



HILDALE LECTURE SERIES

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FROM GENOMICS TO PROTEOMICS: TECHNOLOGIES AND APPLICATIONS OF HIGH- RESOLUTION MASS SPECTROMETRY IN BIOLOGY AND MEDICINE

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Mass spectrometry has a long and illustrious history as an analytical science, even before the development of electrospray and MALDI made MS easily applicable to the study of proteins. Developments over the last few years have steadily increased the scope of MS-based studies in molecular biology but important challenges remain, chief among them, the lack of comprehensiveness compared to oligonucleotide based systems. However, this limitation is now falling away, as I will show with deep proteomic analysis of human cancer cell lines. More than 10,000 different proteins can now be identified in such systems, in a relatively short time, shedding new light on similarities and differences to each other and to in vivo cells. We observe important differences in the gene expression program at the transcriptome and proteome levels, i.e. during the differentiation of stem cells. To track down the mechanistic basis of these differences, we apply RNA-protein interaction screens, which is one example of the expanding area of 'interaction proteomics'. The analysis of post-translational modifications by mass spectrometry is becoming increasingly powerful and here I will discuss recent work related to the systems biology of glucose regulated insulin secretion of beta cells. Apart from elucidating basic signal transduction mechanisms, phospho-proteomics can help elucidate the action of existing and novel diabetic drugs. Finally, I will describe recent developments in 'clinical proteomics', which is showing renewed promise in patient classification in cancer and metabolic diseases.



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**1220, EBLING AUDITORIUM, MICROBIAL
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