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Functional proteomics for biomarker and drug discovery

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In post-genome era having sequence the human genome, one of the most important pursuits is to understand the function of gene-expressed proteins. The overwhelming size and complexity of human proteome requires very high-throughput techniques for rapid analysis. Despite significant advancements in molecular biology and genetic tools, this demand has not been satisfied and only a small fraction of the proteome has been understood at the biochemical level. Systems Biology and Proteomics strive to create detailed predictive models for molecular pathways based upon quantitative behavior of proteins. Understanding these dynamics networks provides clues into the consequence of aberrant interactions and why they lead to diseases such as cancer. Historically, methods capable of collecting quantitative data on biochemical interactions could only be used for one or a few proteins at the time. Protein microarrays allow hundreds to thousands of proteins to be analyzed simultaneously, providing an attractive option for high-throughput studies such as protein-protein interaction, differential protein profiles. Here, a novel approach based on combination of nanotechnology and proteomics tools for biomarker and drug discovery useful for earlier diagnosis and personalized medicine will be presented.

Biography

Manuel Fuentes graduated in Chemistry and Biochemistry from the University of Salamanca (Spain). After his Master's in Biotechnology from University of Bielefeld (Germany), he joined at Biocatalysis Department at National Spanish Research Council (Madrid, Spain) for his PhD Thesis, entitled "Design and development of conjugation and immobilization methods of biomolecules for diagnostic methods useful in Genomics and Proteomics". Afterwards, he moved to Harvard Institute of Proteomics at Harvard Medical School (Boston, EE.UU.), during almost 6 years, when he was working on biomarker and drug discovery in tumor and autoimmune pathologies by using a combination of high-throughput label-free proteomics approaches. In 2009, he joined as a scientist at Cancer Research Center at University of Salamanca, where his research is focused on biomarker and drug discovery in hematological diseases, mainly for personalized medicine. He is co-author of 80 peer-reviewed papers (ISI web of Knowledge) in international journals, 9 licensed international patents, 10 book chapters, and more than 50 invited lectures in national and international meetings. In 2010, HUPPO awarded him as "HUPPO Young Scientist" for his contributions in the field.

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