# Proteins

Proteins are one of the molecular miracles of life, in that these special molecules provide for a myriad of different cellular functions that culminate in life. Proteins provide the framework for muscle contraction and cell structure, chemical communication between and within cells, transport vehicles for other molecules in cells as well as throughout the cardiovascular system, transport channels and passages across membranes, catalysts for chemical reactions, immune function, etc. Within exercise physiology, the contraction dependency on specific protein structure and function attracts a great deal of academic and research attention. However, proteins, and more specifically their amino acid building blocks, also play a major role on cellular energy catabolism. In fact, the longer one exercises, or the more intense the exercise, the greater the role of amino acids in fueling cellular energy transfer. Thankfully, we also know that more intense exercise also provides a large post-exercise stimulus for protein synthesis. Thanks to the connections between exercise, anabolism, muscular strength and dietary protein intake, exercise and protein balance has been a popular topic of research inquiry for more than 40 years. In addition, the measurement of muscular strength and dynamic contractile power development has documented the benefits of exercise training in athletes, as well as previously sedentary and diseased populations.

**Proteins** play a diverse number of life supporting roles in all living entities. For humans, proteins are enzymes, molecule transporters, gas transporters, structures that support muscle contraction, components that provide structure to cells membranes, antibodies that provide immune protection, receptors to hormones and neurotransmitters, a class of hormones, and components involved in the regulation of growth and development. The list could go on and on!!!!

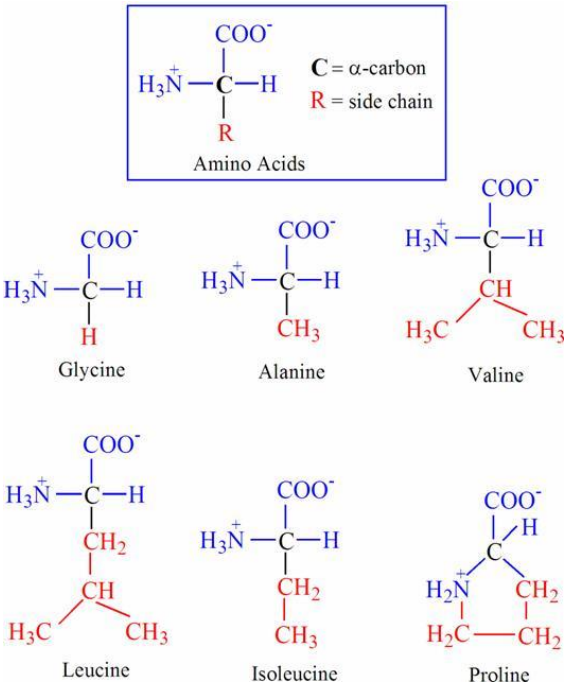


**Figure 1. The structure of amino acids, along with structures for the non-polar aliphatic amino acids**.

Proteins are comprised of small building block structures called **amino acids** (Figures 1 to 5). An amino acid consists of central carbon atom, to which is attached an amino group, a carboxyl group, a hydrogen atom and a side chain (R-group). Differences in the side chain (R-group) from one amino acid to another result in their being 20 different amino acids found within proteins in the human body. For example, due to charge (+'ve vs. –

've vs. neutral) differences between amino acid side chains, amino acids can differ in charge and are classified by this charge as either non-polar, aromatic, polar uncharged, negatively charged, and positively charged (Figures 1 to 5).

The presence of charges on some amino acid side-chains, as well as the presence of a carboxylic acid functional group on all amino acids means that amino acids can bind and/or release a proton thereby functioning as **acids** and **bases**. I will discuss acid-base chemistry and physiology in the section on metabolic acidosis.

The amino acid sequence of a protein is referred to as the **primary structure**. Variations in the sequence and total number of these amino acids allow for a multitude of different proteins within the human body. Due to potential charge (+'ve vs. –'ve vs. neutral) differences between amino acid side chains, the primary structure of amino acids can have unique charge characteristics. Due to charge attraction and repulsion, many primary structures are non-linear, forming repeating shapes such as an alpha-helix, beta-sheets, or globular shapes. Such shapes are referred to as **secondary structures**. For large proteins that have numerous different secondary structures, the resulting complex structure is called a **tertiary structure**. Some large proteins consist of separate protein tertiary structure sub-units or domains. These large multiple unit or domain proteins have a **quaternary structure**, and examples of these structures are provided in Figures 6 to 12.

