Proteins in Food: An Introduction

Introduction

Proteins are the most abundant molecules in cells, making up 50 % or more of their dry weight. Every protein has a unique structure and conformation or shape, which enables it to carry out a specific function in a living cell. Proteins comprise the complex muscle system and the connective tissue network, and they are important as carriers in the blood system. All enzymes are proteins; enzymes are important as catalysts for many reactions (both desirable and undesirable) in foods.

All proteins contain carbon, hydrogen, nitrogen, and oxygen. Most proteins contain sulfur, and some contain additional elements; for example, milk proteins contain phosphorus, and hemoglobin and myoglobin contain iron. Copper and zinc are also constituents of some proteins.

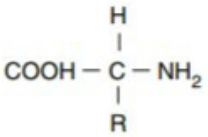
Proteins are made up of amino acids. There are at least 20 different amino acids found in nature, and they have different properties depending on their structure and composition. When combined to form a protein, the result is a unique and complex molecule with a characteristic structure and conformation and a specific function in the plant or animal where it belongs. Small changes, such as a change in pH, or simply heating a food, can cause dramatic changes in protein molecules. Such changes are seen, for example, when cottage cheese is made by adding acid to milk or when scrambled eggs are made by heating and stirring eggs.

Proteins are very important in foods, both nutritionally and as functional ingredients. They play an important role in determining the texture of a food. They are complex molecules, and it is important to have an understanding of the basics of protein structure to understand the behavior of many foods during processing. This chapter covers the basics of amino acid and protein structure. Individual proteins, such as milk, meat, wheat, and egg proteins, are covered in the chapters relating to these specific foods.

Amino Acids

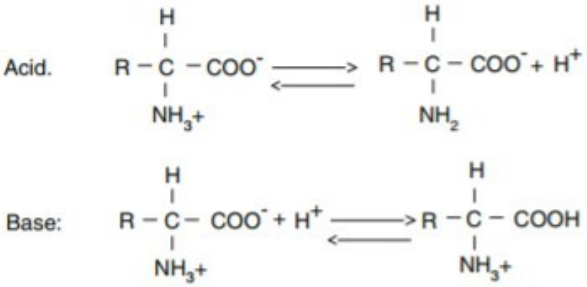
General Structure of Amino Acids

Every ***amino acid*** contains a central carbon atom, to which is attached a carboxyl group (COOH), an amino group (NH_2), a hydrogen atom, and another group or side chain R specific to the particular amino acid. The general formula for an amino acid is



properties depend on the nature of their side chains or R groups.

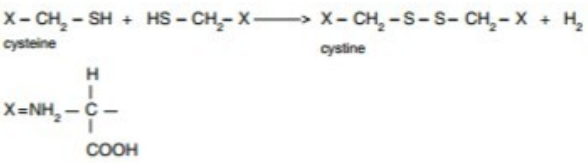
In a solution at pH 7, all amino acids are ***zwitterions***; that is, the amino group and carboxyl groups are both ionized and exist as COO^- and NH_3^+, respectively. Therefore, amino acids are ***amphoteric*** and can behave as an acid or as a base in water depending on the pH. When acting as an acid or proton donor, the positively charged amino group donates a hydrogen ion, and when acting as a base the negatively charged carboxyl group gains a hydrogen ion, as follows:



Categories of Amino Acids

Amino acids can be divided into four categories, according to the nature of their side chains, as shown in Fig. 8.1. The first category includes all the amino acids with ***hydrophobic*** or **nonpolar** side chains. The hydrophobic (water-hating) amino acids contain a hydrocarbon side chain. Alanine is the simplest one, having a methyl group (CH_3) as its side chain. Valine and leucine contain longer, branched, hydrocarbon chains. Proline is an important nonpolar amino acid. It contains a bulky five-membered ring, which interrupts ordered protein structure. Methionine is a sulfur-containing nonpolar amino acid. The nonpolar amino acids are able to form hydrophobic interactions in proteins; that is, they associate with each other to avoid association with water.

