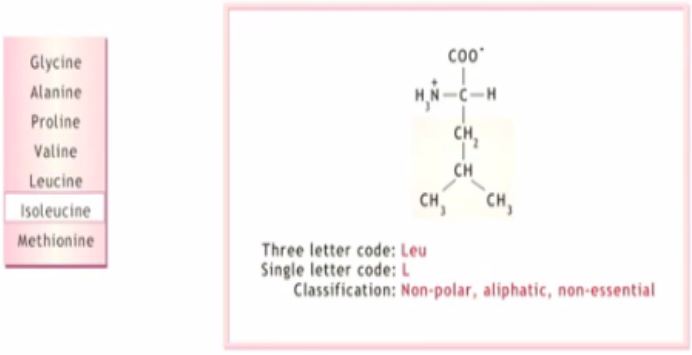

Valine.

**(Refer Slide Time: 08:16)**



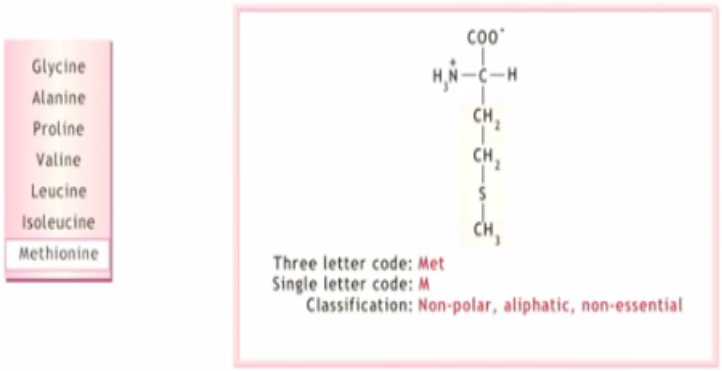

Leucine.

**(Refer Slide Time: 08:18)**



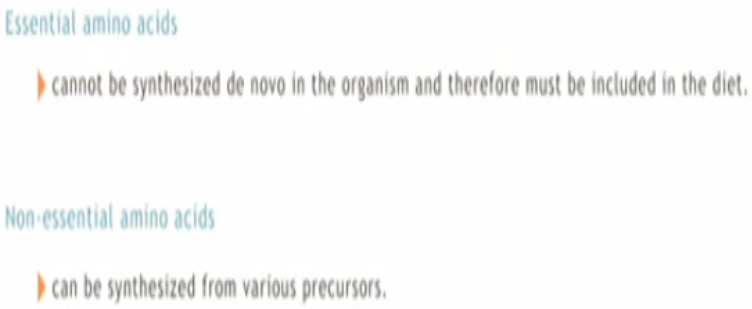

Isoleucine.

**(Refer Slide Time: 08:20)**



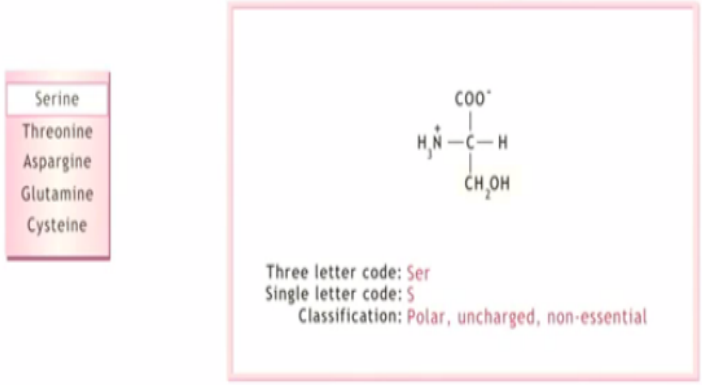

And methionine.

**(Refer Slide Time: 08:23)**



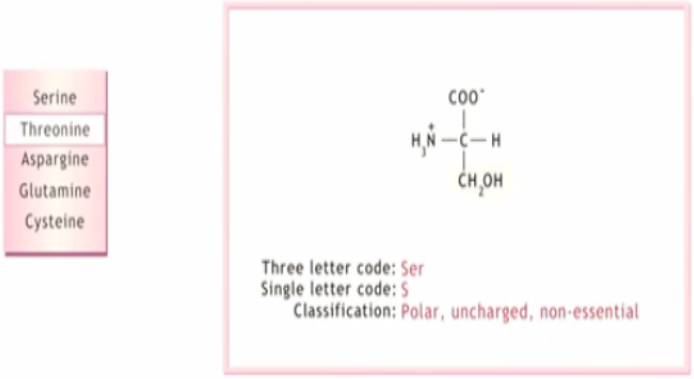

Essential amino acids are those that cannot be synthesized de novo in the organism and therefore, must be included in the diet. Non-essential amino acids on the other hand can be synthesized from various precursors.

**(Refer Slide Time: 08:44)**



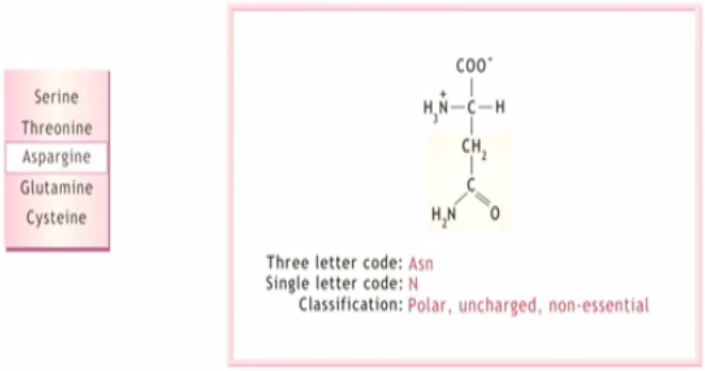

Serine.

**(Refer Slide Time: 08:46)**



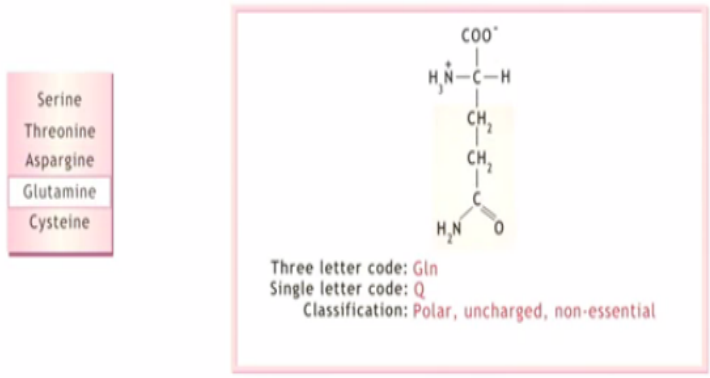

Threonine.

**(Refer Slide Time: 08:48)**



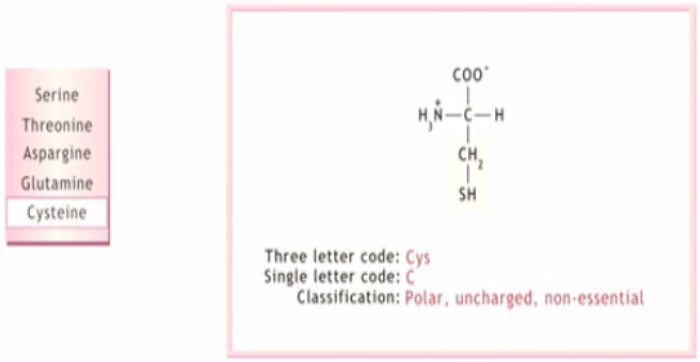

Aspargine.

**(Refer Slide Time: 08:49)**



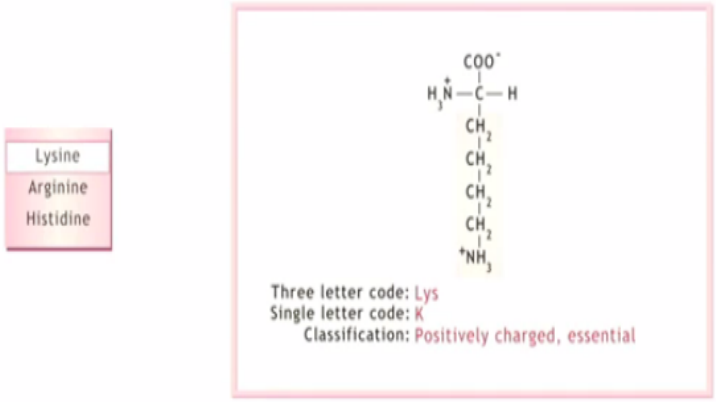

Glutamine.

**(Refer Slide Time: 08:51)**



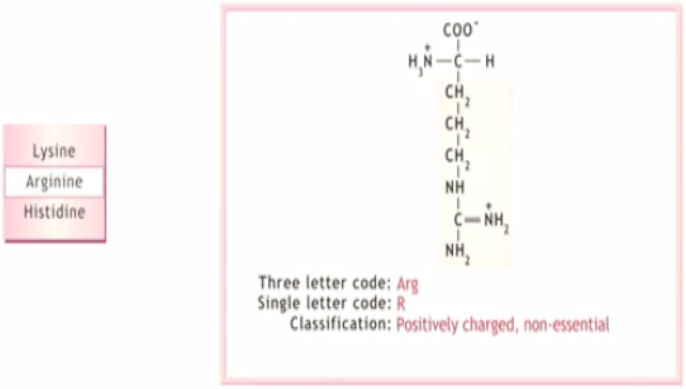

And cysteine consists of polar but uncharged side chains.

**(Refer Slide Time: 08:58)**



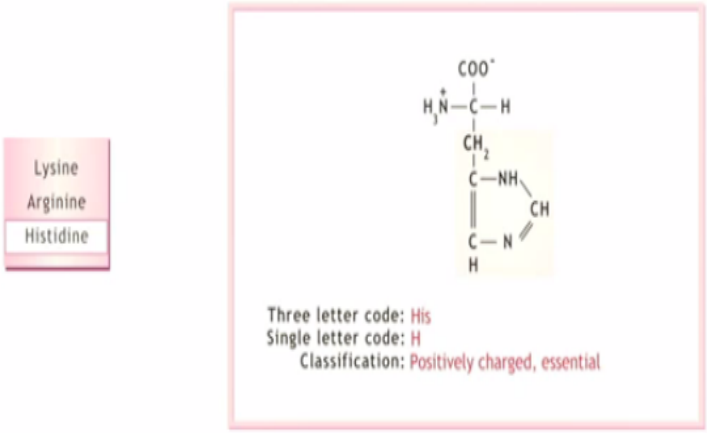

Lysine.

