Research Journal of Pharmaceutical, Biological and Chemical Sciences, 2015, vol.6, N4, pages 25-31

Analysis of Bovine Serum Albumine, Caseine and tryptone proteins hydrolysis by 1H NMR spectroscopy

Bikmullin A., Alimova F., Aganov A., Klochkov V., Usachev K.
Kazan Federal University, 420008, Kremlevskaya 18, Kazan, Russia

Abstract

An adequate estimation of a proteinaceous substrate decomposition is one of the problems, frequently appearing during the protein hydrolysate technology. A combination of high-resolution ^{1}H NMR spectroscopy data with other technics could be a good solution of this problem. In present paper we applied high-resolution ^{1}H NMR spectroscopy method to characterize the degree of protein hydrolysis of the Bovine Serum Albumin, Caseine and Tryptone proteins and propose to use it in a combination with other methods to describe quality of the proteinaceous substrates. Due to the fact that the methods of evaluation of the protein hydrolysis degree are not universal so the combination of methods should be used for precise the description of proteinaceous substrate degradation. Based on the results from one dimensional ^{1}H NMR spectra the hydrolysis of the protein molecules was analyzed by changes in the chemical shifts, multiplicities and line widths in ^{1}H NMR spectra. It was shown that ^{1}H NMR spectroscopy is an effective instrument for analyzing the protein hydrolysis reaction in solution.

Keywords

Bovine serum albumine, Caseine, Hydrolysis, NMR, Proteins, Tryptone