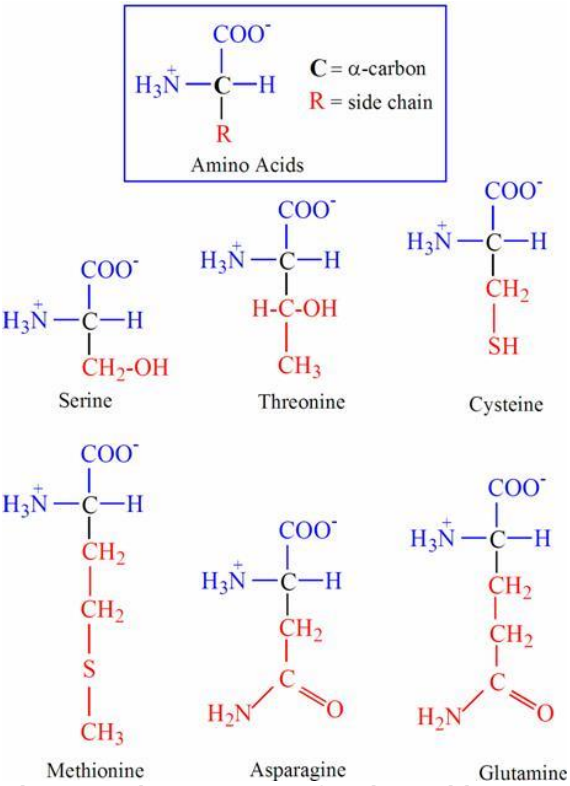


**Figure 2. The structure of amino acids, along with structures for the polar uncharged amino acids.**

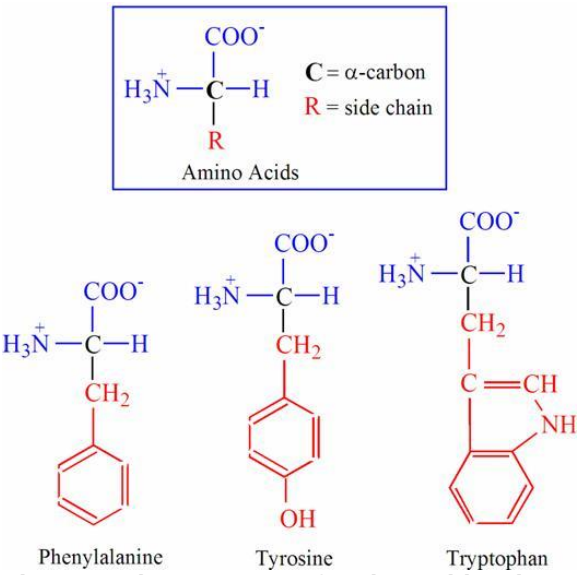


**Figure 3. The structure of amino acids, along with structures for the aromatic amino acids.**

When focused with muscle energy metabolism, proteins must first be broken down (**proteolysis**) into their separate amino acids, and it is the amino acids that are chemically modified for incorporation into glycolysis or the TCA cycle. The main modification of amino acids for use as an energy

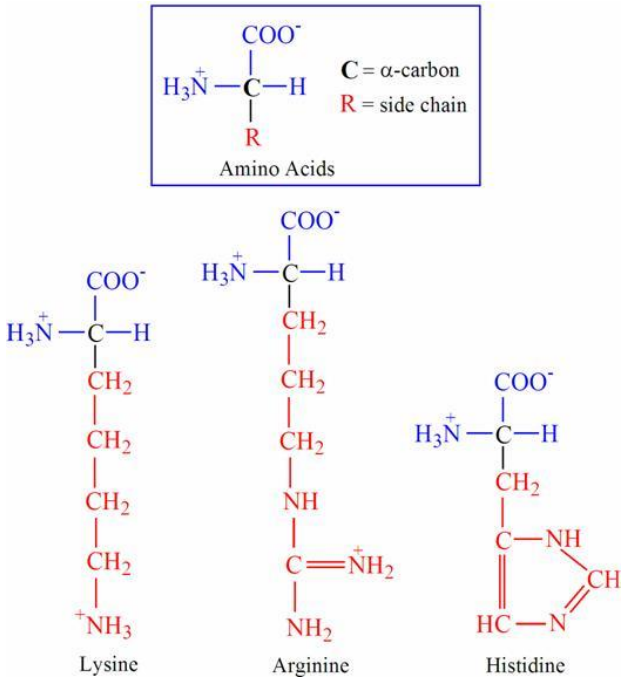


**Figure 4. The structure of amino acids, along with structures for the positively charged amino acids.**

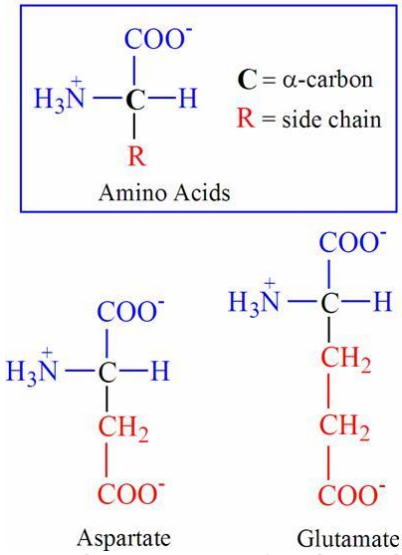


**Figure 5. The structure of amino acids, along with structures for the negatively charged amino acids.**

fuel involves removal of the amine group (**deamination**). The amine group is then either re-used in the cell by addition to other compounds (**transamination**), or converted to ammonia ($NH_4$) where it is removed from the cell and circulated to the liver for subsequent conversion to urea for excretion in urine.

