Peptides

I. Introduction

Peptides constitute one of the two major classes of polymers of amino acids. Proteins constitute the other class. **Peptides** are biopolymers of amino acids in which amino acids are joined by peptide bonds.

II. Differences between peptide and protein

Proteins are also polymers of amino acids. The basic distinguishing feature between peptide and protein is in respect to their molecular weight. Amino acid polymers (polypeptides) with molecular weight greater than 10000 daltons are termed proteins while those with molecular weight less than 10000 daltons are called peptide. In many proteins, two or more polypeptides are linked via covalent (disulfide bridge) or noncovalent hydrophobic interactions.

III. Peptide Bond Formation

Peptides are formed through covalent bonding between two or more amino acids' molecules. As both the amine and carboxylic acid groups of amino acids can react to form amide bonds, one amino acid molecule can react with another and become joined through an amide linkage (Figure 10). This condensation reaction yields the newly formed peptide bond and a molecule of water.

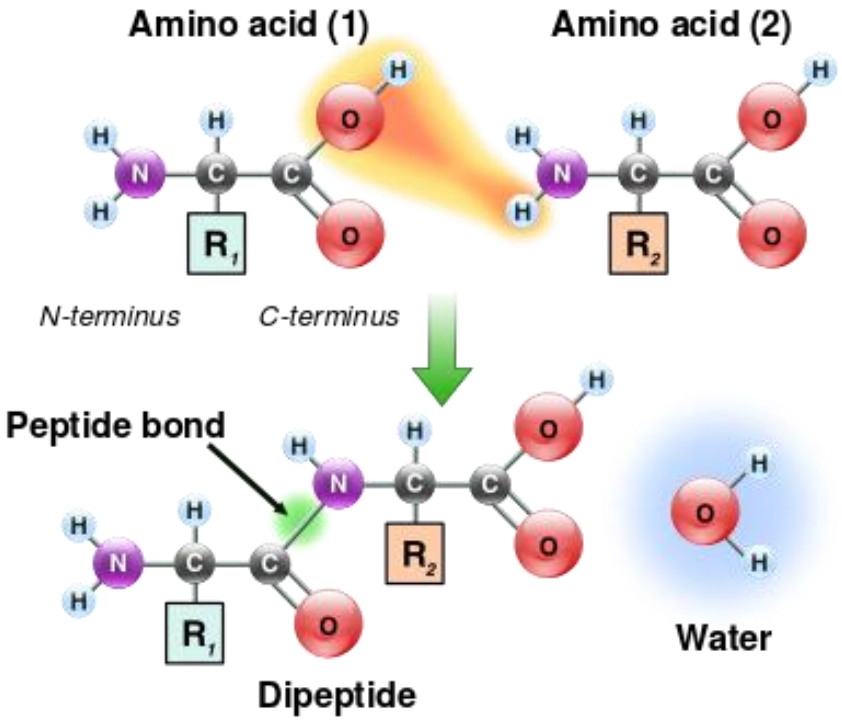


Figure 10: Peptide bond formation.

In cells, this reaction does not occur directly; instead, the amino acid is first activated by attachment to a transfer RNA molecule through an ester bond. This aminoacyl-tRNA is produced in an ATP-dependent reaction carried out by an aminoacyl tRNA synthetase. This aminoacyl-tRNA is then a substrate for the ribosome, which catalyzes the attack of the amino group of the elongating protein chain on the ester bond. As a result of this mechanism, all proteins made by ribosomes are synthesized starting at their N-terminus and moving toward their C-terminus.

However, not all peptide bonds are formed in this way. In a few cases, peptides are synthesized by specific enzymes. For example, the tripeptide **glutathione** is an essential part of the defenses of cells against oxidative stress. This peptide is synthesized in two steps from free amino acids. In the first step, gamma-glutamylcysteine synthetase

condenses cysteine and glutamic acid through a peptide bond formed between the side-chain carboxyl of the glutamate (the gamma carbon of this side-chain) and the amino group of the cysteine. This dipeptide is then condensed with glycine by glutathione synthetase to form glutathione (Figure 11).