The second group of amino acids includes those with **polar uncharged** side chains. This group is ***hydrophilic***. Examples of amino acids in this group include serine, glutamine, and cysteine. They either contain a hydroxyl group (OH), an amide group ($CONH_2$), or a thiol group (SH). All polar amino acids can form hydrogen bonds in proteins. Cysteine is unique because it can form ***disulfide bonds*** (—S—S—), as shown below:



A disulfide bond is a strong covalent bond, unlike hydrogen bonds, which are weak interactions. Two molecules of cysteine can unite in a protein to form a disulfide bond. A few disulfide bonds in a protein have a significant effect on protein structure, because they are strong bonds. Proteins containing disulfide bonds are usually relatively heat stable, and more resistant to unfolding than other proteins. The presence of cysteine in a protein therefore tends to have a significant effect on protein conformation.

The third and fourth categories of amino acids include the charged amino acids. The **positively charged (basic)** amino acids include lysine, arginine, and histidine. These are positively charged at pH 7 because they contain an extra amino group. When a basic amino acid is part of a protein, this extra amino group is free (in other words, not involved in a peptide bond) and, depending on the pH, may be positively charged.

The negatively charged (acidic) amino acids include aspartic acid and glutamic acid. These are negatively charged at pH 7 because they both contain an extra carboxyl group. When an acidic amino acid is contained within a protein, the extra carboxyl group is free and may be charged, depending on the pH.

Oppositely charged groups are able to form ionic interactions with each other. In proteins, acidic and basic amino acid side chains may interact with each other, forming ionic bonds or salt bridges.

Protein Structure and Conformation

All proteins are made up of many amino acids, joined by ***peptide bonds*** as shown below:

Peptide bonds are strong bonds and are not easily disrupted. A ***dipeptide*** contains two amino acids joined by a peptide bond. A ***polypeptide*** contains several amino acids joined by peptide bonds. Proteins are usually much larger molecules, containing several hundred amino acids. They can be hydrolyzed, yielding smaller polypeptides, by enzymes or by acid digestion.

The sequence of amino acids joined by peptide bonds forms the backbone of a protein, as shown below:

- The protein backbone consists of repeating N—C—C units.
- The amino acid side chains (R groups) project alternately from either side of the protein chain.
- The nature of the R groups determines the structure or ***conformation*** of the chain. (In other words, the shape the protein assumes in space.)

Each protein has a complex and unique conformation, which is determined by the specific amino acids and the sequence in which they occur along the chain. To understand the function of proteins in food systems and the changes that occur in proteins during processing, it is important to understand the basics of protein structure. Proteins are described as having four types of structure—primary, secondary, tertiary, and quaternary structure—and these build on each other. The primary structure determines the secondary structure and so on. The different types of protein structures are outlined below.

Primary Structure

The primary structure (***protein primary structure***) of a protein is the specific sequence of amino acids joined by peptide bonds along the protein chain. This is the simplest way of looking at protein structure. In reality, proteins do not exist simply as straight chains. However, it is the specific sequence of amino acids that determines the form or shape that a protein assumes in space. Therefore, it is essential to know the primary structure if a more detailed understanding of the structure and function of a particular protein is desired.

Secondary Structure

The secondary structure (***protein secondary structure***) of a protein refers to the three-dimensional organization of segments of the polypeptide chain. Important secondary structures include the following:

- Alpha helix—ordered structure
- Beta-pleated sheet—ordered structure
- Random coil—disordered structure

The ***alpha (α) helix*** is a corkscrew structure, with 3.6 amino acids per turn. It is shown in Fig. 8.2. It is stabilized by intrachain hydrogen bonds; that is, the hydrogen bonds occur within a single protein chain, rather than between adjacent chains. Hydrogen bonds occur between each turn of the helix. The oxygen and hydrogen atoms that comprise the peptide bonds are involved in hydrogen bond formation. The α-helix is a stable, organized structure. It cannot be formed if proline is present, because the bulky five-membered ring prevents formation of the helix.

The ***beta (β)-pleated sheet*** is a more extended conformation than the α-helix. It can be thought of as a zigzag structure rather than a corkscrew. It is shown in Fig. 8.3. The stretched protein chains combine to form β-pleated sheets. These sheets are linked together by interchain hydrogen bonds. (Interchain hydrogen bonds occur between adjacent sections of the protein chains rather than within an individual chain.) Again, the hydrogen and oxygen atoms that form the peptide bonds are involved in hydrogen bond

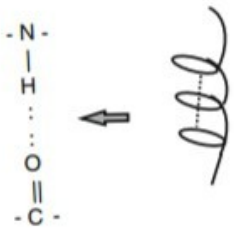


Fig. 8.2 Schematic three-dimensional structure of an α-helix

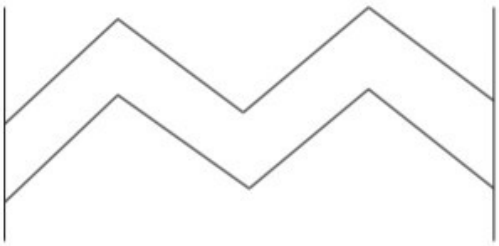


Fig. 8.3 Schematic three-dimensional structure of β-pleated sheets

formation. Like the α-helix, the β-pleated sheet is also an ordered structure.