**(Refer Slide Time: 09:00)**



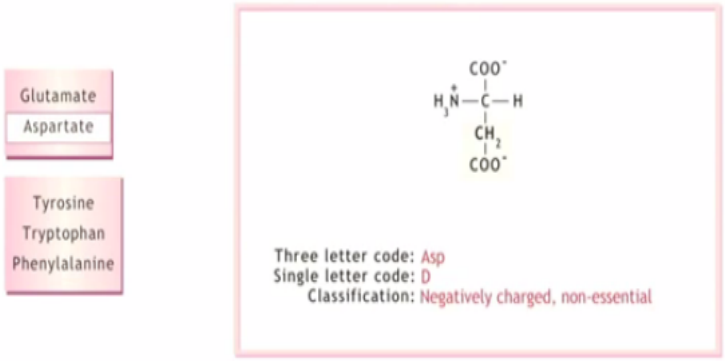

Arginine.

**(Refer Slide Time: 09:01)**



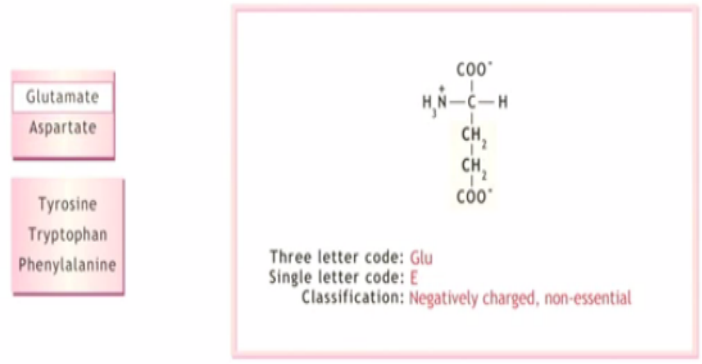

And histidine have positively charged side chains.

**(Refer Slide Time: 09:05)**



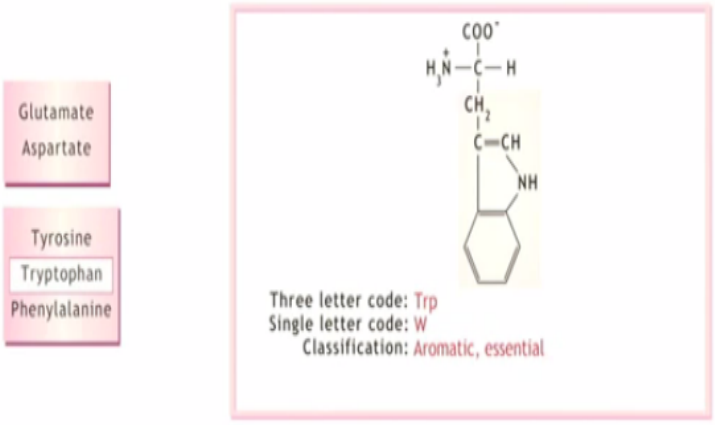

Aspartic acid.

**(Refer Slide Time: 09:07)**



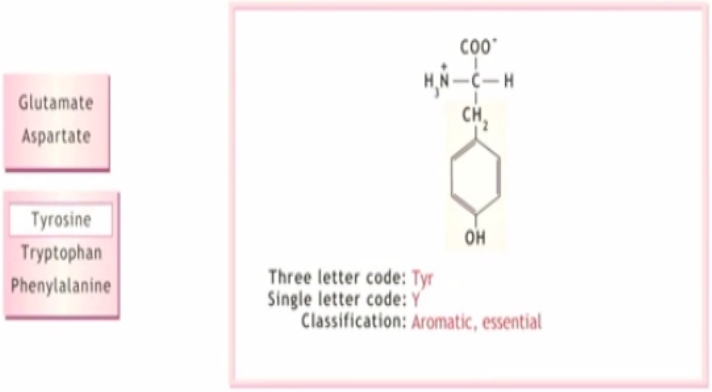

And glutamic acid are polar and negatively charged amino acids.

**(Refer Slide Time: 09:16)**



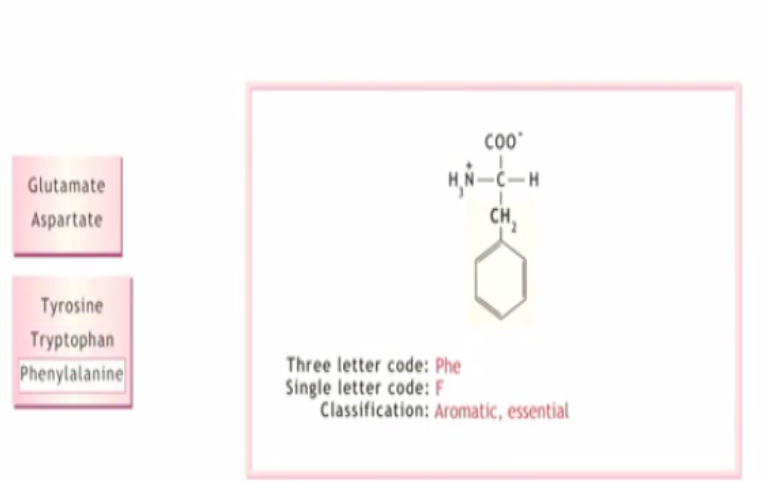

Tryptophan.

**(Refer Slide Time: 09:18)**



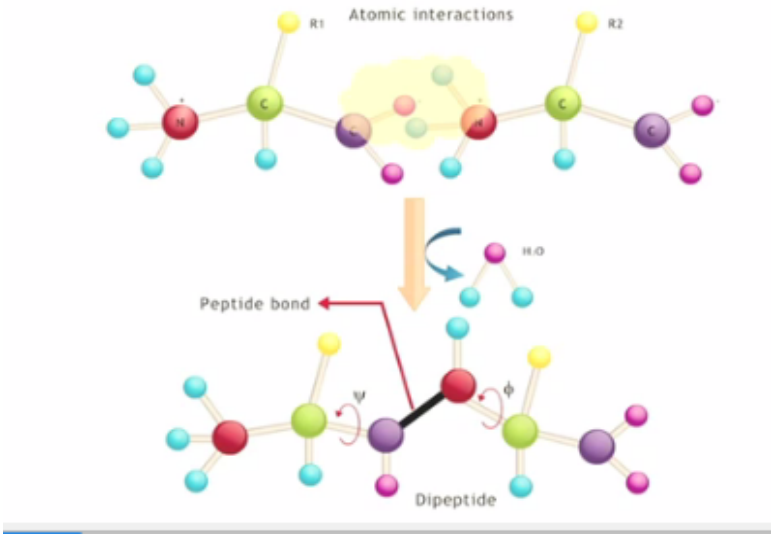

Tyrosine.

**(Refer Slide Time: 09:19)**



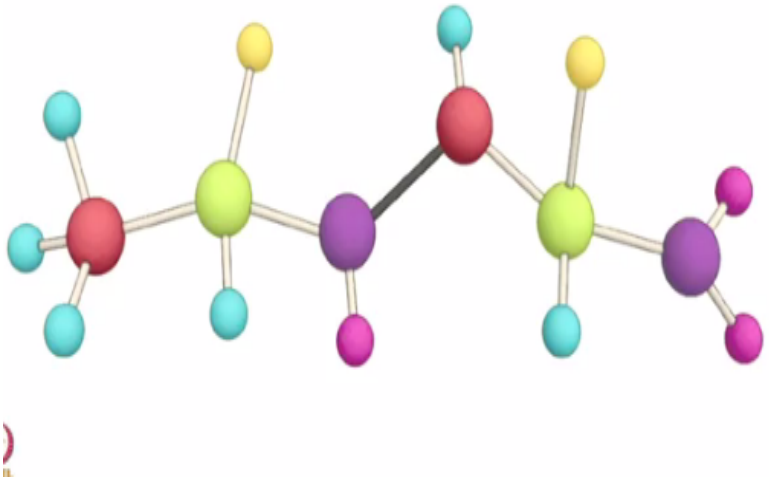

And phenylalanine are all essential amino acids having an aromatic side chain.

**(Refer Slide Time: 09:30)**




Amino acids are the building blocks or monomers that make up proteins, amino acids are oriented in a head to tail fashion and linked together such that the carboxyl group of one amino acid combines with the amino group of another, 2 amino acids joined together by means of such a condensation reaction with a loss of a water molecule forms a dipeptide. Many such amino acids linked together form a polypeptide.

**(Refer Slide Time: 10:14)**



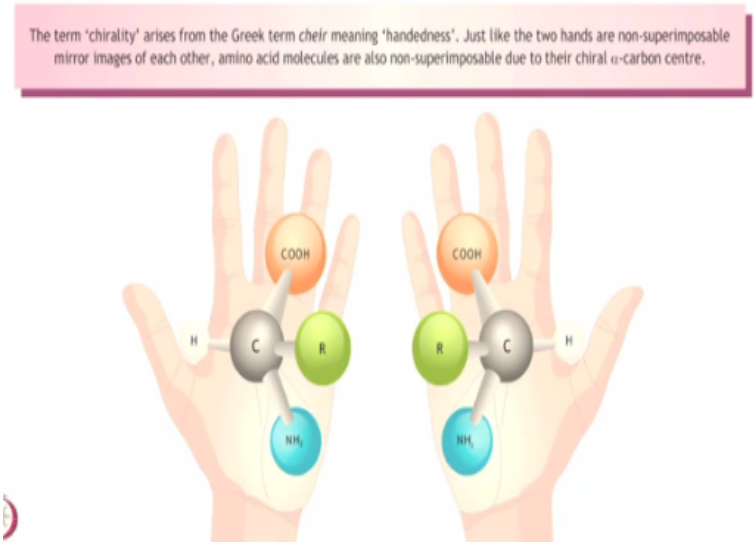
The peptide bond is rigid due to its partial double bond character arising from resonance structures however, the bonds between the alpha carbon and amino and carboxyl groups are pure single bonds that are free to rotate. What are the amino acid properties in relation to isomerism, so let us talk about optical isomerism, just imagine the chiral molecules they interact with the plane polarised light in such a manner that they can rotate the plane of polarization either in the clockwise or the counter clockwise directions.

So, depending on that in which direction the molecule rotates, the plane of the polarization can be designated as plus, you can say dextrorotatory or you can say levorotatory, this nomen clature is not exactly same as the D and L designations, which actually refers to the absolute configurations is specified on the basis of their relationship with D and L glyceraldehyde. Majority of the amino acids which are found in the proteins are of the L configurations.

