

Proxeon Lunch Seminar

Tuesday, March 9, 12:15 – 1:30 pm

Molly Brown (Lower Level 1), Marriott City Center Hotel

[RSVP today to reserve your place.](#)

**Digitizing the Proteome: A Practical Multidimensional LC/MS Approach to
the Analysis of Large Numbers of Human Tumours**

Speaker: Paul Taylor, *The Hospital for Sick Children, Toronto, ON*

Moving from smaller proof of concept type proteomics studies to ones containing larger sample numbers can be challenging. Analysis of a few related samples or a model system can be designed to maximize the number of identified and quantified proteins. Multiple biological and technical replicates can be planned to ensure maximal coverage and good statistical validation scores. When studies are planned with 200+ samples, the simple extrapolation of the same study numbers becomes limiting just considering instrumentation time alone. Rational compromises must be made to attain similar levels of protein identification and statistical validity. Larger studies necessitate that multiple instruments, perhaps at different locations, be operated in a manner that the data can be compared.

The outline for a study in progress (involving 200 human lung tumours) will be presented. It addresses these issues using a robust fully automated on-line 2D MuDPIT protein identification step, a 1D label-free discovery quantitation step and a SRM based validation platform all utilizing the same split-free nano-chromatography system. A unified front end (columns, source and LC-system) ensures multi-instrument reproducibility.