The ***random coil*** is a secondary structure with no regular or ordered pattern along the polypeptide chain. This is a much more flexible structure than either the α-helix or β-pleated sheet. It is formed when amino acid side chains prevent formation of the α-helix or β-sheet. This may occur if proline is present or if there are highly charged regions within the protein.

A protein may contain regions of α-helix, β-sheet, and random coil at different places along the chain. How much of each type of secondary structure it contains depends on the sequence of amino acids or, in other words, on the primary structure of the protein.

Tertiary Structure

The ***tertiary structure*** of a protein refers to the three-dimensional organization of the complete protein chain. In other words, it refers to the spatial arrangement of a protein chain that contains regions of α-helix, β-sheet, and random coil. So, this structure is really an overview of a protein chain, rather than a detailed look at a small section of it. Again, the tertiary structure is built on the secondary structure of a specific protein.

There are two types of protein tertiary structure:

- Fibrous proteins
- Globular proteins

Fibrous proteins include structural proteins such as collagen (connective tissue protein), or actin and myosin, which are the proteins that are responsible for muscle contraction. The protein chains are extended, forming rods or fibers. Proteins with a fibrous tertiary structure contain a large amount of ordered secondary structure (either α-helix or β-sheet).

Globular proteins are compact molecules and are spherical or elliptical in shape, as their name suggests. These include transport proteins, such as myoglobin, which carry oxygen to the muscle. The whey proteins and the caseins, both of which are milk proteins, are also globular proteins. Globular tertiary structure is favored by proteins with a large number of hydrophobic amino acids. These orient toward the center of the molecule and interact with each other by hydrophobic interactions. Hydrophilic amino acids orient toward the outside of the molecule and interact with other molecules; for example, they may form hydrogen bonds with water. The orientation of the hydrophobic amino acids toward the center of the molecule produces the compact globular shape that is characteristic of globular proteins.

Quaternary Structure

Protein quaternary structure, or the quaternary protein structure, involves the noncovalent association of protein chains. The protein chains may or may not be identical. Examples of quaternary structure include the actomyosin system of muscles and the casein micelles of milk. For

more information on these structures, the reader is referred to the chapters on meat and milk, respectively.

Interactions Involved in Protein Structure and Conformation

Protein primary structure involves only peptide bonds, which link the amino acids together in a specific and unique sequence. Secondary and tertiary structures may be stabilized by hydrogen bonds, disulfide bonds, hydrophobic interactions, and ionic interactions. ***Steric*** or spatial effects are also important in determining protein conformation. The space that a protein molecule occupies is determined partially by the size and shape of the individual amino acids along the protein chain. For example, bulky side chains such as proline prevent formation of the α-helix and favor random coil formation. This prevents the protein from assuming certain arrangements in space.

Quaternary structures are stabilized by the same interactions, with the exception of disulfide bonds. As has already been mentioned, disulfide bonds are strong, covalent bonds, and so the presence of only a few disulfide bonds will have a dramatic effect on protein conformation and stability. Hydrogen bonds, on the other hand, are weak bonds, yet they are important because there are so many of them.

Each protein takes on a unique native conformation in space, which can almost be considered as a "fingerprint." As has already been mentioned, the exact folding of the protein into its natural conformation is governed by the amino acids that are present in the protein and the bonds that the side chains are able to form in a protein. The amino acid sequence is also important, as the location of the amino acids along the chain determines which types of bonds will be formed and where, and thus determines how much α-helix, β-sheet, or random coil will be present in a protein. This, in turn, determines the tertiary and quaternary structure of a protein, all of which combine to define its native conformation. Knowledge of protein conformation and stability is essential to understanding the effects of processing on food proteins.

Reactions and Properties of Proteins

Amphoteric

Like amino acids, proteins are ***amphoteric*** (being able to act as an acid or a base) depending on the pH. This enables them to resist small changes in pH. Such molecules are said to have buffering capacity.

