The importance of nitrogen containing substances in biological systems.

Nitrogen is required by plants as part of chlorophyll, which is needed to absorb the light energy to enable the light-dependent reaction of photosynthesis. There are many ways in which plants can be obtained from the environment. One way is nitrogen-fixation. Ammonium can be obtained from nitrogen gas in the air in two ways: via the Haber process (combines nitrogen from the air with hydrogen taken from natural gas into ammonia), or by saprobiontic microorganisms (called Rhizobium, a type of nitrogen-fixing bacteria) which convert the nitrogen gas into ammonium and can occur in anaerobic conditions. The saprobiontic microorganisms may be free-living or attached to the root nodules of certain plants, namely legumes. However, nitrogen-fixation can also occur by lightning, in which atmospheric nitrogen gas in converted into nitrate. The ammonium produced by nitrogen fixation can then be converted into nitrates for plants to use. More saprobiontic organisms, called Nitrosomonas, convert the ammonium to nitrite, which is then converted by another saprobiontic organism (Nitrobacter) to produce nitrate. These reactions required aerobic conditions. However, denitrifying bacteria can convert the nitrate back into nitrogen gas, done by saprobiontic microorganisms (Pseudomonas) in anaerobic conditions. Assimilation occurs

by active transport, using ATP to move the substances against a concentration gradient, in plant roots, as the ammonium and nitrates are taken up. The nitrogen compounds are then converted into plant proteins. If the plants are eaten by a consumer, the consumer will then take in the plant proteins, and convert them into animal proteins using the amino acids absorbed during digestion. Ammonification, or putrification, occurs when dead plants/animals or excrement is broken down by saprobiontic microorganisms to produce ammonium.

Nitrogen is a key component (in both plants and animals) to nucleic acids. Nucleotides are made up of a sugar (deoxyribose in DNA, and ribose in RNA), a phosphate, and a nitrogenous base. The nitrogenous bases are adenine, thymine (uracil in RNA), guanine, and cytosine, and pair up in a complementary fashion: A-T, C-G. Base pairing is fundamental to the processes of transcription. During transcription, the hydrogen bonds between the nitrogenous base pairs are broken by DNA helicase, which allows the double-stranded DNA molecule to unzip and untwist. Free nucleotides can then form complementary base pairs, with 3 hydrogen bonds between C-G, and 2 hydrogen bonds between A-T. Then a polymerase enzyme then condenses phosphodiester bonds between the phosphate and sugar molecules in the nucleotides, forming a strand of mRNA. After introns are spliced out, the mRNA leaves the nucleus through a nuclear pore and goes to the ribosome, where translation occurs. At the ribosome, the mRNA is held in place whilst tRNA molecules with complementary anticodons to the triplets in the mRNA (3 nitrogenous bases). The anticodon has an attached amino acid. Two amino acids are joined together at a time, using a molecule of ATP, to form a peptide bond whilst held by the ribosome. The series of triplet codes code for a protein, which has a primary protein structure (polypeptide chain) determined by the amino acids joined together.

The proteins coded for by the DNA are a key biological molecule that also contain nitrogen, due to amino acids. Amino acids contain a carbon, hydrogen, oxygen, and nitrogen (found in the amine group, and in the R-groups of some amino acids, such as arginine). When proteins are joined together, they are held by a peptide bond which forms between the nitrogen-containing amine group of one amino acid and the carboxyl group of another, to form a peptide bond. Many amino acids joined together in a specific order form a polypeptide chain, which is the primary protein structure. This determines how the chain folds up, forming alpha-spiral-helices or beta-pleats (the secondary structure). The tertiary protein structure is when the protein folds up further, forming hydrogen, ionic, and disulphide bonds. Whilst the hydrogen and ionic bonds can be broken by changes in temperature or pH, the disulphide bridges are strong and covalent, and broken by strongly reducing

agents. The tertiary structure produces the specific 3D shape of the protein, which is vital for the function. Quaternary structure involves multiple polypeptide changes together and can be fibrous or globular. Fibrous proteins tend to be long, thin, and insoluble, with a structural function such as keratin. Globular proteins are spherical and soluble, and have a metabolic function, such as haemoglobin.

These nitrogen-containing proteins, such as haemoglobin, hormones, or enzymes, play very important roles within the human body. Enzyme function is dictated by the tertiary protein structure, as the 3D shape forms the shape of the active site, which must be complementary in shape to a specific substrate in order to form an enzyme-substrate complex (ESC). By forming ESC, enzymes can place strain upon the bond within the substrate, lowering the activation energy required to break them. For example, in the mouth, saliva contained the enzyme amylase is secreted whilst chewing food. Amylase forms ESC with starch molecules found in carbohydrates and breaks it down into maltose. Maltose can then be broken down into glucose in the small intestine, via maltase secreted by the pancreas. Another type of protein is required to absorb glucose in the small intestine. In the epithelial cells of the small intestine, sodium ions are actively transported (using ATP to move the ions against their concentration gradient) out of the epithelial cells into the blood using a carrier protein. Then, due to the reduce sodium ion concentration in the epithelial cell, more sodium ions diffuse in from the lumen of the small intestine down a concentration gradient via a protein channel (facilitated diffusion). However, the protein also transports glucose with the sodium ions, which is co-transport. The glucose can then diffuse into the blood stream, after which it may be converted into glycogen as an energy store (glycogenesis) or transported to respiring cells and used in respiration.

When blood glucose concentration gets too high, the nitrogen-containing hormone insulin is secreted from beta-cells in Islets of Langerhans in the pancreas. The insulin travels in the blood stream and binds to complementary receptors on target cells (such as hepatocytes or muscle cells). This binding causes a change in the tertiary structure of glucose transport carrier proteins, so that more glucose moves into the cell by facilitated diffusion. This is due to an increased number of transport channel proteins in the plasma membrane of the target cell, through which glucose can move. The insulin also activates enzymes that convert glucose to glycogen (glycogenesis) and fat. This causes a decrease in the blood glucose concentration. When blood glucose concentration is too low, another nitrogen containing hormone is secreted, called glucagon, which is secreted by the alpha cells within the pancreas' Islets of Langerhans. The glucagon binds to the complementary receptors on target cells (hepatocytes) and activate enzymes that convert glycogen to glucose (glycogenolysis) or are involved in the conversion of amino acids and glycerol into glucose (gluconeogenesis). Glucose can then leave the cells by facilitated diffusion, through channel proteins, again containing nitrogen.

Other nitrogen containing proteins can be found in muscle cells. Muscle fibres are made up of proteins actin and myosin. In muscular contraction, calcium ions released from the sarcoplasmic reticulum bind to the tropomyosin, causing it to change shape and move away from the actin binding site. The myosin head can then bind to the site. Calcium ions also activate ATP hydrolase, which hydrolyses ATP to form ADP and Pi. The energy released from this hydrolysis reaction causes the myosin head to bend and pull along the actin filament in a rowing motion. Another ATP molecule is hydrolysed to provide the energy to break the actin myosin cross bridge, so that the myosin head can detach and attach further along the filament, continuing the muscular contraction.