**(Refer Slide Time: 11:30)**

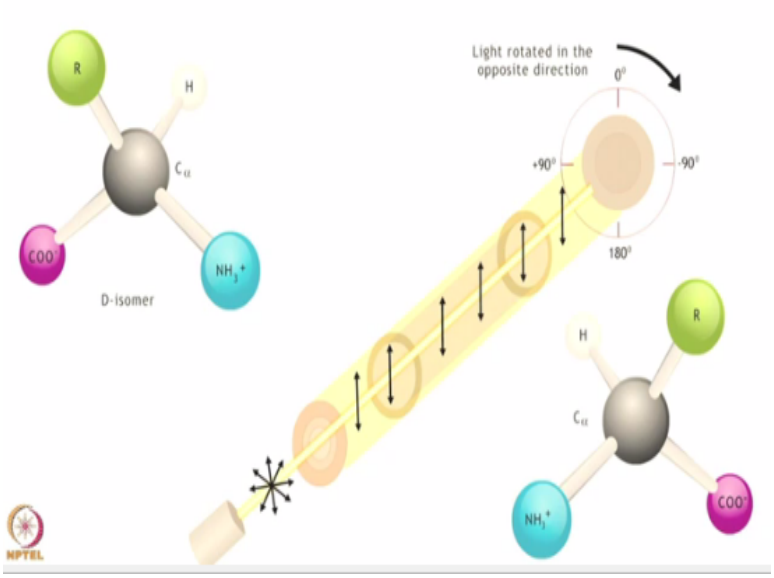

Let us review these concepts in the following animation.

**(Refer Slide Time: 11:36)**



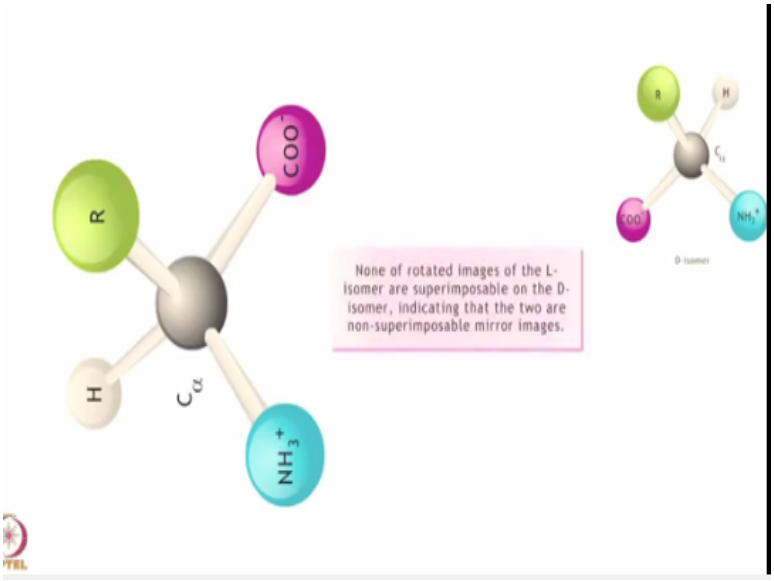

Before learning about the isomerism, let us first know what chirality is; the term chirality arises from the Greek term care meaning, handedness, just like the 2 hands are non-superimposable mirror images of each other, amino acid molecules are also non superimposable due to their chiral alpha carbon centre.

**(Refer Slide Time: 12:10)**




All amino acids except glycine contain an asymmetric centre that makes them chiral in nature due to which they can rotate the plane of polarized light. The 2 enantiomers designated as D and L rotates the plane of polarization in opposite direction.

**(Refer Slide Time: 12:38)**




The 2 enantiomers of amino acids are non-superimposable mirror image due to the spatial arrangement of 4 different groups about the chiral carbon atom, rotation of either isomer about its central axis will never give rise to the other isomeric ring structure. What are the acid and base properties of amino acids? All amino acids they exist in the completely protonated forms in the acidic medium, which is known as the cationic form.

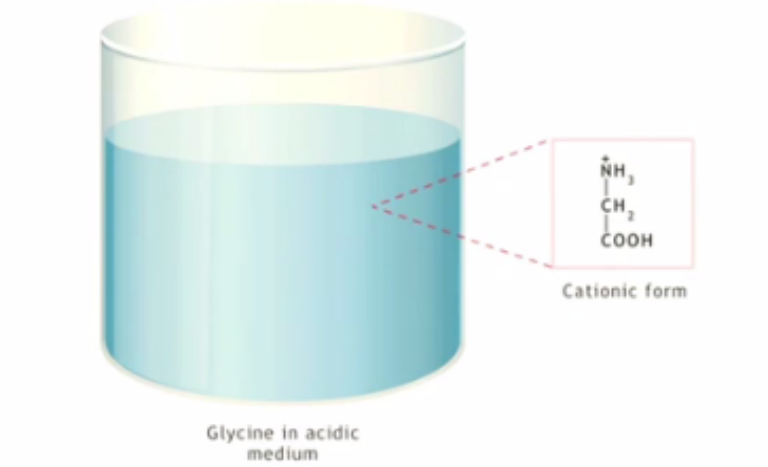
Both amino and the carboxyl groups are protonated and this state in which the amino acids has no net charge that is known as the deuteron, it is neutral because of the presence of NH3+ and COO- groups. What is the anionic form of amino acid? In a highly alkaline medium, all amino acids exist in the anionic form because of the presence of COO- groups, so looking at these properties of cationic and anionic forms and deuterons which are formed one could do titration curve.

So, the number of equivalents of alkali being consumed during the process of addition of alkali to the amino acid solution is plotted against pH of the solution in the flask which is the unique titration curve of each amino acid. The titration curve depicted corresponds to that of glycine.

**(Refer Slide Time: 14:13)**

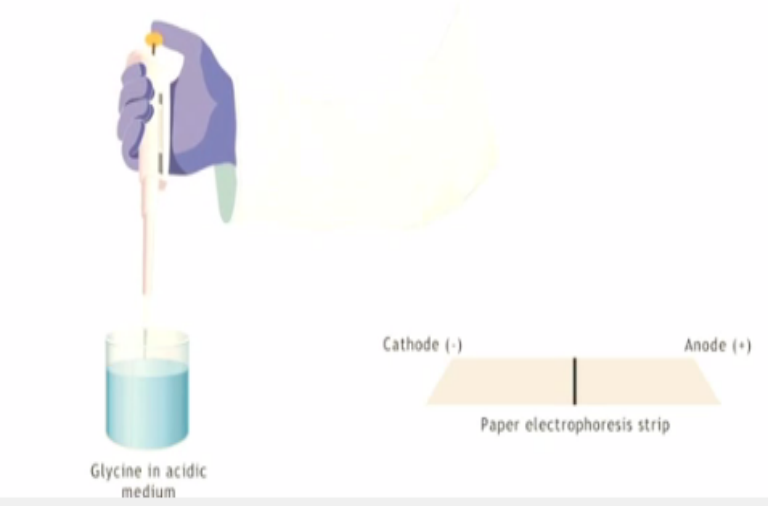

Let us review this concept in animation.

**(Refer Slide Time: 14:17)**



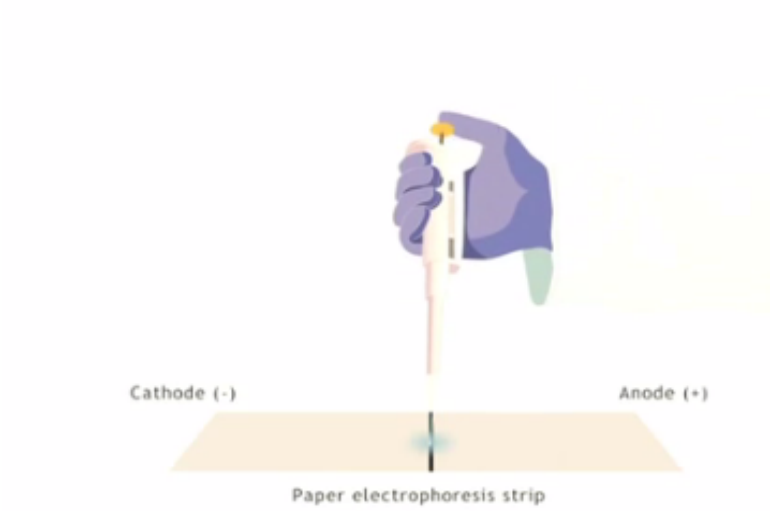

Amino acids in acidic medium exist in the completely protonated form carrying a net positive charge.

**(Refer Slide Time: 14:29)**



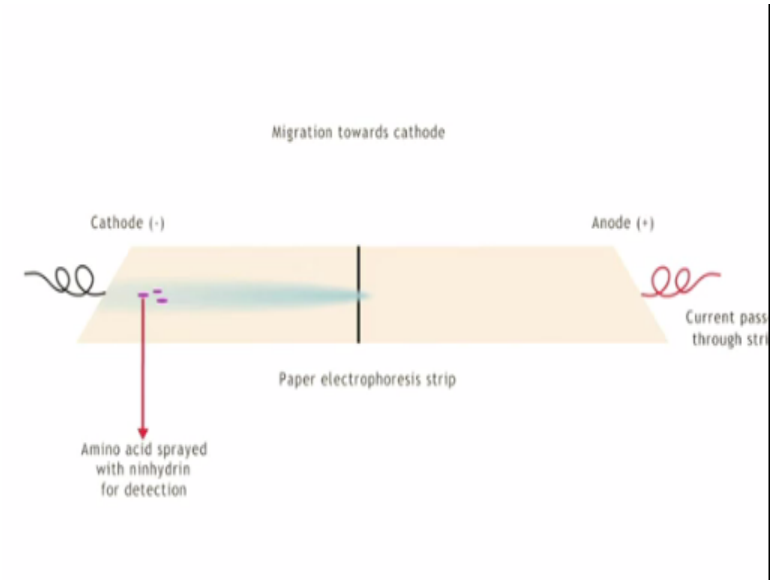

This can be confirmed by means of simple paper electrophoresis, the sample solution is applied at the center of the strip.

**(Refer Slide Time: 14:42)**




And current is passed through it.

**(Refer Slide Time: 14:46)**

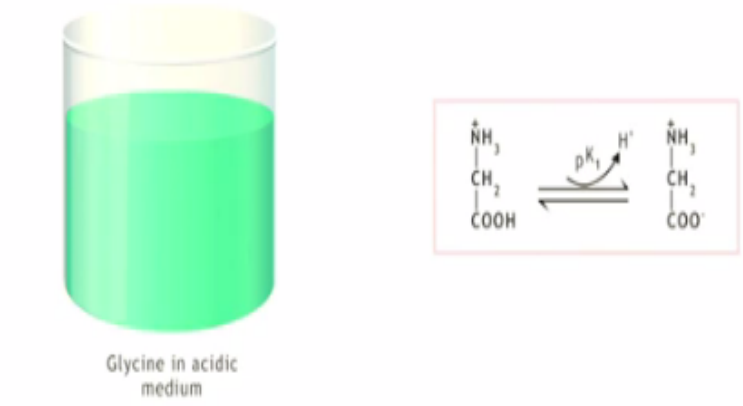



The colourless amino acid solution can be detected by spraying the strip with ninhydrin which gives it a purple colour; migration of the spot towards the negatively charged cathode confirms the net positive charge of the amino acid.

