

## CDISE Seminar

### Introduction in quantitative and clinical proteomics by Christoph Borchers

**December 20, 2019, 10.00 - 12.00**

**Skolkovo Innovation Center**

**Bolshoy Boulevard 30, Bldg. 1 (New Campus),**

**Room E-R2-A5-2030**



#### ABSTRACT

A human proteome is defined as the totality of all expressed body proteins at a current point in time under given conditions. In this regard, although the proteome of a particular organism is relatively constant, it has variations that depend on the state of the organism and the influence of external factors. Proteomics is a large-scale study of the proteome, consisting in the identification and quantification of proteins, which will allow the researcher to scan the entire protein profile of the body, which in turn will provide a direct and complete picture of his health. Accordingly, proteomics has a unique potential in deciphering the basic laws of the structure and function of a person, which is directly applicable to the development of accurate, personalized medicine, especially in the field of oncology, cardiovascular and neurological diseases, and monitoring of personal health.

Quantitative proteomics provides a more effective molecular profile of the body to characterize diseases, determine the prognosis of diseases, and develop and select appropriate treatment methods. The development of absolute, reliable, quantitative methods for determining the proteome is one of the main goals of modern clinical proteomics. Advanced quantitative methods can have a significant impact on biomedical research, leading to the discovery of new biomarkers and proteins of pathological significance.

#### SPEAKER INTRODUCTION

Dr. Christoph Borchers is recognized as a pioneer and leading figure in the development of mass spectrometry-based methods for protein quantification using Multiple Reaction Monitoring (MRM) with more than 25 years of experience. He has also published more than 300 peer-reviewed papers in scientific journals, and is the founder and director of the McGill-Lady Davis Institute Integrated Proteomics Program at the Jewish General Hospital, McGill University, where he is currently a full professor in the Department of Oncology. His research is centered around the improvement, development, and application of proteomics and metabolomics technologies, with a major focus on quantitative targeted proteomics for clinical diagnostics, as well as new mass-spectrometry-based techniques for structural proteomics.

Dr. Borchers received his BS, MSc, and PhD degrees from the University of Konstanz, Germany in 1996. After his post-doctoral training and employment as a staff scientist at NIEHS/NIH/RTP, NC and he became the director of the Duke-UNC Proteomics Facility and held a faculty position at the UNC Medical School in Chapel Hill, NC (2001-2006). He was a Professor in the Department of Biochemistry and Microbiology, and Director of the University-Genome British Columbia Proteomics Centre at the University of Victoria, British Columbia, Canada, where he held the Rix BC Leadership Chair in Biomedical and Environmental Proteomics.

Dr. Borchers is also involved in promoting proteomics research and education through his involvement with HUPO (International Council Member), the British Columbia Proteomics Network (Executive Committee Member, past Scientific Director) and the Canadian National Proteomics Network (Member, past VP External and Chair of the Board of Directors). He is also a Fellow of the Canadian Academy of Health Sciences.

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