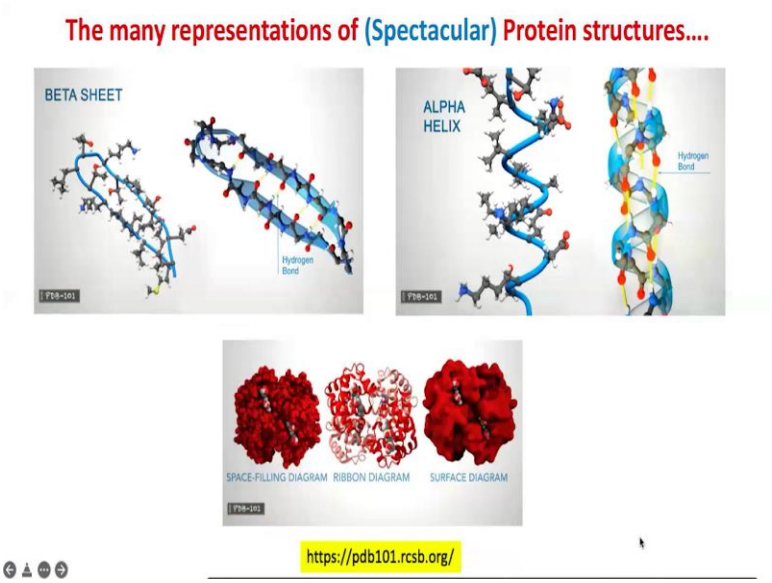
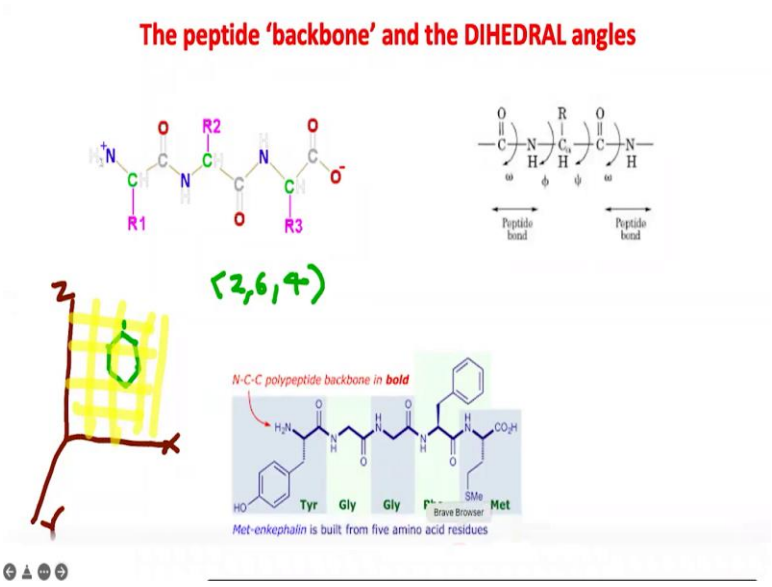
Introduction to Cell Biology
Professor Girish Ratnaparkhi
Professor Nagaraj Balasubramanian
Department of Biology
Indian Institute of Science Education and Research, Pune
Protein Structure, Folding and Function - Part 2

(Refer Slide Time: 00:15)





Student: Sir, please re-explain those diagrams all that space-filling diagram and surface diagram.

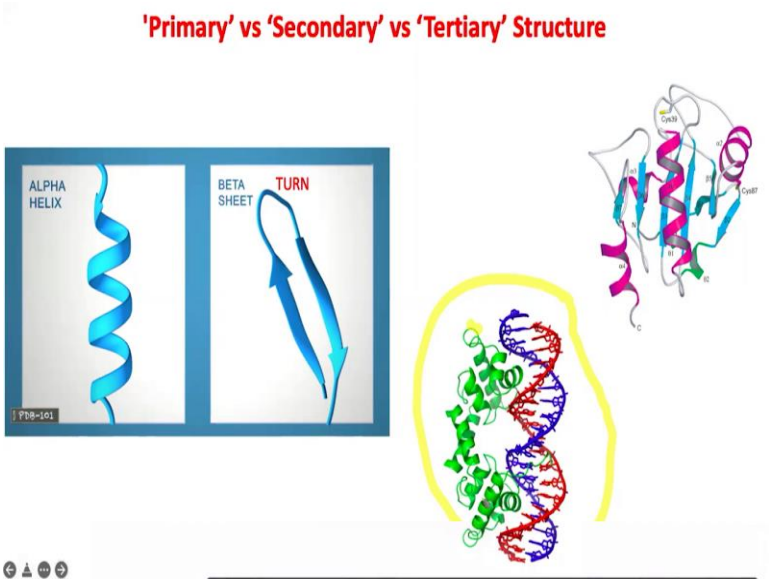
Professor: So, basically, protein is nothing but a repeating unit of these atoms. And the main chain is the heart of the protein, which is the N, C alpha, C prime, N, C alpha, it is a repeat. And

