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Study of proteome heterogeneity and dynamics

Human proteome is tremendously complex and composed from diverse and heterogeneous gene products (proteoforms). Recent developments in mass spectrometry and systematic approaches (technology and methodology) promise to bring new insights into this complexity. A combination of mass spectrometry with classical biochemical separation technologies is particularly attractive for this systematic investigation. Among biochemical methods, two-dimensional gel electrophoresis (2DE) is a most powerful protein separation technique that allows not just separating proteoforms but determining their physic-chemical parameters (pI and Mw). In our study, we performed the panoramic analysis of cellular proteins using a combination of virtual (in silico) and experimental 2DE with high-resolution nano-liquid chromatography-mass spectrometry. This approach is moving proteomics study on the next level of the acquisition of knowledge about proteomes. To get better impression about diversity of proteoforms in a particular proteome, whole gels (not just spots but sections) were analyzed using this approach. This allowed to detecting in a single proteome more than 20000 proteoforms coded by more than 4000 genes. The 3D-graphs showing distribution of these proteoforms including proteoforms of biomarkers in 2DE map were generated. A comparative analysis of these graphs between normal and cancer cells was performed. This analysis showed a high variability and dynamics of proteoforms.

Biography

Stanislav Naryzhny obtained his PhD from the Biophysics Institute in Pushchino, Russia and did his Postdoctoral Studies from St. Petersburg Nuclear Physics Institute (PNPI), Gatchina, Russia and from the Northeastern Ontario Regional Cancer Centre, Sudbury, Canada. He is the Head of Proteomics Laboratory of Petersburg Nuclear Physics Institute at National Research Center "Kurchatov Institute" and also Chief Scientist at Institute of Biomedical Chemistry, Moscow, Russia. He is a protein Biochemist with extensive hands-on experience in academia with strong background in protein structure-function theory and expertise in processes involved in DNA replication, DNA stability and tumorigenesis; protein, protein structure and proteomics analysis employing a wide variety of biophysical and biochemical methods. His area of research lies in the two-dimensional gel electrophoresis (2DE) based proteomics, where he has published more than 40 papers in reputed journals.

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