

**Tuesday 5<sup>th</sup> Dec**

**Venue: LT7A**

**Sponsor: AB/MDS Sciex**

**From proteomics to protein-based biomarkers: A toolbox of opportunity**

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Overcoming the challenges presented to us in our endeavors to identify and characterize proteins in complex media requires advanced analytical tools and workflows. Applied Biosystems has a complete set of tools designed to meet the sensitivity, dynamic range, precision and specificity requirements and has proven itself a leader in pioneering workflows for each challenge. This talk will briefly overview AB's proteomics portfolio including the 4800 MALDI TOF/TOF Analyzer, the QStar® Elite Hybrid LC/MS/MS System, the 3200/4000 Q Trap® LC/MS/MS Systems and the Tempo™ Systems, highlighting the specific proteomics tasks for which each was built. Examples for protein identification, intact protein analysis and post-translational analysis will be shown.

As proteomics itself has matured, as well as the tools that drive the field, many researchers have set their sites on a different end point, the discovery of individual or panels of protein-based biomarkers. This field demands not only the depth of coverage, speed and specificity of proteomics, but also accurate and precise quantification (both relative and absolute). Trying to tackle biomarker research with one tool and/or in one experiment has proven unfruitful causing the pioneers in the field to take a step back and really think about the various stages, their unique needs and the analytical solutions that best fit each bin. Hence, the field of biomarker research has been sub-segmented into discovery, verification and validation. This part of the talk will show how Applied Biosystems' toolbox addresses the needs across these segments. The 4800 MALDI TOF/TOF™ Analyzer or the QStar® Elite Hybrid LC/MS/MS System combined with our novel multiplex-enabled iTRAQ™ Reagents afford simultaneous protein ID and quantification required for the biomarker discovery segment when one is searching for putative markers of disease, efficacy or toxicity. This combination of tools yields unparalleled depth of coverage and precision of quantification that is so critical to this stage of the process. Once a putative panel of markers is found, the next challenge is to verify the specificity of these markers over a larger population set. Taking advantage of the unique capability of the combination of a hybrid triple quadrupole linear ion trap instrument and using our patented MRM Initiated Detection and Sequencing (MIDAS) workflow, this putative panel of biomarkers can easily and rapidly be reduced to the most likely set for the validation stage. This last stage requires absolute quantification and very high throughput. Examples of how iTRAQ™ Reagents used in combination with the Q Trap® Systems for this stage will also be presented.