Isoelectric Point

The ***isoelectric point*** of a protein is the pH at which the protein is electrically neutral (it is denoted by pI). At this pH, the global or overall charge on the protein is 0. This does not mean that the protein contains no charged groups. It means that the number of positive charges on the protein is equal to the number of negative charges. At the isoelectric point, the protein molecules usually precipitate because they do not carry a net charge. (Molecules that carry a like charge repel each other, and thus form a stable dispersion in water. Removal of the charge removes the repulsive force and allows the molecules to interact with each other and precipitate, in most cases.)

The pH of the isoelectric point differs for each protein. It depends on the ratio of free ionized carboxyl groups to free ionized amino groups in the protein.

The isoelectric point is important in food processing. For example, cottage cheese is made by adding lactic acid to milk to bring the pH to the isoelectric point of the major milk proteins (the caseins). The proteins precipitate at this pH, forming curds. These are separated from the rest of the milk and may be pressed and/or mildly salted before being packaged as cottage cheese.

Water-Binding Capacity

Water molecules can bind to the backbone and to polar and charged side chains of a protein. Depending on the nature of their side chains,

proteins may bind varying amounts of water—they have a ***water-binding capacity***. Proteins with many charged and polar groups bind water readily, whereas proteins with many hydrophobic groups do not bind much water. As proteins get closer to their isoelectric point, they tend to bind less water, because reduced charge on the protein molecules results in reduced affinity for water molecules.

The presence of bound water helps to maintain the stability of protein dispersion. This is due to the fact that the bound water molecules shield the protein molecules from each other. Therefore, they do not associate with each other or precipitate as readily, and so the dispersion tends to be more stable.

Salting-in and Salting-out

Some proteins cannot be dispersed in pure water yet are readily dispersed in dilute salt solutions. When a salt solution increases the dispersibility of a protein, this is termed "***salting-in***." It occurs because charged groups on a protein bind the anions and cations of the salt solution more strongly than water. The ions, in turn, bind water; thus, the protein is dispersed in water more easily.

Salting-in is important in food processing. For example, brine may be injected into ham to increase the dispersibility of the proteins. This has the effect of increasing their water-binding capacity, and so the ham is moister and its weight is increased. The same is true for poultry to which polyphosphates are added.

Salting-out occurs at high salt concentrations, when salts compete with the protein for water. The result is that there is insufficient water available to bind to the protein, and so the protein precipitates. This is not normally a problem in food processing. However, it may be a contributing factor to the deterioration of food quality during freezing of foods; during the freezing process, water is effectively removed as ice crystals, and so the concentration of liquid water decreases and the solute concentration increases dramatically. This is discussed in Chap. 17.

Denaturation

Denaturation is the change in the secondary, tertiary, and/or quaternary structure of a protein. There is no change in the primary structure. In other words, denaturation does not involve breaking of peptide bonds. The protein unfolds, yet there is no change in its amino acid sequence.

Denaturation may occur as a result of the following:

- Heat
- pH change
- Ionic strength change (changes in salt concentration)
- Freezing
- Surface changes (occurring while beating egg whites)

Any of these factors may cause breaking of hydrogen bonds and salt bridges. As a result, the protein unfolds and side chains that were buried in the center of the molecule become exposed. They are then available to react with other chemical groups and, in most cases, the denatured protein precipitates. This reaction is usually irreversible; it is not possible to regain the original conformation of the denatured protein.

The changes that produce denaturation are usually mild changes. In other words, mild heat treatment, such as pasteurization or blanching, or small changes in pH are sufficient to change the conformation of a protein.

Denatured proteins normally lose their functional properties; that is, they are unable to perform their normal function in a food. Enzymes are inactivated and so the reactions that they catalyzed can no longer take place. This has important implications in food processing.

Denaturation may be desirable and can be deliberately brought about by food processing. Examples of desirable denaturation include heating beaten egg white foams to form meringues, adding acid to milk to form cottage cheese, or inactivating enzymes by heat, as occurs when vegetables are blanched before freezing.

Blanching is a mild heat treatment that denatures and inactivates enzymes that would cause rancidity or discoloration during frozen storage.

Sometimes denaturation is undesirable. For example, frozen egg yolks are lumpy and unacceptable when thawed because the lipoproteins denature and aggregate. Overheating of foods can also cause unwanted denaturation. Food processors must be careful to utilize processing methods that do not cause unnecessary deterioration of food quality due to protein denaturation.

