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**“Large-scale proteomics:
From cultivating cells to high-
performance-computing”**

05 June 2012, 11:00 (s.t.)

Venue: 2nd Floor Seminar Room
Institute of Molecular Biology (IMB)
Johannes Gutenberg University Campus Mainz

All are welcome to attend

Abstract:

Liquid chromatography (LC)- mass spectrometry (MS) has become the analytical platform of choice for large-scale quantitative proteome analyses. In shotgun proteomics experiments, both, protein identification and protein quantification are performed on the level of peptides, and computational methods are heavily involved in the processing and the analysis of the complex and large LC-MS data.

Due to recent advances in the whole proteomics workflow, but especially in the MS technology and software, the quality and comprehensiveness of such experiments is ever increasing. In this talk, we will discuss the proteomics workflow with recent applications to perturbation studies in cancer research, where the dynamic proteomic response of human cancer cells to Sorafenib (a multi-kinase inhibitor) was profiled using high-accuracy mass spectrometry. We will also elaborate on the role of quality control and software development in large-scale proteomics.

Furthermore, recent work on new statistical algorithms for the identification of modified peptides will be presented. In summary, the talk will focus on the essential and growing importance of the interplay of mass spectrometry and computational methods in proteomics.