FURTHER DEVELOPMENT OF HIGH-SENSITIVITY TARGETED MRM ASSAYS FOR PEPTIDE AND PROTEIN QUANTIFICATION

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Discovery phase proteomics has generated numerous candidate protein markers for a wide variety of biological processes and disease types. To assess the viability of these protein expression changes requires the analysis of a larger number of samples, preferably in a targeted fashion, and hence the use of MRM has become routine. Specific peptides from the proteins of interest are targeted as surrogate markers for that protein, in a screening assay using a triple quadrupole mass spectrometer operating in the multiple reaction monitoring (MRM) mode.

The MRM method which is used to detect specific ions from target molecules has the capability to simultaneously quantify large numbers of proteins with good limits of quantification (LOQ) and linear dynamic range. In this mode of analysis the sensitivity and dynamic range are improved and providing sufficient data points across a chromatographic peak are recorded then quantitation is accurate (CV 5-10%). This high sensitivity coupled with the specificity/selectivity afforded by MRM transitions allows extensive panels of peptide biomarkers to be monitored in a single experiment from complex mixtures.

We will describe the development and implementation of novel high-sensitivity MRM assays for large scale peptide quantification.