Hydrolysis of Peptides and Proteins

Hydrolysis of proteins involves breaking peptide bonds to form smaller peptide chains. This can be achieved by acid digestion, using concentrated acid. This may be appropriate in protein research, but it is not an option in food processing. Hydrolysis is also catalyzed by ***proteolytic*** enzymes. Examples of such enzymes used in foods include ficin, papain, and bromelain, which are used as meat tenderizers. They hydrolyze muscle protein or connective tissue, making meat more tender. It is important to control the duration of time that they are in contact with the meat so that too much hydrolysis does not occur. Too much hydrolysis would make the texture of the meat soft and "mushy" (see Chap. 9).

Another example of a proteolytic enzyme is rennet, which is used to make cheese (see Chap. 11). This enzyme is very specific in its action, hydrolyzing a specific peptide bond in the milk protein. The result of this hydrolysis reaction is aggregation of the milk proteins to form curds, which can then be processed into cheese. (This enzyme continues to act as a proteolytic agent during cheese aging in conjunction with natural enzymes from milk and the starter cultures. Their combined action results in flavor and texture development in aged cheeses.)

Maillard Browning

Maillard browning is the reaction that is responsible for the brown color of baked products. A free carbonyl group of a reducing sugar reacts with a free amino group on a protein when heated, and the result is a brown color. The reaction is highly complex and has a significant effect on the flavor of foods as well as the color. It is known as nonenzymatic browning, because the reaction is not catalyzed by an enzyme. (Maillard browning must be distinguished from enzymatic browning, which is the discoloration of damaged fruits or vegetables and is catalyzed by an enzyme such as phenol oxidase; enzymatic browning is discussed in Chap. 7.)

The Maillard Reaction is favored by the following:

- High sugar content
- High protein concentration
- High temperatures
- High pH
- Low water content

Maillard browning is responsible for the discoloration of food products such as powdered milk and powdered egg. Before drying, eggs are usually "desugared" enzymatically to remove glucose and prevent Maillard browning (see Chap. 10).

The reaction causes loss of the amino acids lysine, arginine, tryptophan, and histidine, as these are the amino acids with free amino groups that are able to react with reducing sugars. With the exception of arginine, these are essential amino acids. (The body cannot make them, and so they must be included in the diet.) Therefore, it is important to retard the Maillard Reaction, particularly in susceptible food products (such as food supplies sent to underdeveloped countries) in which the nutritional quality of the protein is very important.

Enzymes

All enzymes are proteins. Enzymes are important in foods, because they catalyze various reactions that affect color, flavor, or texture, and hence quality of

foods. Some of these reactions may be desirable, whereas others are undesirable, and produce unwanted discoloration or off-flavors in foods.

Each enzyme has a unique structure or conformation, which enables it to attach to its specific substrate and catalyze the reaction. When the reaction is complete, the enzyme is released to act as a catalyst again. All enzymes have an optimal temperature and pH range, within which the reaction will proceed most rapidly. Heat or changes in pH denature the enzymes, making it difficult or impossible for them to attach to their respective substrates, and thus inactivating them.

If an enzymatic reaction is required in food processing, it is important to ensure that the optimal pH and temperature range for that enzyme is achieved. Outside the optimal range, the reaction will proceed more slowly, if at all. Heat treatment must therefore be avoided. If this is not possible, the enzyme must be added after heat treatment and subsequent cooling of the food.

On the other hand, if enzyme action is undesirable, the enzymes must be inactivated. This is usually achieved by heat treatment, although it may also be accomplished by adding acid to change the pH.

Examples of desirable enzymatic reactions include the clotting of milk by *rennet*, which is the first step in making cheese (Chap. 11). Ripening of cheese during storage is also due to enzyme activity. Ripening of fruit is also due to enzyme action (Chap. 7). Other desirable enzymatic reactions include tenderizing of meat by proteolytic enzymes such as *papain*, *bromelain*, and *ficin* (Chap. 9). These enzymes are obtained from papaya, pineapple, and figs, respectively.

As was mentioned earlier, these enzymes catalyze hydrolysis of peptide bonds in proteins. They are added to the meat and allowed to work for a period of time. The reaction must be controlled, to prevent too much breakdown of the proteins. The optimum temperature for these enzymes occurs during the early cooking stages. (Hydrolysis proceeds very slowly at refrigeration temperatures.) As meat is cooked, the enzymes promote hydrolysis. However, as the internal temperature continues to rise, the enzymes are inactivated and the reaction is stopped.

