

Waters Corp. Lunch Seminar

Tuesday, March 9, 12:15 – 1:30 pm

Mattie Silks (Lower Level 1), Marriott City Center Hotel

RSVP by visiting Waters Corp. exhibit booth on Sunday or Monday.

Is Selectivity Important?

Introducing a Novel Mass Spectrometer and Data Acquisition Strategy for Proteomics

Organizer

Roy Martin, Waters Corporation

Liquid chromatography- mass spectrometry has been widely adopted as the tool for the qualitative and quantitative analysis of complex peptide mixtures. A typical analysis involves either a data dependant analysis, selecting peptides in real-time as they elute from the LC column, or more recently data independent acquisition modes. Either approach has been applied to a wide range of mass spectrometer systems, including quadrupoles, ion-traps and time-of-flight systems. The nature of the MS utilized dictates the specificity of the precursor and fragment ion information provided for qualitative identification (databank searching) or quantitative comparisons. Here we will discuss the importance of specificity (resolution and mass accuracy) on the results obtained. With the new Synapt G2 HDMS system data can be acquired at 15,25 or 45K resolution, using a high-duty cycle parallel sequencing approach (LC-MS^E) up to 20 spectra/second. This generates data from all species entering the gas cell simultaneously, irrespective of sample complexity, recording data at low collision energy and, in the subsequent scan, at elevated collision energy. The challenge of this method is then to correlate fragment ions with a precursor, especially for species with similar chromatographic retention times. Hence, specificity is vitally important, and a bigger issue than speed or sensitivity. One way to increase this specificity is to use Ion mobility spectrometry adding a further dimension of gas phase separation. Here, we demonstrate for the first time how incorporating IMS into our LC-MS^E strategy results in increased protein identification numbers.