**(Refer Slide Time: 15:08)**

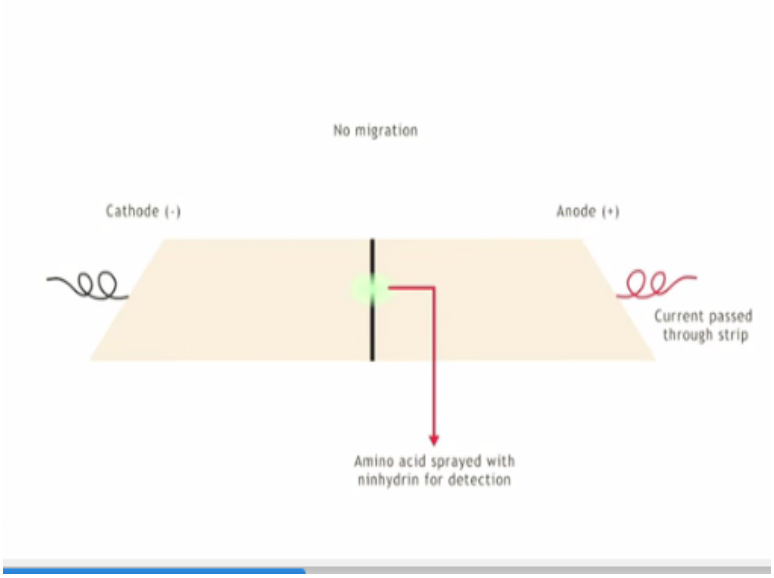

All amino acids exhibit a characteristic titration curve with distinct PK values, 0.1n NaOH is added to the acidic amino acid solution.

**(Refer Slide Time: 15:24)**



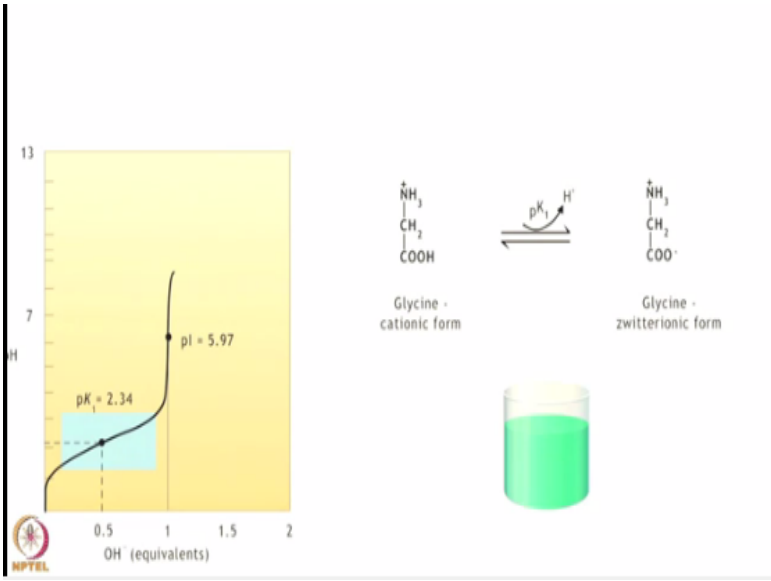

The cationic form of the amino acid is gradually converted into its neutral.

**(Refer Slide Time: 15:36)**



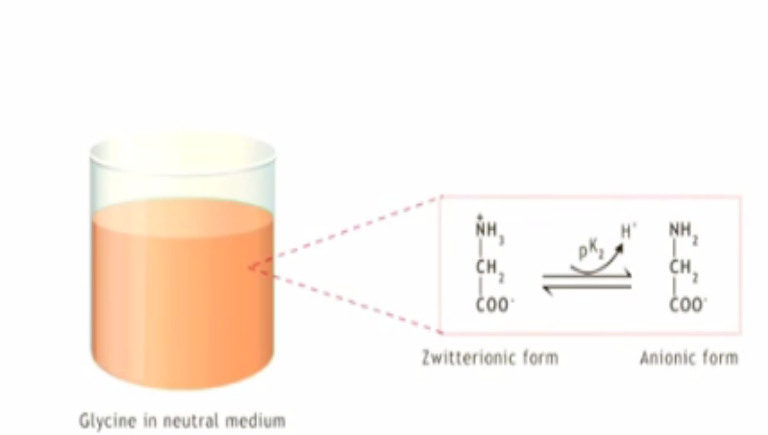

Or zwitter ionic form by loss of a proton from its COOH group, this can again be confirmed by electrophoresis where there is no migration of the samples spot.

**(Refer Slide Time: 16:00)**

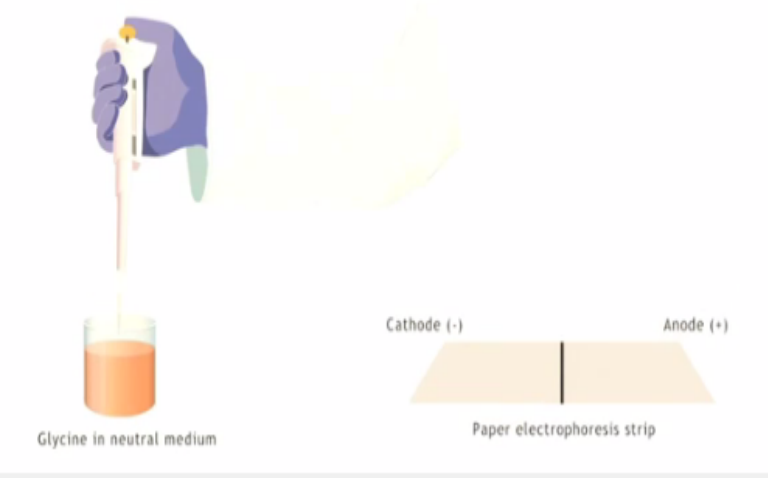



Number of equivalence of alkali being consumed is plotted against the pH of the amino acid solution to obtain the titration curve, pK1 of glycine is found to be 2.34 that is, it starts to lose its carboxyl group proton at this pH.

**(Refer Slide Time: 16:27)**

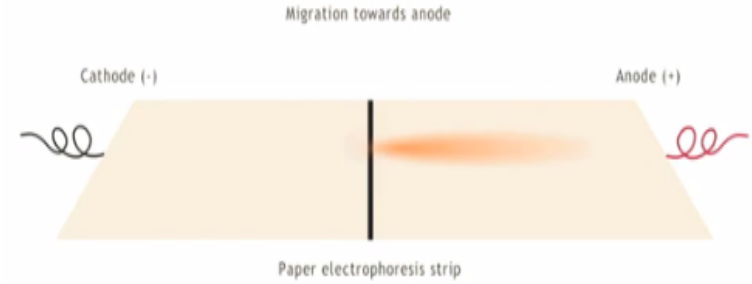



**(Refer Slide Time: 16:45)**



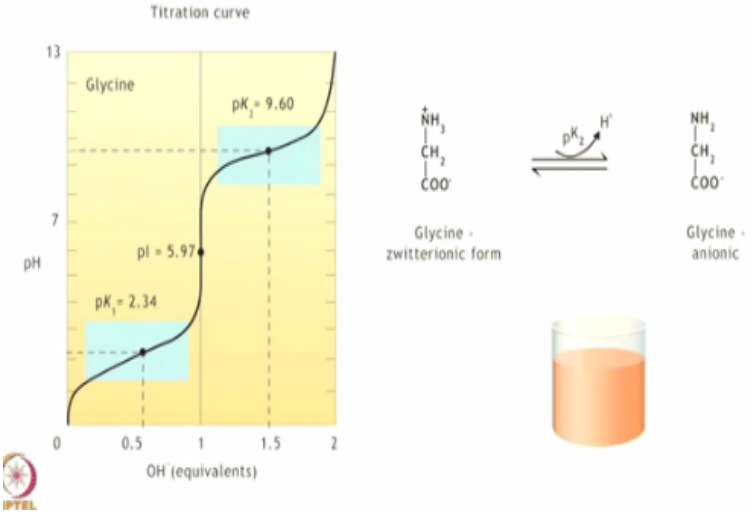

Removal of the proton from the amino group constitutes the second stage of the titration curve; continued addition of alkali to the amino acid solution gradually converts the zwitter ionic form into the anionic form.

**(Refer Slide Time: 16:49)**




Migration of the sample spot towards the anode during electrophoresis confirms this.

**(Refer Slide Time: 16:57)**



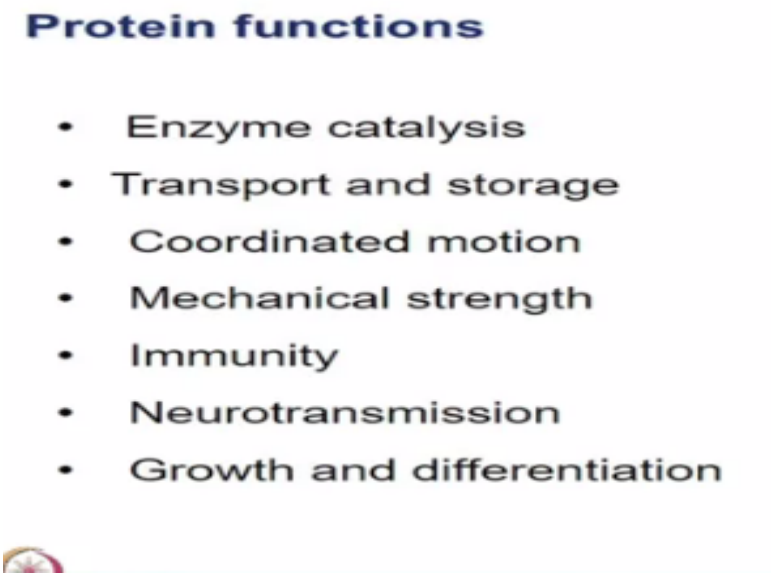

The pK2 of an amino acid is obtained by continued addition of alkali to the neutral solution of the amino acid, pK2 of glycine is found to be 9.6, some amino acids having positively or negatively charged side chains will have pK1, pK2 and pKr, which corresponds to ionization of the side chain, these amino acids have good buffering capacity around 1 pH unit on either side of the pK values.

