Structure and function of proteins

ASSIGN BUSTER

Whichever essay topic macromolecule you pick, you will need to outline the variety of structures in that family of macromolecules it may be useful to use diagrams for this, you will then need to explain how and where they are used in the cell and, where appropriate link macromolecule structure to function. You will also need to briefly outline where the molecules come from e. g. are they derived from the diet or synthesised within the cell. You should also include an explanation of how these molecules can contribute to health and/or disease.

Structure and Function of Proteins

INTRODUCTION

Proteins are large macromolecules which consist of hydrogen, carbon and oxygen; proteins are polymeric chains that are built from monomers known as amino acids. Proteins have a major function in a living organism, for example, the replication of DNA, catalysing metabolic reactions (catalyst); stimulus response and also transporting molecules form one place to another. There are 20 different types of amino acids which synthesize proteins, however the function and different properties of each type of protein is due to the precise sequence and structure of the amino acids present. (Petsko and Ringe. 2004. Pp. 8)

Each amino acid consists of a central carbon atom (C), which is attached to a hydrogen atom (H), an amino group (also known as NH2 group), a carboxyl group (- COOH, this gives up a proton hence why this is known as an acid) and also a unique side chain or R group.

Amino acids are linked linearly via covalent peptide bonds, short chain amino acids are known as peptides whereas long chain formations of amino acids are called polypeptides, where the peptide bond is formed between the carboxyl group of one amino acid and the amino group on the neighbouring amino acid. This reaction occurs as a condensation reaction where there is a removal of a hydrogen atom from the amino group of one amino acid and the removal of a -OH group from the carboxyl acid from another amino acid forming a water molecule (Fig 1). (Andrew. 2001. Pp. 13)

The unique side chain or R group is what disguises one amino acid from another; the overall structure and properties of the proteins are therefore dependent on sequence of the R group of each amino acid (Campbell and Farrell. 2011. Pp. 61). Furthermore these variations of the R group and also the arrangements of the other amino acids would form a number of different polypeptides. Each protein consists of a different number of these polypeptide chains which are folded into complex three dimensional shapes therefore different proteins would have different shapes.

There are four levels of protein organization found in polypeptides; these structures are known as: primary structure, secondary structure, tertiary structure and also quaternary structure.

Primary structures is the basic structure of the levels of organization, the primary structure is the linear arrangements/sequence found of the amino acid in the protein, and also could be thought of as the covalent linkages found in the polypeptide chain or the protein, such as a disulphide bond (Vickie and Christian. 2008. Pp. 148).

The secondary structure is the areas of folding found within the protein, where there is an ordered arrangement of the amino acids in some localized regions of the polypeptide molecule; hydrogen bonds play a vital role in stabilizing the folding patterns which are found in the protein molecule (Lieberman and Marks. 2009. Pp. 92). Although the conformation of each protein molecule are considered unique, there are two main types of secondary structure, or folding patterns, that are often present; these are the alpha helix and the parallel and anti-parallel beta-pleated sheets, these two folding patterns are common due to the hydrogen bonding occurs between the N-H and C= O groups in the backbone of the polypeptide (Albert's. Bray. Hopkins. Johnson. Lewis. Raff. Roberts. And Walter. 2010. Pp. 127). However there are a number of other secondary structures, but the alpha helix and the beta sheets are the most stable form of secondary structures found. Furthermore there may be a number of these two types of secondary structure found in a single polypeptide chain.

An alpha helix is spiral structure where this could be either a right handed or left handed spiral, in which the peptide bonds are found to be Trans conformational and planar, it would also be found that the amino group of each of the peptide bonds is generally in the upward position where as the carboxyl group points in the downwards position.

An alpha helix structure is generated when a single polypeptide chain has turned around itself to form a rigid cylinder where a hydrogen bond is formed between every fourth amino acid (fig 1. 2), which links the C= O group of one peptide bond to the N-H group on another amino acid (fig 1. 2).

There are two types of beta sheets; parallel and anti-parallel beta sheets. The Beta pleated sheets are extended polypeptide chains with another neighbouring polypeptide chain extending either parallel or anti-parallel to each other, this occurs due to the hydrogen bonds being formed between the segments of the polypeptide chain so are essentially place side by side. (Bradley and Calvert. 2006. Pp. 7). The parallel beta sheets is when the structure is shown to consist a polypeptide chain and neighbouring polypeptide chain that would run in the same direction (from the N-terminus to the C-terminus), is known as the parallel beta sheet (Fig 2. 1), whereas when the polypeptide chain runs in the opposite direction of that of its neighbouring chain, it is known as an anti-parallel beta sheet (Fig 2. 2).