Although useful as meat tenderizers, proteolytic enzymes may be undesirable in other circumstances. For example, if a gelatin salad is made with raw pineapple, the jelly may not set, due to action of *bromelain*, which is contained in pineapple. This can be prevented by heating the pineapple to inactivate the enzyme before making the gelatin salad.

Additional examples of unwanted enzymatic reactions include enzymatic browning, which occurs when fruits and vegetables are damaged, due to the action of *polyphenol oxidase*, and produces undesirable discoloration (Chap. 7). Development of off-flavors in fats and fat-containing foods may also be a problem in some circumstances, and this may be caused by *lipase* or *lipoxygenase* (Chap. 12).

Enzymes are inactivated in fruits and vegetables prior to freezing by a mild heat process known as blanching (Chap. 17). The fruits or vegetables are placed in boiling water for a short time, in order to inactivate the enzymes that would cause discoloration or development of off-flavors during frozen storage.

CULINARY ALERT! Do not add fresh pineapple, papaya, kiwi, or other fruits containing proteolytic enzymes to a gelatin gel, or it will not set! Canned fruit of these fruit varieties is not generally available yet it yields better results than fresh.

Functional Roles of Proteins in Foods

Proteins have many useful ***functional properties*** in foods. A functional property is a characteristic of the protein that enables it to perform a specific role, or function, in a food. For example, a protein with the ability to form a gel may be used in a food with the specific intention of forming a gel, as in use of gelatin to make jelly.

- Phosphoproteins—for example, casein (milk protein); phosphate groups are esterified to serine residues.
- Glycoproteins—for example, κ-casein; a carbohydrate or sugar is attached to the protein.
- Lipoproteins—for example, lipovitellin, in egg yolk; a lipid is attached to the protein.
- Hemoproteins—for example, hemoglobin and myoglobin; iron is complexed with the protein.

Protein Quality

Press Release on New Protein Quality Measurement FAO proposes new protein quality measurement.

The Food and Agriculture Organization of United Nations (FAO) has released a report recommending a new, advanced method for assessing the quality of dietary proteins. The report, "Dietary protein quality evaluation in human nutrition," recommends that the Digestible Indispensable Amino Acid Score (DIAAS) replace the Protein Digestibility Corrected Amino Acid Score (PDCAAS) as the preferred method of measuring protein quality.

The report recommends that more data be developed to support full implementation, but in the interim, protein quality should be calculated using DIAAS values derived from fecal crude protein digestibility data. Under the current PDCAAS method, values are "truncated" to a maximum score of 1.00, even if scores derived are higher.

Protein is vital to support the health and well-being of human populations. However, not all proteins are alike as they vary according to their origin (animal, vegetable), their individual amino acid composition and their level of amino acid bioactivity. "High quality proteins" are those that are readily digestible and contain the dietary essential amino acids in quantities that correspond to human requirements.

"Over the next 40 years, three billion people will be added to today's global population of 6.6 billion. Creating a sustainable diet to meet their nutritive needs is an extraordinary challenge that we won't be able to meet unless we have accurate information to evaluate a food's profile and its ability to deliver nutrition," said Paul Moughan, Co-director of the Riddet Institute, who chaired the FAO Expert Consultation.

"The recommendation of the DIAAS method is a dramatic change that will finally provide an accurate measure of the amounts of amino acids absorbed by the body and an individual protein source's contribution to a human's amino acid and nitrogen requirements. This will be an important piece of information for decision makers assessing which foods should be part of a sustainable diet for our growing global population."

Using the DIAAS method, researchers are now able to differentiate protein sources by their ability to supply amino acids for use by the body. For example, the DIAAS method was able to demonstrate the higher bioavailability of dairy proteins when compared to plant-based protein sources. Data in the FAO report showed whole milk powder to have a DIAAS score of 1.22, higher than the DIAAS score of 0.64 for peas and 0.40 for wheat.