**(Refer Slide Time: 17:45)**


After discussing about amino acids, now let us move on to the proteins, so what are proteins? These are linear polymers which are built of monomers of amino acids and they have wide range of functional group which accounts for various protein function and then that reactive properties are very crucial for the enzyme and the protein function. There are many properties like protein-protein interaction, protein bio molecular interaction which generates a synergistic capability which may not be obtained just by studying an individual protein.

And therefore, it becomes very crucial to study proteins together and then, you know one need to understand the (()) (18:27) in totality, proteins are governing that function.

**(Refer Slide Time: 18:32)**



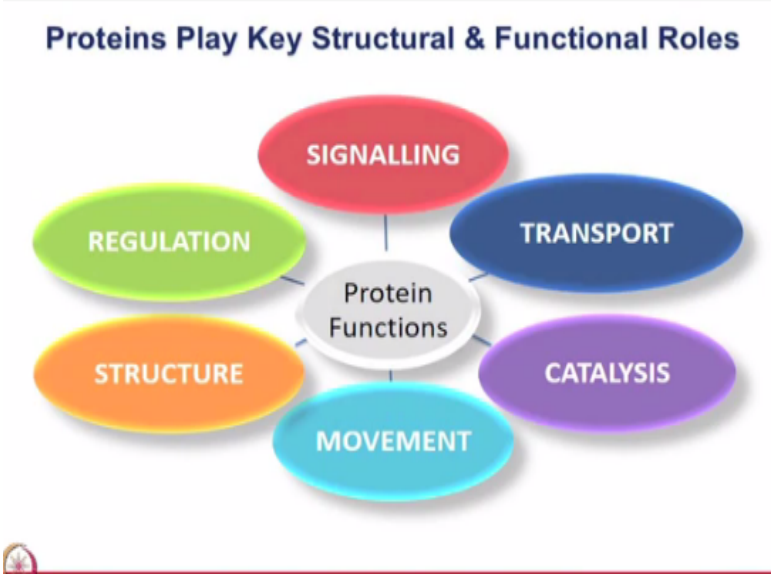
So, understanding protein function is key to biology, let us look at some of these key characteristics here like enzyme catalysis, where enzymes catalyses all the biochemical reactions by increasing rate of reactions, so enzymatic catalysis is the process when enzymes catalyse all biochemical reactions by increasing the rate of reactions. There are proteins which are involved in the transport and storage processes.

The proteins which can transport the small molecules like oxygen, iron etc. proteins are also involved in doing the coordinated motion for example, muscle contraction, bacterial chemotaxis, chromosomal movements, sperm propulsion etc. all of these are coordinated motion which are governed by different proteins, where its mechanical strength is also governed by the different proteins.

For example, with skin and bones by the collagen proteins and here, with the keratin protein, I discussing about protein function, proteins are also involved in the immunity process for example, antibodies which exemplify the specificity of protein, protein and protein ligand interactions. They are also involved in neurotransmission which is in the response of cells to these stimuli in the nerve cells.

In the process of growth and differentiation for example, the transcription factors; they are involved in the gene expression processes during growth and development.

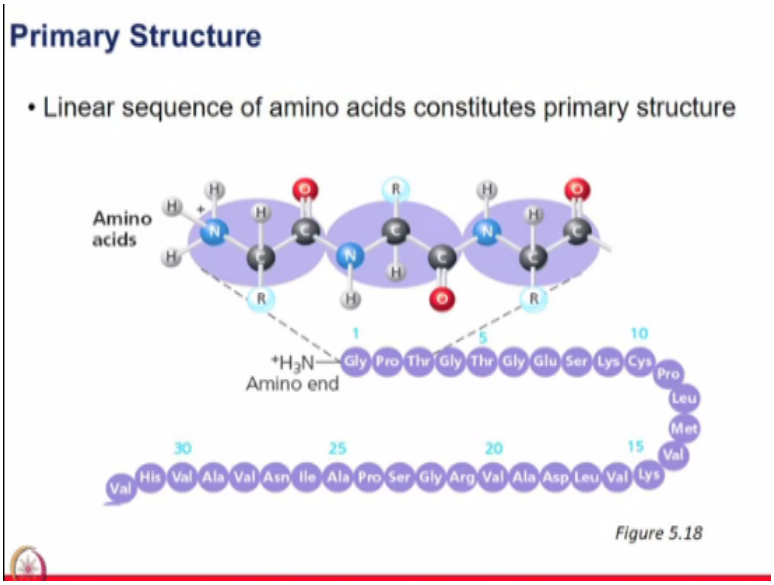
**(Refer Slide Time: 19:57)**




So, I am sure you appreciate that you know, proteins play key structural and functional role and they define you know, wide range of functions involved in signalling, transport, catalysis, movement, structure, regulation etc. Let us now discuss about different levels of protein structures. So, the primary structure refers to the sequence of amino acids, the secondary structure refers to the locally folded regions.

The tertiary structure refers to the overall folding of the protein structures and quaternary structure refers to all the interaction between individual protein subunits in a multi subunit complex.

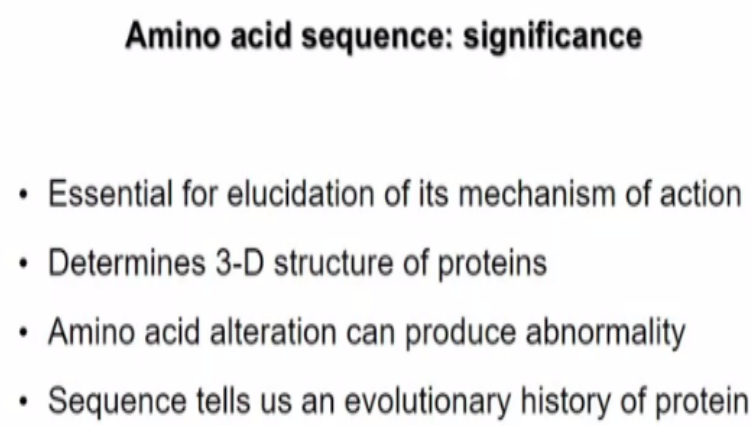
**(Refer Slide Time: 20:34)**



Let us start with each of these structural details of proteins, let start with primary structure. The sequence of amino acids are joined together by the peptide bond, which forms a linear polymer constituting the primary structure of the protein, the linear polypeptide chains are often cross-linked, most commonly by the cysteine bonds and then they are linked together to form a cysteine unit.

The first primary structure that was deduced that was for a protein insulin, which was discovered by scientist Frederick Sanger. So, what does the significance of these, you know primary structure or the amino acid sequences.

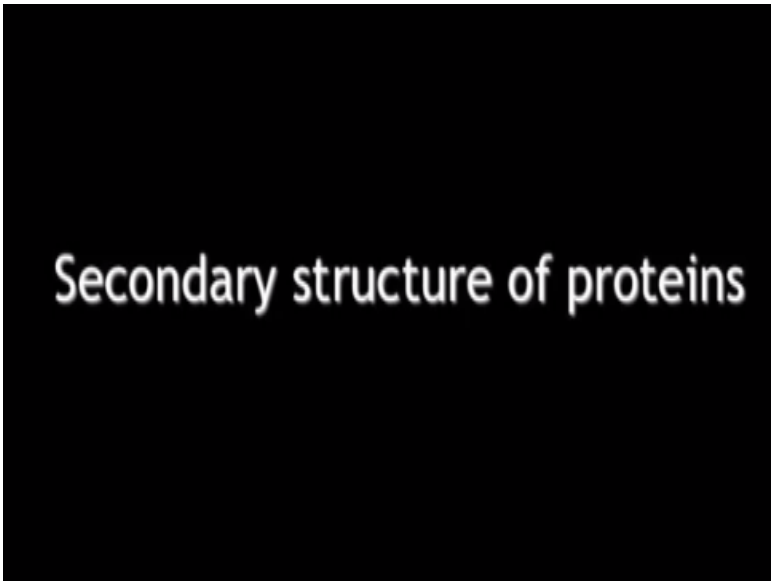
**(Refer Slide Time: 21:16)**




It is essential for the elucidation of its mechanism of action, it also determines the 3 dimensional structure of the proteins, the amino acid alteration can produce certain abnormalities in the individuals and diseases like you know, sickle cell anaemia is one of the example in which how the amino acid alteration could you know, just for single amino acid change could lead to you know, certain abnormality.

The sequences also tell us an evolutionary history of the protein and lot of evolutionary relationship of organisms could be established looking at their amino acid sequences.

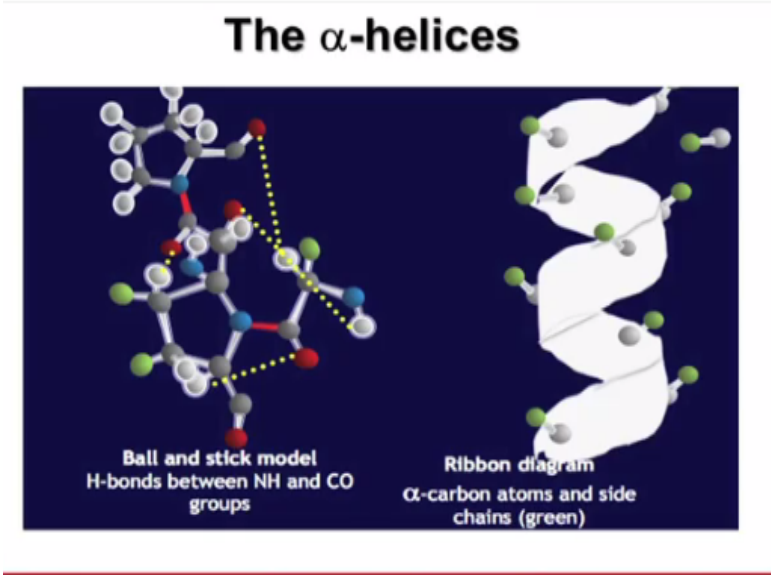
**(Refer Slide Time: 21:51)**




Let us now talk about secondary structures; the folding of a polypeptide backbone by means of internal hydrogen bonds between nearby amino acid residues that gives rise to a regular arrangement which is defined as the secondary structure of proteins. The different type of alpha helices and beta sheets which are most commonly observed in the secondary structure of proteins due to their highly favourable phi and psi angles which is described by the Ramachandran plots.