The beta sheet are stable structures that produces a very rigid, pleated structure; this is due to the beta sheet being stabilized by hydrogen bond being formed between the amino group on one polypeptide chain and the carboxyl group on the adjacent chain.

Beta sheets have many different properties and functions, where this type of secondary structure is found in protein which their function would require strength, for example; this type of structure gives silk fibres their extraordinary tensile strength, beta sheets would also be found in the exoskeleton of insects which allows them not to freeze in cold conditions by providing the insect with an anti-freeze protein which forms a flat surface with a number of hydroxyl groups, the protein can therefore bind with the ice crystals which would prevent the growth of the crystals and therefore the insect does not freeze.

The tertiary structure of a protein is the full three dimensional structure of the arrangements of atoms found within the polypeptide chain, this structure is the final geometric shape that protein assume and would be the highest level structure that a protein can attain, the structures include the alpha helix, beta sheets, random coils and also other structures such as loops and folds, which are formed between the N-terminus and the C-terminus. (Stoker, H. S. 2012. Pp. 726)The tertiary structure is mainly stabilized by the formation of disulphide bonds, this is also known as a disulphide bridge because these bonds are formed by oxidation reaction of the side chains of cysteine, by oxidizing the two thiol groups (SH) which would form a disulphide bond (S-S) (fig 3).

The tertiary structure is the most important of all the structural levels of enzymes activity, where the tertiary structure of an enzyme would consist of all the peptide bonds, ionic bonds, hydrogen bonds and also the disulphide bonds therefore when all these types of bonds are combined, this would produce a three dimensional structure. The function of an enzyme require a three dimensional structure for the active site of the enzyme, the area of the enzyme that combines with a substrate, and cause a specific reaction to speed up.

However a mutation in the genetic code could lead to a human disease by disrupting the tertiary structure of the protein causing the protein or enzyme to be denatured (the enzyme would lose its catalytic power). If a protein loses its tertiary structure it could also lead to diseases such as cystic fibrosis, where there is a disruption in the CRTR protein.

The quaternary structure of a protein is the arrangements of many different types of coiled and folded polypeptides to form a unique functional protein and is stabilized by several non-covalent bonding, where some of these types of bonding are also found in tertiary structures, for example; hydrogen bonding, Van Der Waals interactions, hydrophobic interactions, ionic interactions and also disulphide bonding. This structure can only occur if there is more than one polypeptide chain present in a complex protein these are called multimers.

The Quaternary structures are usually found in biologically active proteins for example, in the pigment of haemoglobin, which is found in the red blood cells, contain two types of polypeptide chains but with a total of four tightly packed polypeptide chains which are alpha 1, 2 and beta 1, 2, where these are arranged in a globular fold. Each haemoglobin molecule contains four haem molecules where there is one attached in each subunit, so that oxygen would bind on the centre of each haem molecule (a total of 4 oxygen molecules) and when the oxygen binds to the haem group, the conformation of the haemoglobin protein changes (forming oxyhaemoglobin) where these changes in structure on one site of the protein may cause changes at a distant site, this type of protein which changes structure is referred as an allosteric protein. (Roberts. Reiss. Monger. (2000). Pp. 28-35)

However there is a genetic mutation that could affect the quaternary structure of a protein, an example is sickle cell anaemia where there is a single point mutation in the nitrogen base in a codon where the hydrophobic amino acid valine is coded in instead of the hydrophilic amino acid, glutamic,

therefore this small change in the genetic code causes a normally round red blood cell to be a sickle shape.

CONCLUSION

The structure of proteins plays a major and useful role in the functioning of the human body when it comes to the specific functions of the amino acids. There are a wide variety of functions that are accomplished by proteins, from enzyme activity to transportation and immune responses (such as antibodies). However the functions of proteins are affected in a major way if the conditions or structure of the amino acids are slightly changed for example, if conditions such as the temperature were to change slightly (increasing), an enzyme would lose its tertiary shape and would become denatured; therefore the catalysing reaction would slow down dramatically ie the decrease in the rate of reaction due the less than ideal condition surrounding the enzyme, this would therefore cause a reduction in specific reaction. Furthermore as long as the conditions and the structure of the polypeptide chains remain constant, the functioning’s of the protein molecules and, in turn the living organism, will not be affected.