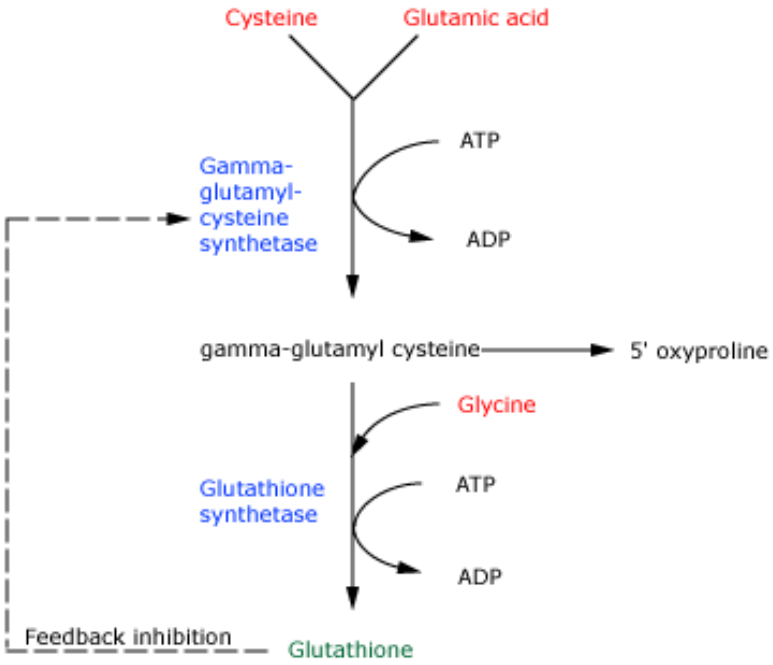


Figure 11: Glutathione formation.

IV. Nomenclature of peptides

In a peptide, amino acid residue is linked to its neighbour in a head-to tail manner, forming linear polymer. The end of the linear polymer with a free α-amino group is the N-terminus while the amino acid residue at this end is called the amino terminal (or N-terminal) residue. In the same way, the opposite end of the polymer with a free carboxyl group and its terminal

amino acid are called the C-terminus and carboxyl-terminal residue respectively.

A peptide is named according to the amino acid residues in it and usually begins with the N-terminal residue. Thus, the pentapeptide in Figure 12 below is named serylglycyltyrosylalanylleucine and abbreviated as ser-Gly-Tyr-Ala-Leu or SGYAL (using one-letter abbreviation).

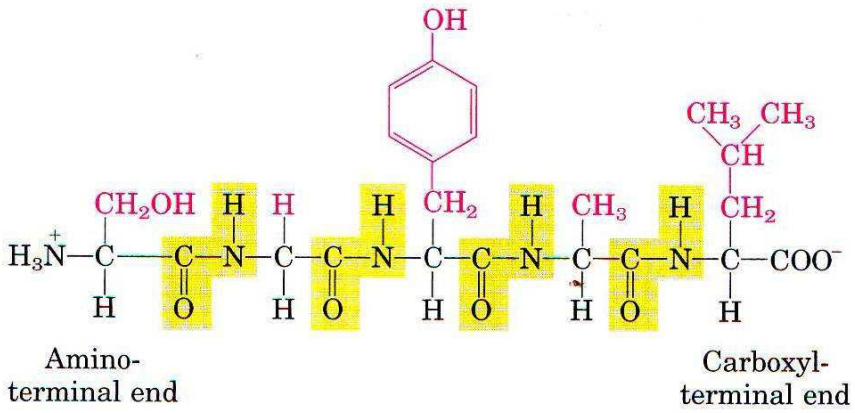


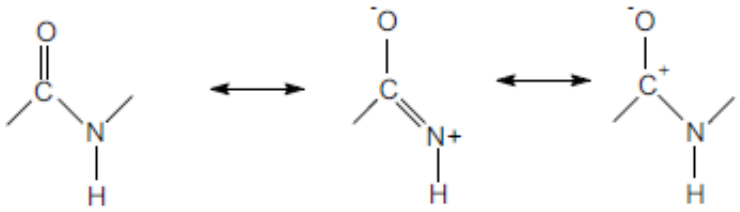
Figure 12: A Pentapeptide showing the N- and the C- termini

In describing the amino acid sequence of a peptide, it is customary to place the amino-terminal residue at the left and the carboxyl-terminal residue at the right. Again, residues are numbered from the N-terminus with the N-terminal residue as 1.

V. Properties of peptide bond

The three-dimensional structure of protein is dependent upon the properties of the amide linkages between amino acid units. The peptide bond possesses the following properties:

1) Peptide group is a resonance hybrid of the following structures:



Apart from the second and third properties mentioned below, another consequence of resonance of peptide bond is that the oxygen atom acquires partial negative charge and the NH group partial positive charge. These opposite ends of the dipole tend to associate to form hydrogen bonds which are very important in stabilizing protein structure.

2) It is rigid and plainer. This arises from resonance interactions.

3) It is a partial double bond. This is also due to resonance.

4) Except in few exceptions, it assumes the trans conformation in which successive C_α atoms are on opposite sides of the peptide bond joining them.

5) It is 1.32 angstrom (Å) in length. This value is in between that of single bond (1.49 Å) and that of double bond (1.27 Å).

Study Questions

1) **What are the differences between peptide and protein?**

2) **Explain the glutathione formation.**

3) **State the properties of peptide bond.**

References

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David L.N. & Michael M.C. Lehninger Principles of Biochemistry. 4th Edition. New York: W. H. Freeman and Company, 2005. Chapter 3.