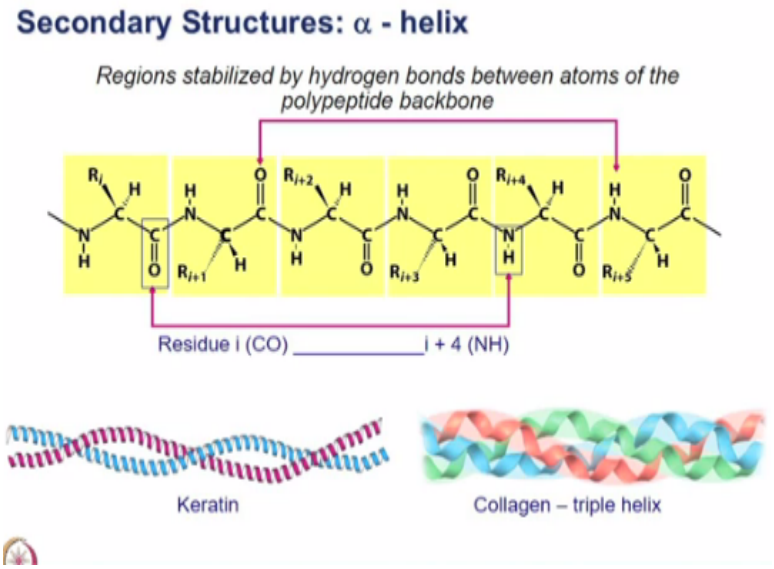
The amino acid prolene, it tends to disrupt the helix and it is often found you know, bending in the structure which is known as the reverse turn or the beta bends, let us look at the alpha helices first. So, proteins have variable helices contents.

**(Refer Slide Time: 22:39)**



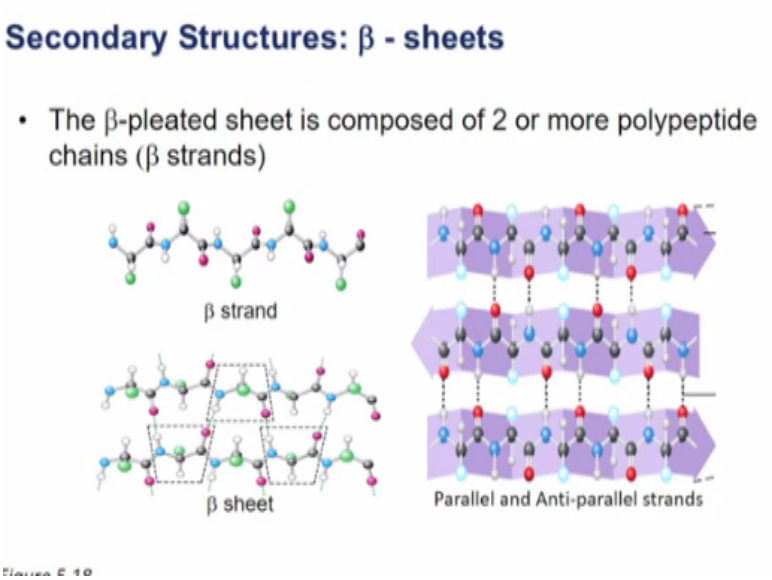
The alpha helices is a rod like structure, the main chain is tightly coiled around helical axis and the side chains they are extended outwards which is away from the helical axis that specific hydrogen bonds which can stabilize this helical codes to make alpha helices bonds.

**(Refer Slide Time: 23:00)**




The alpha helix is formed in the regions which are stabilized by the hydrogen bonds between atoms of the polypeptide backbones and residue the carboxyl group of the, the first amino acid with the NH group of the fourth is forming this bond and similar thing of the alpha helix could be seen in different examples whether it is a keratin protein or it is collagen protein, when you can see even double helix or triple helix is being present and they actually you know provide a lot of a strength to these protein structures.

**(Refer Slide Time: 23:32)**




Beta sheets; these are another common periodic structural motives, which are fully extended structure, they are parallel or antiparallel and we can see the structures of starting from you know the parallel and the antiparallel beta strands, so the beta pleated sheet is composed of 2 or more polypeptide chains shown in this on the screen is the beta strand on the top and the beta sheet.

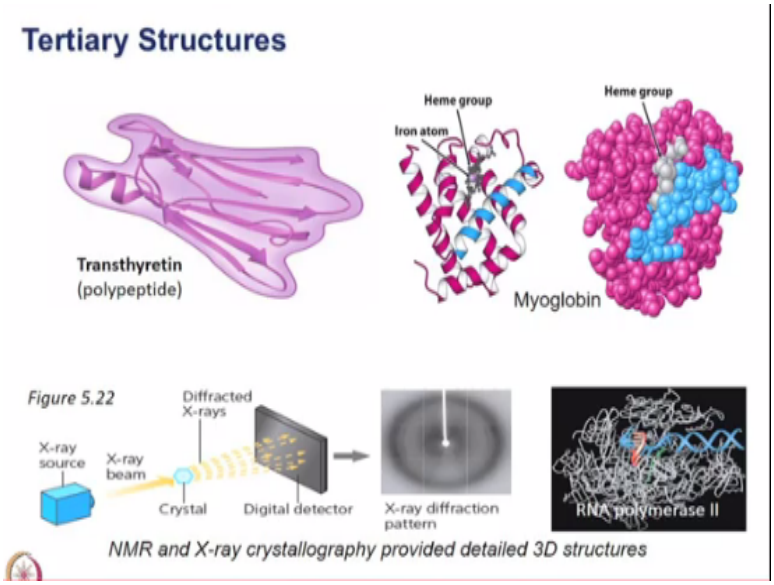
**(Refer Slide Time: 23:58)**

One of the examples shown here is the spiders silk fiber which is one of the structural protein which contains beta pleated sheets, let us move on to tertiary structures now. The tertiary structures refers to the interactions especially hydrophobic, electrostatic, hydrogen bonds etc. between amino acid side chains which are located far apart in the polypeptide sequence and that

causes the protein to fold resulting into a 3 dimensional arrangement of atoms which is known as tertiary structure.

The folding takes place in such a manner that the hydrophobic residues they get buried to form the core while the hydrophilic amino acids they remain on the surface in contact with the polar surroundings, so there are numerous interactions which specialises a tertiary structure of the proteins.

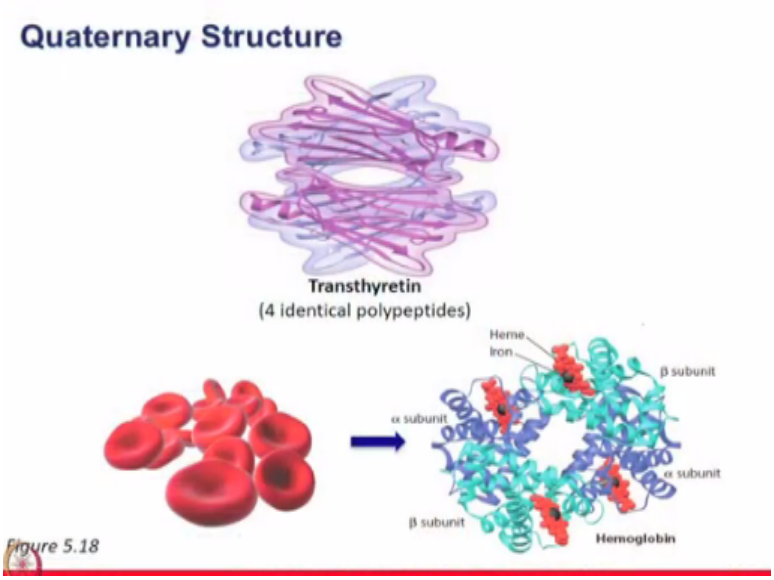
**(Refer Slide Time: 24:52)**




And that is shown here in some of the examples especially for the myoglobin and transthyretin proteins, these structures could be studied using NMR and x-ray crystallography which provides the detailed 3 dimensional structures. So, what are quaternary structures? Many proteins have more than 1 polypeptide chains also called a subunit that are assembled together by various interactions like electrostatic, Van Der Waals, disulphide bonds and that gives rise to the quaternary structure.

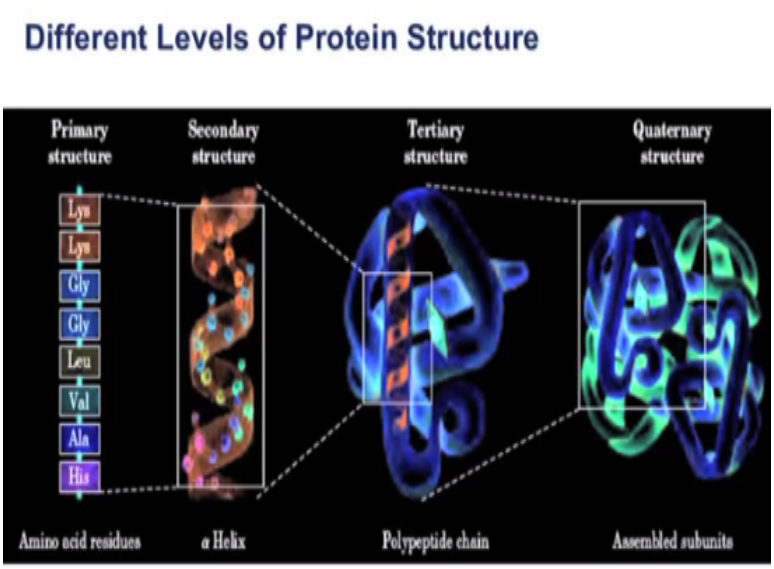
So, quaternary structure is referring to the interactions between individual protein subunits in a multi subunit complex and it actually, provides a final level of protein structure, it also depicts the special arrangements of subunits and their interactions and how these polypeptide chains assemble to form these multi sub unit structures.

**(Refer Slide Time: 25:46)**




Shown here are the examples of hemoglobin and transthyretin.

**(Refer Slide Time: 25:51)**

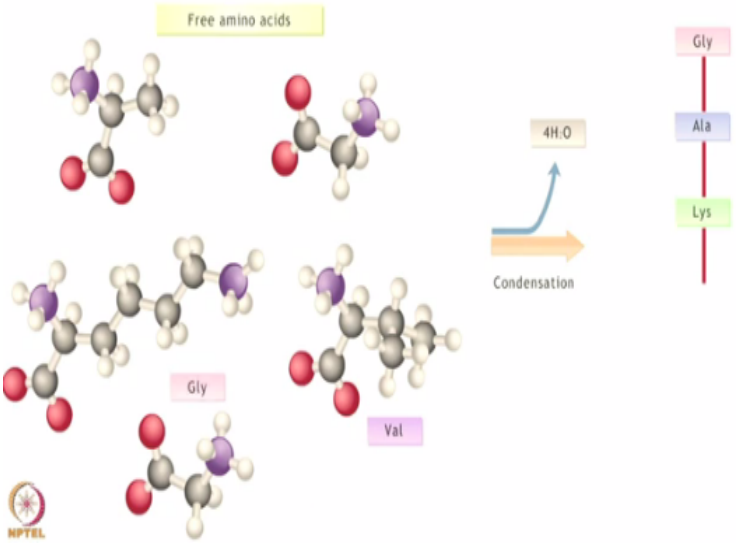



So, this is how we can summarize these different levels of protein structures, we have primary structure, secondary structure, tertiary structure and the quaternary structure.

