

## SYMPOSIUM 1 - CANCER

### FOCUS: HAEMATOLOGICAL MALIGNANCIES

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## Clinical Proteomics

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Clinical proteomics aims to apply the large-scale characterization of protein profiles performed on patient samples (cells, tissues and fluids) for prediction, diagnosis, prognosis, and therapeutic management & monitoring of treatments. Coupling the vast knowledge obtained by mapping both the human genome and proteome with technological breakthroughs in CRISPR/Cas9 genome editing have fuelled the anticipation of a personalized, individualized, precision medicine in the near future. The spectacular advances in sample preparation using liquid biopsy and the improvements in sensitivity and robustness of instrumentation based on mass spectrometry (MS), together with the development of the powerful tools in dataset analysis have established the foundation for adoption of recent discoveries into the clinical setting. The capability to quantify more accurately and precisely the profile of entire proteoforms (all proteins including their modified forms) from clinical specimens provide a source of multi-parametric data that can give insights into the underlying mechanisms of a disease for informative translation into patient care. To apply proteomics discoveries in the clinic requires proper experimental study design, standardization of proteomic platforms, improvement of biospecimen collection & processing, and provision of systematic data analysis tools to convert data sets into easily interpreted information that answers the most important clinical questions. To harness the power of clinical proteomics, it is necessary to set up a clinical system comprising of a more automated, sensitive, robust, accurate, reliable, easy-to-operate and cost-effective MS-based platforms that will become an integrated part of the clinical laboratory. The medical revolution goal is to characterize every human disease one patient at a time, yielding a novel-targeted medicine for smarter decisions and investment of resources.

Back to [Table of Contents](#)