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Manipulating trypsin digestion conditions to accelerate proteolysis and simplify digestion workflows in development of protein mass spectrometric assays for the clinical laboratory

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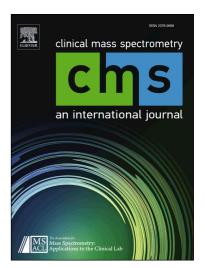
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## **ACCEPTED MANUSCRIPT**

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Manipulating trypsin digestion conditions to accelerate proteolysis and simplify digestion workflows in development of protein mass spectrometric assays for the clinical laboratory

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#### **Abbreviations:**

Canada

MS: mass spectrometry; LC: liquid chromatography; MRM: multiple reaction monitoring; DP: declustering potential; CE: collision energy; apoA1: apolioprotein A-1; RBP4: retinol-binding protein 4; TTR: transthyretin/prealbumin; CO9: complement component 9; CRP: C-reactive proteins; HEPES: 4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid; AA: ammonium acetate; IAA: iodoacetamide; DTT: dithiothreitol; AMBIC: ammonium bicarbonate; SDC: sodium deoxycholate; TPCK: tosyl phenylalanyl chloromethyl ketone; ACN: acetonitrile; Q1 ion: precursor ion; Q3 ion: product ion; PTMs: post-translational modifications

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