two different pieces of an amino acid form peptide bond, which I will define little more clearly. So, these are atoms in space. And these atoms in space along the polypeptide chain, you basically have different side chains, that is all that is varying, whereas the main chain remains pretty uniform throughout the polypeptide.

Now, let me see if I can get, explain this to you a little more clearly. So, the way I am going to explain this to you is to ask you to imagine a X, Y, Z grid or three dimensional graph paper, with this being, let us say, the x-axis, this being the z-axis, and this being the y-axis. And this is basically coordinate space. And in this coordinate space, at any point, if you have any atom over here, and let us just draw a benzene ring sort of ring over here, these atoms can be given specific points in the grid of this X, Y, Z grid.

So, there will be an X, Y, Z three dimensional grid and each atom over here can be given a three letter code, which corresponds to X, Y and Z. So, let us just say that, for example, this atom over here is 2, 6, 4. So, you can give specific locations in space in a X, Y, Z coordinate plane for any atom in space.

(Refer Slide Time: 2:11)

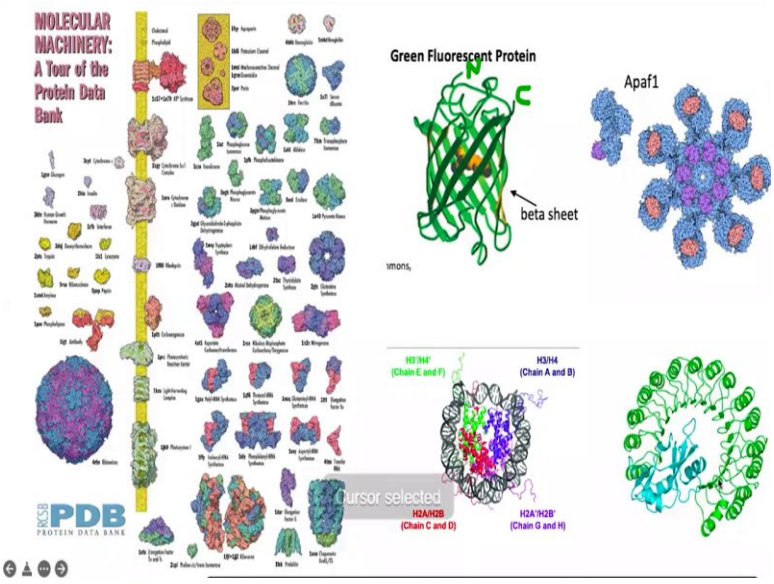


So, now, all the structures which are solved by crystallographers, and let us just look at one of them, let us look at this structure over here. For this structure, every atom in the structure after the structure was solved using crystallography, has been given a specific location in space. So

this entire structure in a file is nothing but X, Y, Z spot for this atom, X, Y, Z spot for this atom, and so on and so forth.