**(Refer Slide Time: 25:59)**

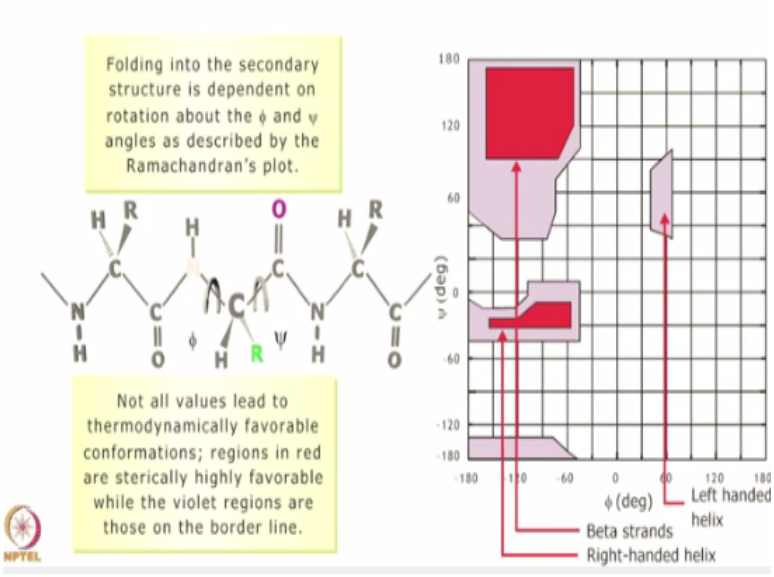

Let me explain you this in more detail in the following animation.

**(Refer Slide Time: 26:05)**



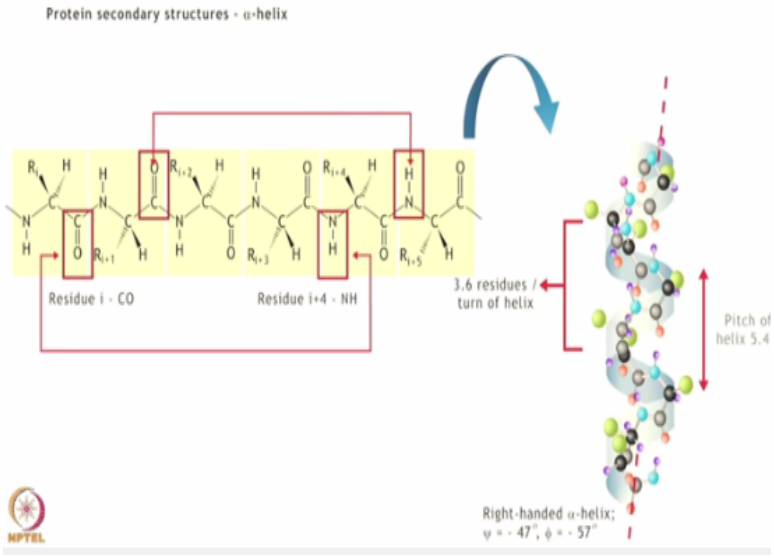

Amino acids are joined together in a head to tail arrangement by means of peptide bonds with a release of water molecules; this linear sequence of amino acids constitutes the primary structure.

**(Refer Slide Time: 26:24)**




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 favourable confirmations. The Ramachandran's plot defines these regions of favourability.

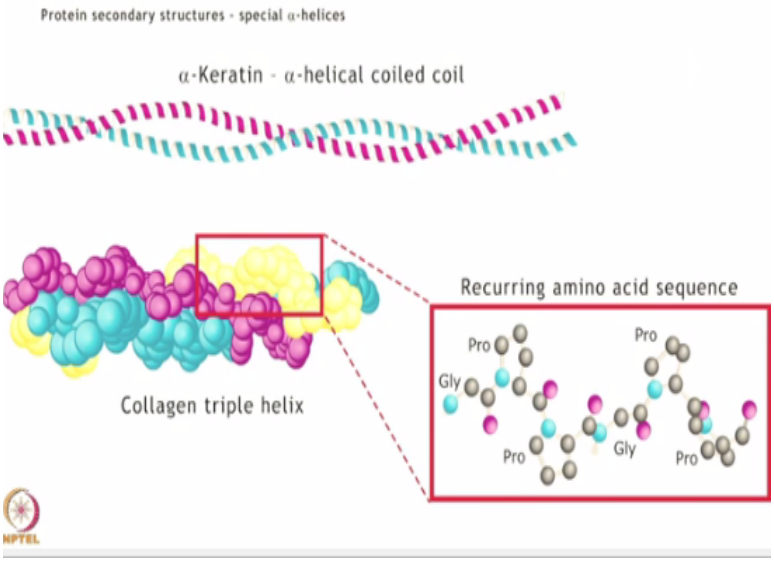
**(Refer Slide Time: 26:51)**




Amino acids along the polypeptide backbone interact through hydrogen bonds leading to secondary structures, the alpha helix has intrachain hydrogen bonds between the H of NH and O of CO in every fourth residue. Most alpha helices are right handed since this conformation is energetically more favourable. The amino acid proline which has a 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.

[Amino acids along the polypeptide backbone interact through hydrogen bonds leading to secondary structures; the alpha helix has intra chain hydrogen bonds between the H of NH and O of CO in every fourth residue. Most alpha helices are right handed since this conformation is energetically more favourable, the amino acid proline which has a 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.]

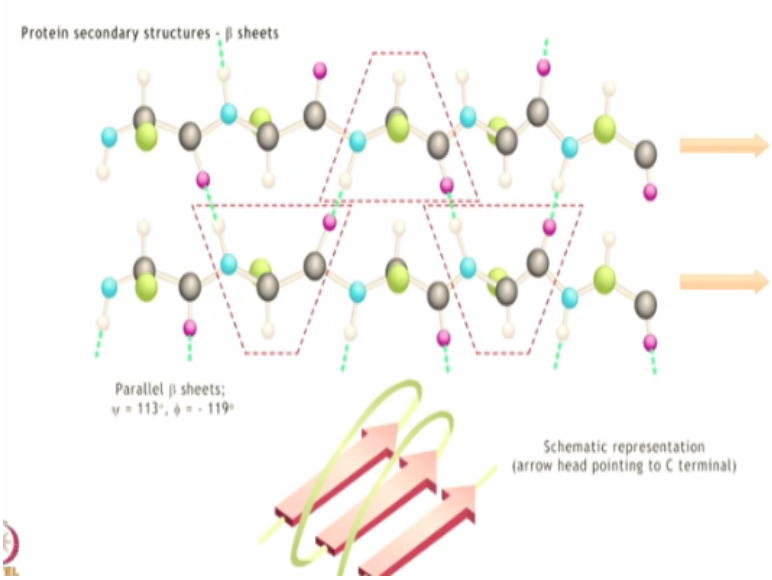
**(Refer Slide Time: 28:43)**




Alpha helices can also wind around each other to form stable structures such that their hydrophobic residues are buried inside while the polar side chains are exposed to the aqueous environment. Alpha carotene, the major protein component of hair consists of 2 such coiled coils forming a left handed super helix, collagen which is a fibrous component of skin, muscle etc. consists of 3 such coiled alpha helices.

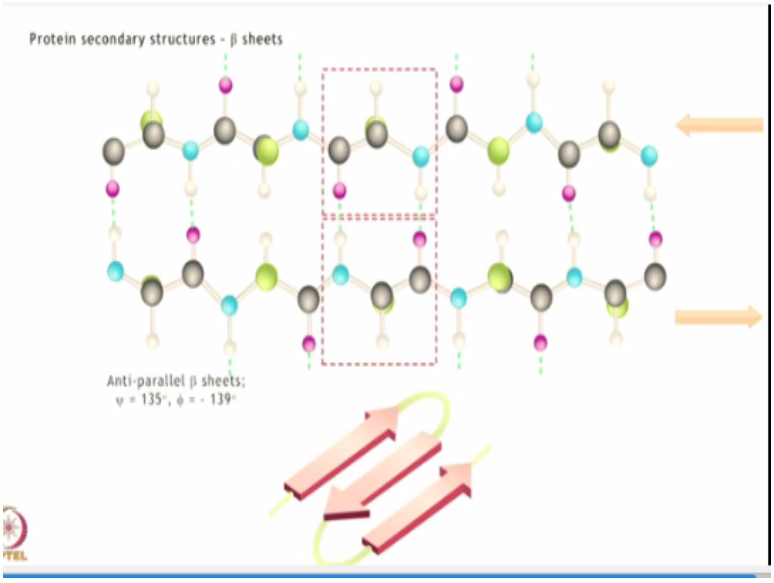
It has a characteristic recurring amino acid sequence of glycine, proline, hydroxy proline with glycine appearing at every third residue.

**(Refer Slide Time: 29:42)**



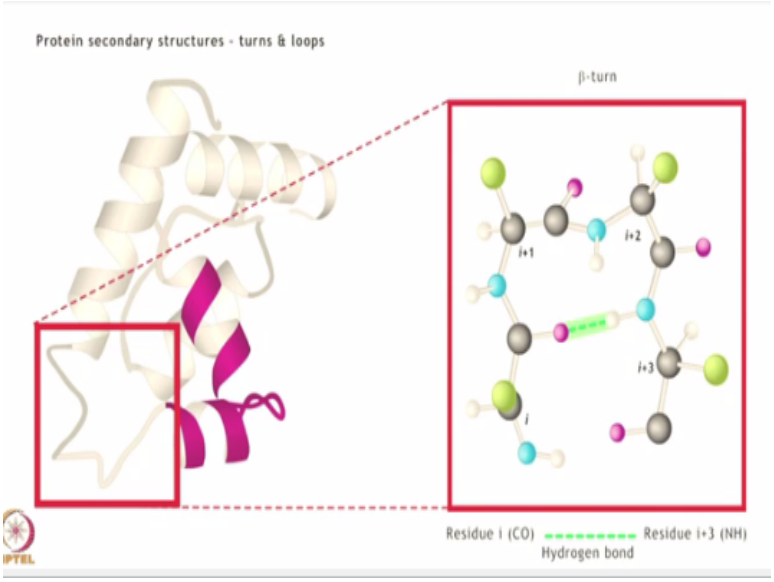

Beta pleated sheets discovered by Pauling and Corey is another common secondary structure with periodic repeating units, it is composed of 2 or more polypeptide chains with their side chains oriented above and below the plane, it is an extended structure with hydrogen bonds between the chains stabilizing it.