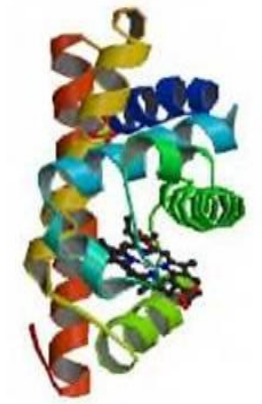

**Figure 6. The three dimensional structure of seal myoglobin.**

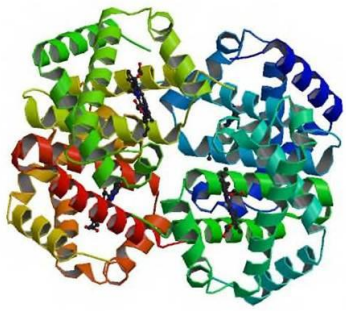

**Figure 7. The three dimensional structure of deoxyhemoglobin.**

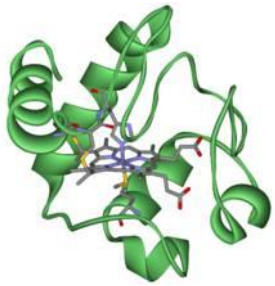

**Figure 8. The three dimensional structure of cytochrome C.**

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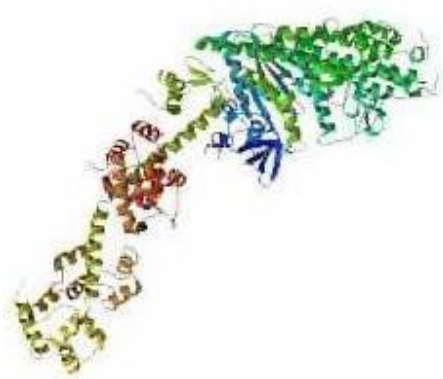

**Figure 9. The three dimensional structure of myosin heavy chain.**

**Figure 10. The three dimensional structure of calmodulin.**

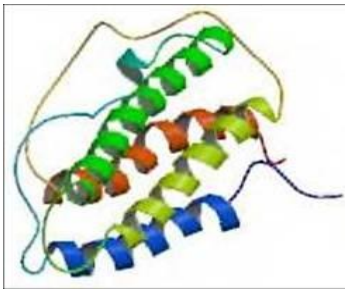

**Figure 11. The three dimensional structure of erythropoietin.**

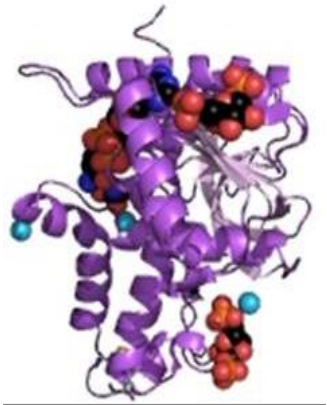

**Figure 12. The three dimensional structure of lactate dehydrogenase.**

## Glossary Words

**proteins** are large and often complex molecular structures comprised of multiple amino acids connected end to end, and sometimes also characterized by more complex covalent bond arrangements.

**amino acids** are the basic molecular “building blocks” of proteins, which consist of a central carbon atom, to which is attached an amino group, a carboxyl group, a hydrogen atom and a side chain (R-group).

**acids** are molecules that can release a proton for pH conditions < 7.0.

**bases** are molecules that can bind a proton for pH conditions > 7.0.

**primary structure** is the sequence of amino acids of a protein.

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**secondary structures** are the next level of complex structure to that of the primary structure, which is formed by the charge distribution of amino side chains of a protein causing attraction and repulsion of specific regions of the amino acid chain, and in turn the formation of more complex non-linear arrangements of the amino acids.

**tertiary structure** is the next level of complexity in structure to the secondary structure, where different regions of the amino acid chain form different secondary structures.

**quaternary structure** refers to the complex structure of some proteins that have multiple tertiary structures.

**proteolysis** is the enzymatic breakdown of protein.

**deamination** refers to the removal of the amine group from amino acids.

**transamination** refers to the transfer of the amino group from one amino acid to another, or to a carbon chain that eventually results in amino acid synthesis.