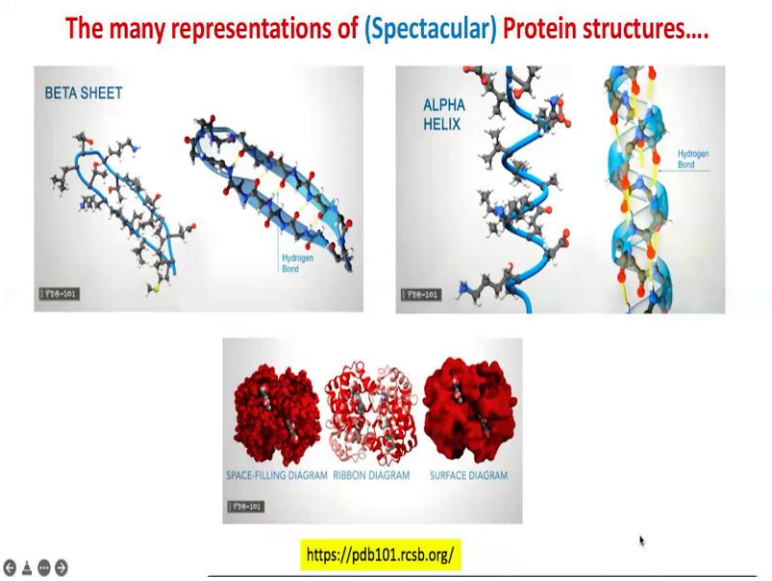
Now, we are basically dealing with carbon, nitrogen, oxygen, and sulfur, not too many atoms. And these atoms are organized in the main chain in a very specific way. And all these colorful representations are doing are using the atomic coordinates, which I have tried to explain to you, using the fact that the folded state of secondary structure of proteins are very standard. They are either helices or turns or beta sheets. And then represent them as simple pictures which can be appreciated by people who are not, let us say, specialized.

(Refer Slide Time: 3:14)



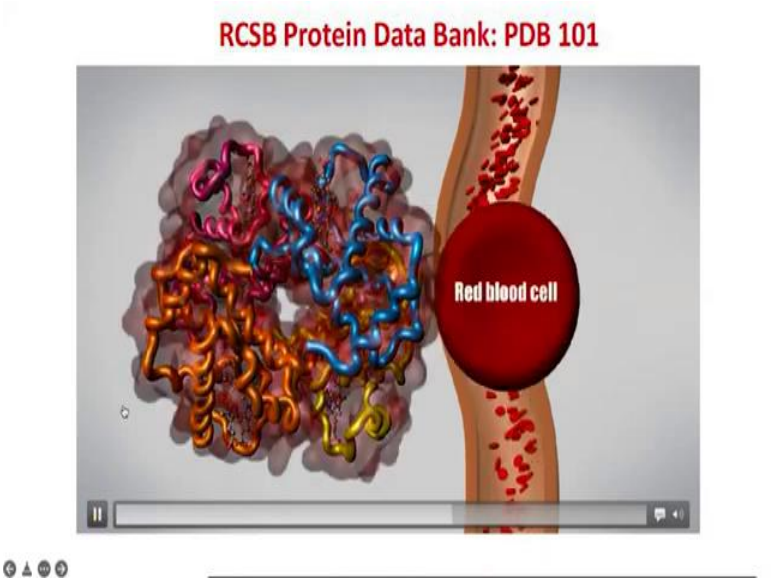
So, for example, the green fluorescent protein over here, if you say that this is where the N terminus starts, which I am not completely sure of over here, and let us say the C terminus ends over here, the green fluorescent protein is nothing but a series of beta sheets which are stacking against each other. And this representation called as a ribbon representation allows you to visualize what the protein looks like. And remember, this is at the level of atoms. So, you are visualizing it in a simple manner. And in the same way, you can look at a nucleosome, you can look at a ribosome and inhibitor and so on and so forth.

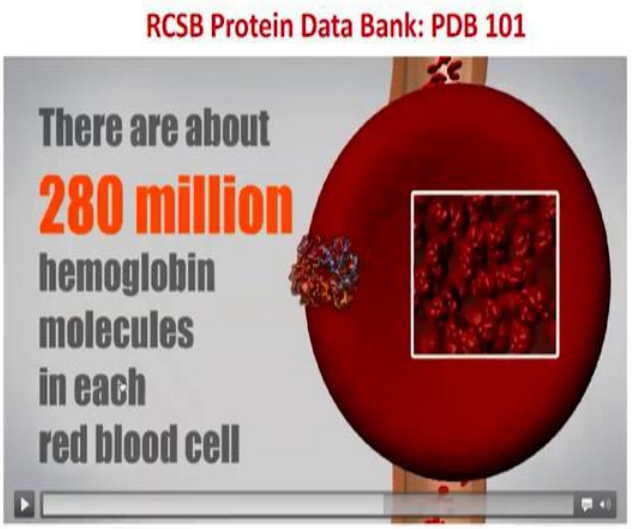
(Refer Slide Time: 3:53)



