Proteins

Slide 2 Proteins carry out a multitude of functions in living organisms. They provide support, act as catalysts for chemical reactions, carry oxygen in our blood, defend us from infection, allow movement, and regulate cell activities, to name a few. Nearly all of the genes in an organism's DNA code for proteins!

Slide 3 All proteins in all organisms are composed of amino acids bound together in varying sequences. The basic structure of all amino acids is the same. They all have a central carbon, an amino group, and a carboxyl group. Attached to the central, or alpha carbon, amino acids also have an R group which is different for each amino acid. The structure and properties of the different R groups are what make the amino acids different from one another.

Slide 4 Polypeptides are polymers of amino acids, linked by a peptide linkage. Peptide linkages result from condensation reactions. A peptide linkage, which is a covalent bond, forms between the carbon atom of the carboxyl group of one amino acid and the nitrogen atom of the amino group on the other amino acid. When this bond forms, 2 hydrogens from the amino group and one oxygen from the carboxyl group are removed to form a water molecule. Any two amino acids can be linked together in this way, regardless of the structure of the R groups because the R groups are not involved in the formation of the bond. Polypeptides can range from rather small chains of less than a hundred amino acids to massive proteins with nearly 5,000 amino acids linked together.

Slide 5 All living organisms use the same 20 amino acids to form all the proteins necessary to carry out their life functions. As you begin to understand the incredible array of protein functions, this fact will become even more amazing. On the other hand, the 20 amino acids can be thought of as an alphabet. Our English alphabet has 26 letters, and we can spell a huge number of words from that seemingly small set of letters. Try carrying around an unabridged dictionary sometime. In the same way amino acids can be linked together in an almost infinite number of different sequences to form different proteins. Remember that any 2 amino acids can be linked together using a peptide linkage because the amino and carboxyl groups on every amino acid are the same. The R groups, however, are quite diverse. This slide shows the chemical structure of each of the R groups, and gives some information about the properties of those R groups. Note that some R groups are charged, some are polar, some are hydrophobic, and some are hydrophilic. The different chemical properties of the R groups determine how different amino acids interact, and ultimately how a protein interacts with its environment and other molecules

These chemical interactions among R groups will become important when we talk about the secondary and tertiary structure of proteins.

Slide 6 Proteins have several levels of structure – primary, secondary, tertiary and quaternary. We will discuss each level in the next few slides

Slide 7 The primary structure of a protein is simply its amino acid sequence. This primary structure, however, ultimately determines the secondary and tertiary structure of the protein because the positions of the various R groups determine how parts of the polypeptide will interact with each other.

Slide 8 A protein's secondary structure is formed by hydrogen bonding between different amino acids along the polypeptide. In some cases regular patterns of hydrogen bonding will lead to the formation of patterns called alpha helices or beta pleated sheets. These structures are formed by hydrogen bonding between slightly polar parts of the polypeptide backbone. An alpha helix is a right-handed coil characteristic of structural proteins such as the keratins that are found in hair. Beta pleated sheets form when two polypeptides are lying alongside each other or a single polypeptide is bent back along itself. The chains are stabilized by hydrogen bonding. Many proteins contain regions of both alpha helices and beta pleated sheets.

Slide 9 Structures such as alpha helices and beta pleated sheets are commonly bent and folded together to contribute to the tertiary structure of proteins such as this RNA polymerase enzyme. Tertiary structure depends on the interactions among the various R groups on the amino acids. These interactions may encompass any of the chemical interactions we discussed earlier, including covalent bonds called disulfide bridges between sulfur-containing cysteine amino acids, hydrophobic and van der Waals interactions among amino acids with hydrophobic R groups, and ionic salt bridges between positively and negatively charged R groups. All of these interactions serve to fold the protein into its final, functional form. Remember that the shape of the protein is vital to its function.

Slide 10 Quaternary structure is found in complex proteins that contain more than one polypeptide chain. This slide shows hemoglobin which is made up of 4 different polypeptide chains. These distinct chains are held together by a combination of interactions, including ionic and hydrogen bonds, as well as hydrophobic and van der Waals interactions.

Slide 11 Because the secondary, tertiary and quaternary structure of proteins depends largely on comparatively weak bonds, the higher structure of proteins is sensitive to environmental conditions such as temperature and pH that can disrupt those bonds. For instance, proteins may denature at high temperatures because hydrogen bonds and van der Waals forces become unstable at elevated temperatures. When proteins denature, they lose their folded shape and are unable to perform their functions. When you have a high fever, for example, proteins in your body may begin to denature and become unable to perform important bodily functions. When your temperature returns to normal, the proteins will usually fold back into their customary shapes. Changes in pH can cause similar denaturation and renaturation processes.

Denatured and newly formed proteins are sometime in danger of becoming misfolded because they may be exposed to other molecules with which they can interact. A number of diseases, including Alzheimer's, have been shown to involve misfolded proteins. To protect a protein that has not yet attained its correct shape, proteins called chaperonins form a sort of cage around the protein to limit inappropriate interactions while the protein is folding into its functional form.