DIAAS determines amino acid digestibility, at the end of the small intestine, providing a more accurate measure of the amounts of amino acids absorbed by the body and the protein's contribution to human amino acid and nitrogen requirements. PDCAAS is based on an estimate of crude protein digestibility determined over the total digestive tract, and values stated using this method generally overestimate the amount of amino acids absorbed. Some food products may claim high protein content, but since the small intestine does not

Nutrition: See More in Specific Food Commodity Chapters

Nutrition comes into play with new product introductions—both original products and reformulations. "... nearly every fat has been implicated in some sort of dietary brouhaha. Carbohydrates, well, steer clear of sugars and starches, and be wary of fibers that might cause digestive upset. Water seems safe—for now.

And then there's protein .... Protein is a key factor in satiety, so it can help battle the bulge. ... one of the strongest nutritional trends for 2013 and beyond. And ... not just by adding high-protein ingredients like meat, eggs or beans, but purified sources, like dairy proteins, and vegetable proteins, including soy, canola and even the dreaded gluten." (Kuntz 2013)

What Foods Are in the Protein Foods Group?

All foods made from meat, poultry, seafood, beans and peas, eggs, processed soy products, nuts, and seeds are considered part of the Protein Foods Group. Beans and peas are also part of the Vegetable Group.

Since the Great Depression adequate protein intake has not been a concern for most Americans, as meat, poultry and other forms of animal protein are readily available and even typically, overconsumed. (Berry 2012)

Conclusion

Proteins are complex molecules that are widely distributed in all foodstuffs. It is important to understand their conformation and reactions in order to know how they will behave during food processing and to understand how to maximize their functional properties. This is especially true of protein-rich foods, where the quality of the final product depends to a large extent on the treatment of the protein during processing and handling. This chapter has focused on general properties of food proteins. More details of the composition and functional properties of some specific food proteins are given in the ensuing chapters.

Notes

Water-binding capacity The ability of a protein to bind water; this ability depends on the number of charged and polar groups along the protein chain.

Zwitterion Contains a positively charged group and a negatively charged group within the molecule.

Peptide bond Bond formed by the reaction of the amino group of one amino acid and the carboxyl group of another.

Polypeptide Several amino acids joined together by peptide bonds.

Protein primary structure Specific sequence of amino acids along the protein chain, joined by peptide bonds; the covalently bonded protein backbone.

Protein quaternary structure The noncovalent association of protein chains to form a discrete unit.

Protein secondary structure Three-dimensional arrangement of sections of the protein chain; secondary structures include the α-helix, β-pleated sheet, and random coil.

Protein tertiary structure Three-dimensional arrangement of the whole protein chain; the shape that a protein chain assumes in space; includes fibrous and globular structures.

Proteolytic Breaks down or hydrolyzes proteins.

Random coil A protein secondary structure that exhibits no regular, ordered pattern.

Salting-in Addition of a dilute salt solution to improve the dispersibility of a protein.

Salting-out Addition of a concentrated salt solution to precipitate a protein.

Steric effects Effects caused by the size and shape of the amino acids comprising the protein chain; spatial effects; for example, bulky

Amino acid Building block of proteins; contains an amino group, a carboxyl group, a hydrogen, and a side chain, all attached to a central carbon atom.

Amphiphilic A molecule that contains both hydrophobic and hydrophilic sections.

Amphoteric Capable of functioning as either an acid or as a base depending on the pH of the medium.

Alpha helix Ordered protein secondary structure: corkscrew shape, stabilized by intrachain hydrogen bonds.

Beta-pleated sheet Ordered protein secondary structure; zigzag shape, stabilized by interchain hydrogen bonds.

Conformation The specific folding and shape that a protein assumes in space.

Denaturation Changes in the conformation (secondary, tertiary, or quaternary structure) of a protein caused by changes in temperature, pH, or ionic strength, or by surface changes.

Dipeptide Two amino acids joined by a peptide bond.

Disulfide bond Strong covalent bond formed by the reaction of two thiol (SH) groups.

Functional property Characteristic of the molecule that enables it to perform a specific role in a food. Examples of functional properties of proteins include solubility, thickening, binding, gelation, foaming, and emulsifying capacity.

Hydrolysis Breaking of one or more peptide bonds in a protein to form smaller polypeptide chains.

Hydrophilic Water-loving; characteristic of polar and charged groups.

Hydrophobic Water-hating; characteristic of nonpolar groups.

Isoelectric point pI; the pH at which the overall charge on a protein is zero; the number of positive charges is equal to the number of negative charges; the protein is most susceptible to denaturation and precipitation at this pH.

Maillard browning The free carbonyl group of a reducing sugar and the free amino group of a