

Abstract

This work investigates the behavior of system peaks in chip electrophoresis. The aim of this work was to propose a suitable separation environments with regard to the position and number of system peaks.

In the theoretical introduction we first deal with processes taking place in the separation of proteins by SDS-PAGE method, its miniaturization and provide an overview of current application of this method. Then there is briefly summarized the issue of system zones.

System peaks were observed in the three separation systems. The behavior of the system zones was first investigated theoretically in PeakMaster program and results were then verified experimentally by means of Agilent 2100 Bionalyzer.

In the experiments there was recorded larger number of system peaks than should correspond to the theoretical composition of the systems. Due to this fact it was not possible to fully identify the theoretical results from PeakMaster with the results from real experiments.