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## A Novel Algorithm to Track lons or Peptides Found by LC/MS in Multiple Injections of Multiple Complex Biological Samples

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### **Overview**

#### Purpose:

Track isotope ions or peptides (EMRT: Exact Mass Retention Time) from the Waters<sup>®</sup> Protein Expression System for quantitative studies of peptides/ proteins

#### Keys of technology:

- •Data is acquired by the Protein Expression System. The collision cell of the Micromass<sup>®</sup> Q-Tof Ultima Mass Spectrometer is operated in alternating low energy (to produce mutiple peptide ions) and elevated energy mode (to produce all fragmentation ions from multiple peptides)
- •Lock mass and < 10 ppm mass accuracy of the Q-Tof instrument
- •Low energy data (parents) and elevated energy data (daughters) are linked together by retention time
- •Exact mass and retention time are used to track ions or peptides between injections and samples

**EMRT:** Exact Mass Retention Time **MPDS:** Protein Expression System Standards

Introduction



## **Methods**



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