

PW19 Generation of unique protein specific MRM signatures; Using peptide information from alternate scanning LC-MS data to drive MRM development.

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Novel workflow improves the utility of MRM based peptides in discovery experiments

Proteomics research has resulted in the discovery of a large number of differentially expressed proteins. These proteins, or in some cases panels of proteins, must be validated in wider sample sets, or a greater number of related clinical conditions in order to determine their utility as specific markers. Detection and quantitation of these proteins from complex biological mixtures is challenging only due to the inherent complexity associated with the number of tryptic peptides generated, but the dynamic range in protein concentration present.

We previously described, how, using an alternate scanning LC-MS strategy on a Q-ToF mass spectrometer we can derive a comprehensive peptide inventory of precursor ions, product ions, peak area intensities and associated physio-chemical properties. Here we show how this experimental data (precursor and fragment m/z values, intensity and retention time) can be utilized to empirically determine a list of unique 'proteotypic' tryptic peptides for each protein i.e. those peptides, which uniquely identify a protein in a database from a complex sample.