TITLE: **"A Tale of Proteomics, Disease Mechanisms & Data Mountains"**

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ABSTRACT:
Cell regulation and disease mechanisms can now be studied in unprecedented detail, combining high throughput '*omics*' techniques, including mass spectrometry (MS) based proteomics and RNA seq with image-based phenotypic assays using microscopy. If properly designed, these methods provide the opportunity for making unbiased, system-wide, quantitative measurements of gene expression and phenotypes that underpin mechanisms causing disease. The opportunity here is clear: modern quantitative proteomics in particular can reveal detailed insights into proteome dynamics, providing a flexible suite of quantitative assays that we can use to characterize, system-wide, a multi-dimensional array of '*Protein Properties*'. Thus, time-dependent measurements, with isoform resolution, of protein abundance, subcellular protein localization, turnover rates, post-translational modifications, cell cycle variation and specific protein complexes and protein-protein interactions etc. allow a detailed characterization of cell phenotypes in both healthy and diseased cells. One of the major challenges in using proteomics and other '*omics*' methods to study molecular mechanisms affecting biological regulation is how to manage, analyse and integrate the huge volumes of complex, quantitative data that are generated. I will describe some of the current projects in which we are doing quantitative proteomics to study gene expression mechanisms relevant to cancer, immune cells and nutritional responses in humans and in model organisms. I will also review our progress in building user-friendly, computational tools for the effective management and sharing of large, multidimensional data sets with the life sciences and biomedical research community.