

Markery nowotworowe badane metodami proteomiki w osoczu i surowicy krwi

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Tumor markers studied with proteomic methods in blood and serum plasma

Summary

Proteins are major components that directly determine phenotypes of cells and organisms, in either normal or pathological conditions. Because of numerous post-translational events that modify structure and function of proteins, the knowledge of genomes is only at the beginning of understanding of the full complexity of biological systems. “Proteomics” is the study of proteomes, which addresses proteins’ 3D structure, function, and their inter- and intracellular communication. Among primary goals of proteomics, there is discovery of biomarker for various human disease conditions. Plasma and serum are considered to be the source of choice in molecular diagnostics. The development of cancer involves transformation and proliferation of altered cell types that produce unique proteins and enzymes, which can significantly modify the pattern of serum peptides and proteins. The serum protein/peptide profiles that could be registered using different analytical methodologies appear to carry important information with direct clinical applicability. Importantly, such peptide profiles itself could become a new kind of potential tumor marker. These approaches are promising, but the results obtained are still preliminary. For example, detection of disease markers in the blood proteome could be hampered by its extremely low concentrations and the presence of a few abundant components (e.g., albumin and immunoglobulins), and thus development of more specific and sensitive analytical methods is still required. Nevertheless, identification of serum proteomic patterns or molecular signatures specific for different cancer types, stages and responses to therapy is possible at this moment. This article provides a comprehensive overview of current methodologies used for cancer biomarkers detection in blood proteome.

Key words:

proteomics, human proteome, biomarkers, ELISA, mass spectrometry, MALDI-TOF, LC/ESI/MS/MS molecular signature of cancer

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