**(Refer Slide Time: 30:13)**



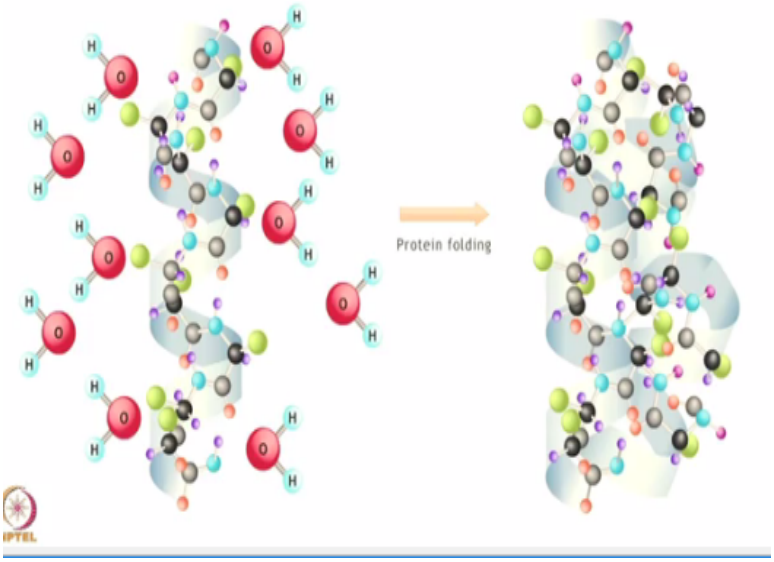

Amino acids in parallel beta sheets which run in the same direction interact with 2 different amino acids on the adjacent strand through hydrogen bonds; amino acids in anti-parallel strands on the other hand interact with only one amino acid on an adjacent strand.

**(Refer Slide Time: 30:40)**



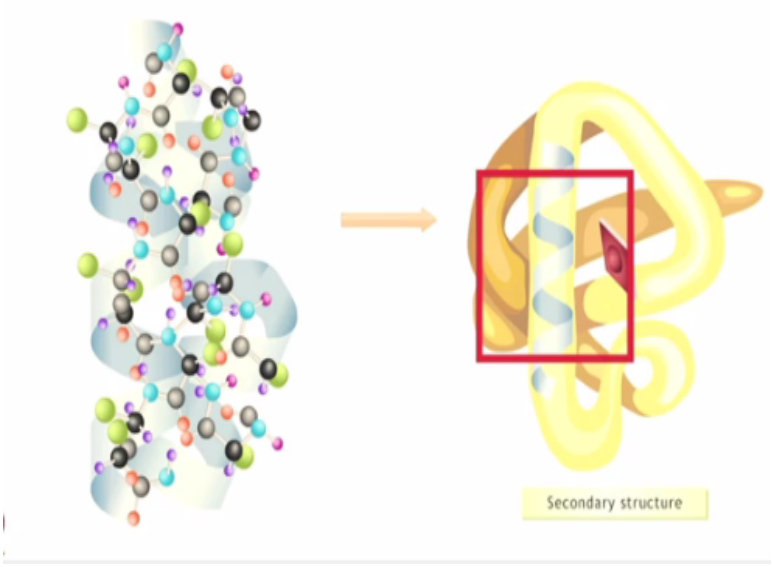

Almost all proteins exhibit a compact globular structure which is possible only if there are turns or loops between the various regions, beta turns, which are the most commonly observed turned structures consist of rigid well defined structures that usually lie on the surface of the protein molecule and interact with other molecules. A combination of secondary structures such as the helix turn helix which consists of 2 alpha helices separated by a turn is also observed and these are known as super secondary structures or motives.

**(Refer Slide Time: 31:32)**



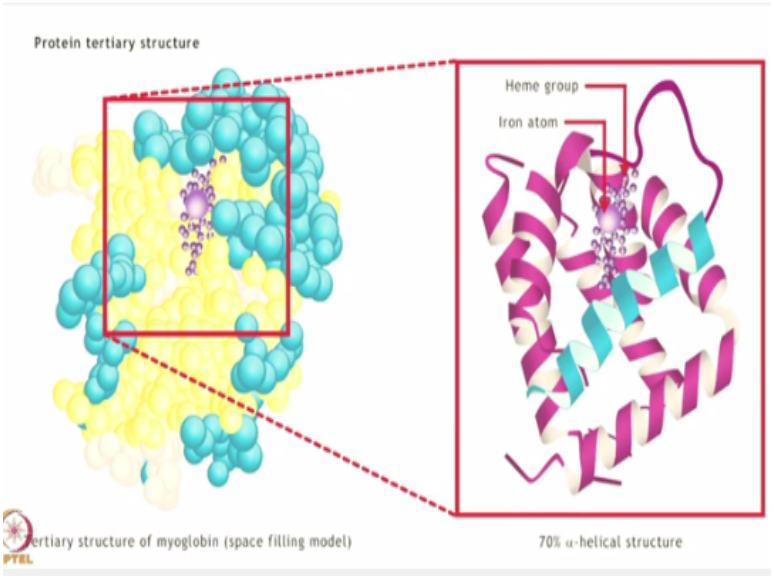

Amino acids located far apart on the polypeptide chain interact with each other by means of hydrogen bonds, electrostatic interactions, disulphide bridges etc. allowing the protein to fold 3 dimensionally in space giving rise to the tertiary structure.

**(Refer Slide Time: 31:58)**



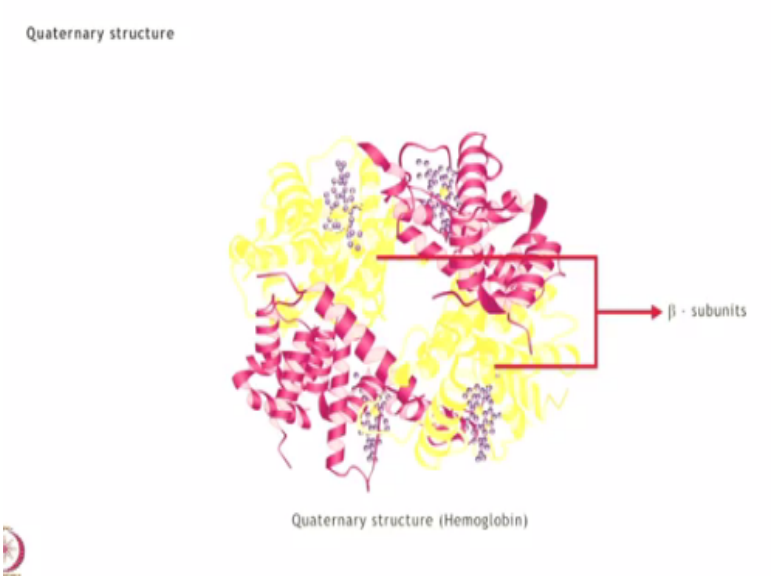

Folding takes place such that the hydrophobic residues are buried inside the structure while the polar residues remain in contact with the surroundings.

**(Refer Slide Time: 32:11)**




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, hydrophobic residues are found buried inside the structure, while the polar amino acids are found on the surface, 70% of the 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 give it a compact structure.

**(Refer Slide Time: 32:56)**



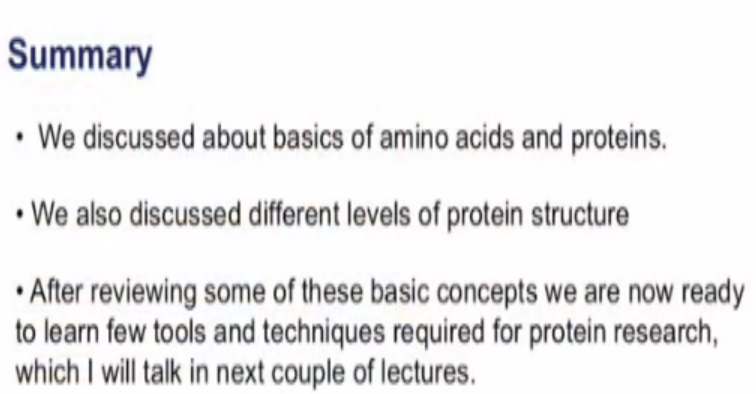

Different subunits or polypeptide chains interact with one another and are held together by means of ionic, electrostatic van der Waals etc. interactions, such multi subunit proteins are said to have a quaternary structure, the final level of protein structure. So, today in this lecture I try to refresh you about some of the basic concepts of amino acids and proteins of course, this whole subject needs not more detailed study.

But you know just to give you some basics and some idea, the kind of diverts side chain groups present in amino acids and why they are so crucial and why these studying proteins are so difficult because of the so much uniqueness in these amino acids and 20 different forms, they give rise to many different type of proteins and studying the proteins they therefore, becomes on one hand very crucial but also becomes very challenging.

In case of DNA studies, we had only 4 base pairs to study ATGC, in case of amino acids we have 20 combinations to a study, we do not have the techniques like polymerase chain reaction which we have studied earlier, in case of DNA technologies which could just simply amplify the DNA molecule, we do not have techniques like that in the case of the protein technologies maybe you can start with you know small amount of protein and amplify that to obtain the huge amount of protein.

So, these are many challenges to study the proteins and proteins are usually very dynamic, they are very labile, sometime they are you know, very short life, so studying proteins becomes very challenging and therefore, knowing their basics and properties are very crucial.

**(Refer Slide Time: 34:41)**




I just try to give you some glimpse of these structure of the different levels of protein structures; primary, secondary, tertiary and quaternary and intention is that after reviewing some of these basic concepts, you should go back, read the textbooks in much more detail and then you are more prepared to actually learn the tools and techniques which are employed to study proteins especially for the various type of protein research and proteomics research.

So, in the next couple of lectures, I am going to talk about different technologies, how they are trying to study the proteins and why, you know the complex protein mixtures especially at the proteome level and to do that different type of protein properties are being utilized. So, in the next couple of lectures we have more you know technology based understanding and then these basic concepts will be very useful over there, thank you.

**(Refer Slide Time: 35:29)**

## References

• Campbell Biology - Reece, Urry, Cain, Wasserman, Minorsky, Jackson 10th Edition, Cummings

•*Acknowledgment*

•Animations: In house animations OSCAR project IIT Bombay