

Food chemistry assignment

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Functions of proteins are clearly seen when they interact with other processes in the food system.

The forms of interactions may include solute, solvent, and protein molecules or other substances dispersed in the solvent like air or oil. The existence of proteins is seen in the lowest kinetically achievable state of free energy. The free energy found in the proteins may be the lowest to be achieved by the protein in a good time frame. The structure of protein depends highly on the environment. This leads to the protein assuming different conformations like the changes in environmental conditions. Important factors are temperature, ionic strengths, dielectric constant, PH and existence of different molecules such as fat, air and denaturants.

One of the ways used by the proteins in lowering free energy is removing the hydrophobic groups from the aqueous environment. This may lead to a decrease in free energy in the proteins. The hydrophobic binding strength is sensitive to the temperature changes and dielectric constant. These changes can influence the structures of the protein. The primary, secondary and tertiary structures of the protein are dynamic and not rigid.

Within the protein, there are rotational freedoms about the bonds and the entropy gain from this freedom reduces the native's structure free energy. There are also other parts of the protein structures that are evened out by secondary forces that are weak and are mainly free in assuming different conformations. These conformations lead to high free energy structures. Hence, it makes them unstable and to have a short life. As a dynamic entity, a protein may be anticipated in sampling the different structures constantly.

These structures are to some extent different from the native conformation and may lead to situations where the system's free energy increases. An increase in free energy leads to the protein refolding spontaneously in a low free energy state. Environmental changes may make alternate structures becoming to become low in free energy, and this leads to protein denaturation. For the protein to show that it is functioning, it is supposed to interact with the food system components. For the interactions to take place properly, the protein is supposed to be free and move all over the system.

On the other hand, it is supposed to change its structure in a way that interactions may be allowed with added components. Emulsions are uneven mixtures of immiscible liquids. Emulsified droplets can be evened out by adding molecules that are partly soluble in both stages. In different foods, an amount of small emulsifier molecules can be used in serving these functions. Proteins that are likely to unfold at the interface may be used in serving the same functions. Protein coats the droplet of the lipid and issues an energy barrier in a phase separation and particle association.

Molecular Characteristics of Globular Proteins Globular proteins are formed by amino acid chains that are compacted and folded into intricate chains resembling spheres. These proteins do not have systematic structures. There may be one or two chains that come together in usual ways. Additionally, there may be parts of these chains that have helical, random or pleated structures. Common globular proteins are hemoglobin, insulin, myoglobin, egg albumin, enzymes and serum globulins. These proteins have a 3 dimension molecular structure and are divided mostly into three or four points.

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There is a primary structure that is the amino acids sequence which forms a peptide chain. This peptide chain can be folded in a repetitive fashion and ordered way. The structures having this repetitive fashion and ordered way are referred to as secondary structures. Turns and helices are the vital categories of secondary structures. Turns are categorized as secondary structures despite the fact that they have ordered but no repetitive structures.

The tertiary structure is the general globular protein 3D structure that is produced by the helices being folded. It is also produced by folding the sheets on themselves with loops and turns leading to the formation of folds. For the globular proteins folded conformation to be maintained, non-covalent molecular attractions are needed. Hydrogen bonds are examples of visualizing and both types are found in the globular proteins. Attractive forces found in the salt bridges are needed in preserving other tertiary structures. Disulfide bond is an example of the covalent bond that can be used in preserving the tertiary structure as well as linking two or more peptide chains collectively.

Other globular proteins have quaternary structures. They are formed when two or more added globular protein molecules link to form a multimeric unit. A used and known example of a protein having quaternary structure is hemoglobin. The tertiary structures in the globular proteins are characterized by the amount of layers of the peptide backbone that exist and the attractive forces produced by these layers. To sum up the whole discussion, other vital characteristics are the existence of disulfide bonds of intrinsically segments

that are unstructured or chelated metal ions in the absence of backbone layers.

Backbone layers found in the central part of the structure is a feature in some of the globular proteins. The location and the number of layers differ for various proteins, but in all the globular proteins the hydrophobic forces found in these layers are vital in retaining the tertiary structure. The ribbons used show the amino acid chain backbone having different amino acids represented by shading. The side chains of the amino acids fill in the structure.