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THE WAY TO DEEP COVER OF HUMAN PROTEOME IN GENE-CENTRIC MODE

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Currently, great interest is paid to the identification of "missing" proteins that have not been detected in any biological material at the protein level (PE1). Using the UPS1 and UPS2 Sigma Aldridge sets as the “gold standard”, we characterized mass spectrometric approaches from the point of view of sensitivity (Sn), specificity (Sp) and accuracy (Ac). This sets consists of 48 high purity human proteins without SAP or PTM. UPS1 set consists of the same 48 proteins at 5 pmols each, in UPS2 proteins were unified into five groups in accordance with their molar concentration, ranging from 10-11 M to 10-6 M. Single peptides from the ninety-two and ninety-six percent of all set proteins could be detected in a pure solution of UPS2 and UPS1, respectively, by Selected reaction monitoring with stable isotope-labeled standards (SRM SIS). We also found that in the presence of a biological matrix such as *E.coli* extract or human blood plasma (HBP), SRM SIS makes it possible to detect from 63% to 79% of proteins of the UPS2 set (sensitivity), with the highest specificity (~100%) and an accuracy of 80%. To increase the sensitivity of shotgun and SRM SIS monitoring samples were fractionating by RP using chromatography under alkaline condition (2D-LC_alk). It is shown that this technique allows the SRM SIS to detect 98% of the the single peptides from the proteins present in the pure solution of UPS2 (47 out of 48 proteins). When the extracts of *E-coli or P. Pastoris* are added as biological matrixes to the UPS2, 46 and 45 out of 48 proteins (~95%) can be detected respectively. The combination of the 2D-LC_alk SRM SIS and shotgun technologies allows to increase the sensitivity up to 100% in case of the proteins of UPS2. The usage of that technology can be a solution for identifying the so-called "missing" proteins and, eventually, creating the deep proteome of a particular chromosome of tissue or organs. Data in PASSEL PASS01192 and PRIDE PXD007643.

Biography

Professor, Scientific Advisor of Institute of Biomedical Chemistry, Was born January 10, 1940, in Kashin, Kalinin (Tver) region – scientist, biochemist. A.I. Archakov had organized a scientific school to study molecular organization and functioning of oxygenase cytochrome P450-containing systems, molecular mechanisms of the structure and function of membranes and biological oxidation. Under the guidance of A. I. Archakov, the institute's members have developed a fundamentally new pharmaceutical composition “Phosphogliv” with antiviral activity for the treatment of liver diseases of various etiology. A.I. Archakov's present-day/current areas of expertise relate to research in the field of post-genomic technologies, nanobiotechnologies, proteomics, development of approaches to create personalized medicine of the future. A.I. Archakov is the pioneer in the development of proteomics in Russia. Currently, he is the international “Human proteome” project coordinator in Russia/ the coordinator representing Russia in the international “HP” project.

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