So, the take home over here is that you can visualize set of coordinates in space, which is the folded state of a protein, using either a ribbon diagram, a space filling diagram, a surface diagram or many, many other variants are there. But you have to remember that all of these are just representations of atoms in space. And the exact locations of the atoms in space relative to each other has been done by a crystallographic experiment, where x-ray crystallographer has purified protein, made a crystal, pointed x-ray beams on that crystal, got a diffraction pattern, and using a Fourier transform, and adding the missing phrases generated a three dimensional folded protein. And the three dimensional state of a folded protein relates to the function the protein does.

(Refer Slide Time: 4:53)





And in the movie you saw some very nice animation of hemoglobin and you saw where the iron atom was and you could understand that the tertiary structure of hemoglobin, maybe I can just go there, basically gives you an idea of its function.

So, here is a structure of hemoglobin. This is a sort of a tube diagram rather than a ribbon diagram. The main chain is shown as a tube. The side chains are not shown here at all, but you can see all the heme atoms, the four major heme groups and these are what are going to bind oxygen and carry out function inside the red blood cells of your blood.

So, was that explanation clear enough?

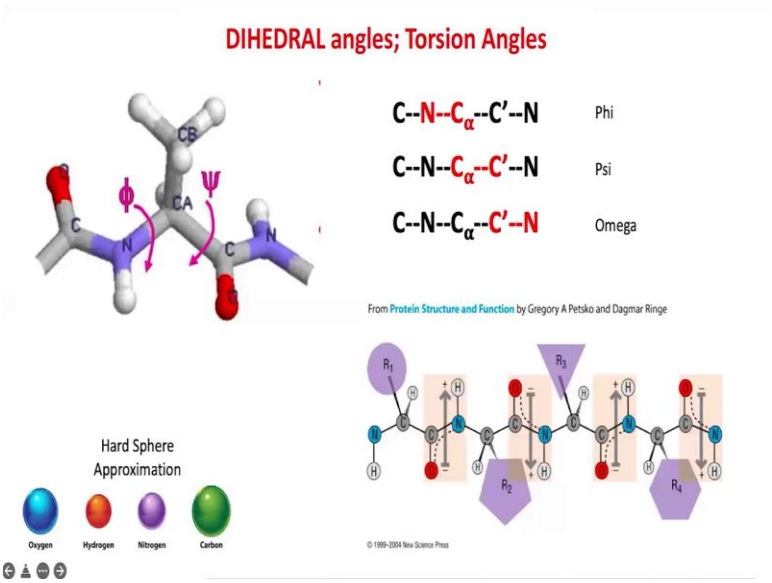
Student: Yes, sir.

Professor: Was that a yes or a no?

Student: Sir, it was nearly clear. Thank you, sir.

Professor: Okay sure.

(Refer Slide Time: 05:48)



Student: Sir, when you talked about the secondary structures, you have your alpha and beta sheet, is there any criteria for protein preferring alpha over beta or different protein preferring beta over alpha or they are just two forms simply no correlation.

Professor: So, the secondary structure elements are to a large extent defined by the sequence of amino acids and there will be some sequences which will preferentially fold into alpha helix. There will be some sequences which will be found only in beta sheets. So, you can actually predict not very well, it is not 100 percent prediction, but let us say 70 percent prediction. If I give you a linear sequence of amino acids, you can look at the sequence and say, oh, this is way to form alpha helix.

And how can we say that, because thousands, tens of thousands of protein structures have…

Student: You are not audible between.

Professor: Tens and thousands of protein structures have been solved. And one can just look at the sequences of all the structures, all the stretches which have alpha helices and say we have now looked at 10,000 alpha helices and there is always these four amino acids in alpha helices and they are always in this sequence. Therefore, whenever we see the sequence, it is a alpha helix. Is that clear?

Student: Thank you, sir.