AUTOMATION OF SAMPLE PREPARATION FOR MASS SPECTROMETRY IN BIOMEDICAL PROJECTS

Nazariy Souchelnytskyi and **Serhiy Souchelnytskyi**
Qatar University, Qatar

Analysis of separated full-length proteins may be more informative as compared to a shotgun peptidomics approach. However, automation of separation and identification of proteins is a serious challenge. When LC-MS/MS approach is well-automated, 2DE and MS/MS demands a lot of hands-on work. We will present our experience in development of automation for sample preparation for MALDI TOF mass spectrometry. Examples will show applications of the sample preparation robotics in studies of protein nitration, phosphorylation and expression in human cancer cells and breast tumor biopsies. Separation of proteins was performed by 2D gel electrophoresis, and for sample preparation were used liquid handling stations. By incorporation in the proteomics workflow of robotics stations, we enhanced capacity of sample preparation in at least 10 folds. Tecan and Genomics Solution robotics were used, and will be presented as examples of technical solutions.

BIOGRAPHY

Nazariy Souchelnytskyi studied at the Royal Institute of Technology (Stockholm), Uppsala University and Nakademin (all in Sweden). Mr. Nazariy Souchelnytskyi has been working as a proteomics core facility manager at the Ludwig Institute for Cancer Research (Uppsala, Sweden), Karolinska Institutet and Karolinska University Hospital (Stockholm, Sweden). Mr. Nazariy Souchelnytskyi is a Chief Technology Officer at Oranta CancerDiagnostic AB (Sweden). He has 9 publications in the application of proteomics and mass spectrometry in biomedical research.

Nazariy.Souchelnytskyi@gmail.com

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