The study of the protein expression, by means of proteomic techniques, is broadly applied in human disease. Proteomic tool allow the classification of disease on a molecular basis, that is essential to understand the mechanisms involved in the onset of the diseases, to identify proteins alterations and to discover new diagnostic biomarkers.

Currently most current diagnostic tests are based on the detection and quantification of single protein in body fluids. A common feature for these biomarkers is their relatively low predictive value, so that they cannot be used alone for diagnosis but they have to be supported with other clinical procedure as usually a biopsy. Instead the direct availability of a panel of biomarkers, in particular in the serum, is an important feature in clinical practice, because to collect the sample is possible with minimal need for invasive tests.

The application of proteomic markers can allow diagnosis in early stages, when the disease have the highest probability to be cured, and may change the fate of thousands of patient.

We performed proteomic analysis of biological fluids such as serum, dialysis fluid and ultra filtrate using SELDI-ToF and 2D-PAGE.

The dialysis and ultra-filtrate fluids, unlike urine, allows to analyze the profile of uremic toxins without the dominance of particular abundant proteins such as albumin and immunoglobulins. Many of the retained solutes affect biological and biochemical systems which are essential for quality of life and survival, thereby generating a process of gradual endogenous intoxication.

We examined proteome profiles and identify differentially expressed proteins with different types of dialysis membranes, studies were conducted in dialysis and ultra-filtrate fluids of 10 patients at different times of emodialysis treatment. This study was done in collaboration with the Nephrology Unit of the Hospital of Modena.

We used the same proteomic tools to study protein profiles with the aim of isolate and identify a set of proteins differentially expressed to be used as diagnostic biomarkers for discriminate among different groups in lung cancer. Proteomic profiles were obtained in serum samples of patients with non-small cell lung cancer (NSLC). To facilitate the biomarker discovery we performed the proteomic analyses of serum after depletion of high abundant proteins using different fractionation techniques. The preliminary results showed differences in proteomic and peptide pattern among NSLC patients group and the patient group with positive PET-CT but without cancer.. This study is in collaboration with the thoracic surgery division of Policlinico di Modena.