ABSTRACT

Proteomics is a set of analytical methods which enable qualitative and quantitative characterization of the proteome. Expression proteomics quantitatively compares proteomes of cells, tissues, body fluids or other biological materials to find differencies in protein expression and, based on these differencies, to describe the biological processes occuring in investigated organisms.

An initial material for expression proteomic studies are complex mixtures containing thousands of proteins, which are analyzed using separation (electrophoretic and chromatographic) methods, and identified, possibly quantified using mass spectrometry.

The aim of this Thesis is to demonstrate the application of the tools of expression proteomics in solving diverse challenges in biomedicine. We employed various proteomic approaches and tools for studying molecular mechanisms of human diseases using pacient biological samples, or a model organism and a cell culture. We were conducting three different research projects, namely: A quest for potencial molecular targets for selective elimination of TRAIL-resistant mantle cell lymphoma cells; Investigation of molecular mechanisms of heart failure using a rat model of the disease induced by volume overload; and Searching for diagnostically usable serum biomarkers of ovarian cancer. Results of our three projects are discovery of molecular „weakness“ of resistant cells which has a potencial as a therapeutic target for the selective elimination of such cells, suggestion of two highly potential therapeutic targets for treatment of heart failure and identification of a new potential biomarker of ovarian cancer.

We demonstrated that with a suitable experimental design and pointed evaluation of gained results proteomics provides significant insight into the physiological and also pathological molecular processes and carries a huge potencial in the fields of basic and applied biomedical research.

key words: expression proteomics, mass spectrometry, two-dimensional electrophoresis, mantle cell lymphoma, TRAIL, drug resistance, heart failure, ovarian cancer, biomarker