Two thick salmon steaks are shown against a light blue background. The top steak is positioned slightly behind and to the right of the bottom one, creating a sense of depth. Both steaks show the characteristic pinkish-orange color of the flesh and the darker skin on the bottom side.

Protein Chemistry

A detailed image of a fish head, likely a salmon, is shown in profile, facing left. The fish has a silvery, metallic sheen on its scales and a prominent eye. The head is cut off at the snout, and the jaw is slightly open, revealing a pinkish interior. The background is a solid light blue.

Ph.D & Msc Students

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Lectur e 5

Analysis of Proteins

Proteins differ from each other according to the type, number and sequence of amino acids that make up the polypeptide backbone. As a result they have different molecular structures, nutritional attributes and

Determination of Overall Protein Concentration

Kjeldahl method

The Kjeldahl method was developed in 1883 by a Danish chemist called Johann Kjeldahl. A food is digested with a strong acid so that it releases nitrogen which can be determined by a suitable titration technique. It is usually considered to be the standard method of determining protein concentration. The Kjeldahl method can conveniently be divided into

Digestion

Distillation

Titration



Organic nitrogen is converted into NH_4^+



NH_3 is distilled and retained in a receiver vessel



Nitrogen is determined

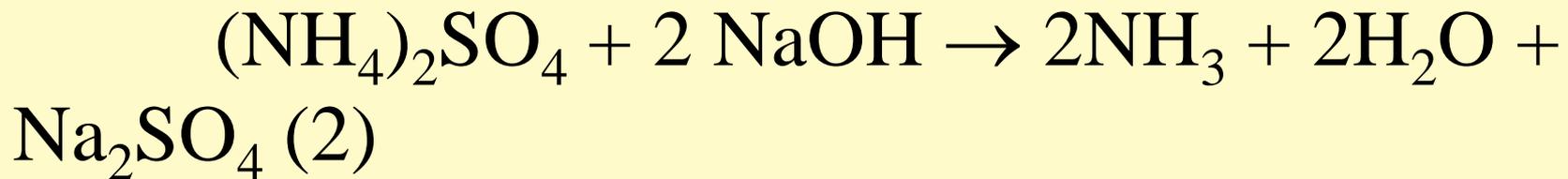
Principles

Digestion

The food sample to be analyzed is weighed into a digestion flask and then digested by heating it in the presence of sulfuric acid (an oxidizing agent which digests the food), anhydrous sodium sulfate (to speed up the reaction by raising the boiling point) and a catalyst, such as copper, selenium, titanium, or mercury (to speed up the reaction)

Distillation (neutralization)

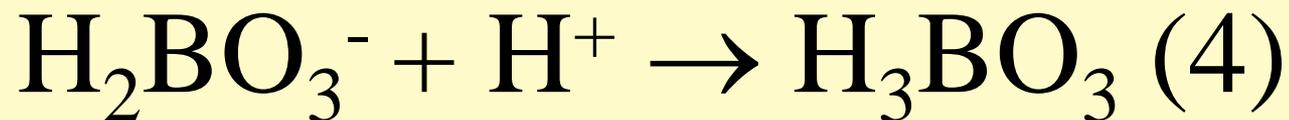
After the digestion has been completed the digestion flask is connected to a receiving flask by a tube. The solution in the digestion flask is then made alkaline by addition of sodium hydroxide, which converts the ammonium sulfate into ammonia gas:



The ammonia gas that is formed is liberated from the solution and moves out of the digestion flask and into the receiving flask - which contains an excess of boric acid. The low pH of the solution in the receiving flask converts the ammonia gas into the ammonium ion, and

Titration

The nitrogen content is then estimated by titration of the ammonium borate formed with standard sulfuric or hydrochloric acid, using a suitable indicator to determine the end-point of the reaction.



The concentration of hydrogen ions (in moles) required to reach the end-point

- When boric acid is used as the receiving solution the equation is:

$$\% \text{ Nitrogen} = \frac{(\text{ml standard acid} - \text{ml blank}) \times \text{N of acid} \times 1.4007}{\text{weight of sample in grams}}$$

- When standard acid is used as the receiving solution, the equation is:

$$\% \text{ Nitrogen} = \frac{[(\text{ml standard acid} \times \text{N of acid}) - (\text{ml blank} \times \text{N of base})] - (\text{ml standard base} \times \text{N of base}) \times 1.4007}{\text{weight of sample in grams}}$$

If it is desired to determine % protein instead of % nitrogen, the calculated % N is multiplied by a factor, the magnitude of the factor depending on the sample matrix. Many protein factors have been developed for use with various types of samples. Here you can see the % Nitrogen, the Protein factor and the % Prote

<https://www.itwreagents.com/uploads/2018011>

<https://info.gbiosciences.com/blog/topic/protein-estimation>

Food	% Nitrogen	Factor	% Protein
Wheat flour	2.4	5.7	13.7
Red beans	3.4	6.25	21.2
Milk	0.5	6.38	3.3
Egg	2	6.25	12.5
Fish	2.6	6.25	16

Advantages and Disadvantages

Advantages. The Kjeldahl method is widely used internationally and is still the standard method for comparison against all other methods. Its universality, high precision and good reproducibility have made it the major method for the estimation of protein in foods.

Disadvantages. It does not give a measure of the true protein, since all nitrogen in foods is not in the form of protein. Different proteins need different correction factors because they have different amino acid sequences. The technique is