

**Speciation of Five Arsenic Metabolites in Urine Using High Performance Liquid Chromatography and Post Column UV Digestion Coupled with Hydride Generation Atomic Fluorescence Spectrometry (HPLC-UV-HGAFS)**

Bin Chen<sup>1</sup>, Zorimar Rivera-Nunez<sup>2</sup>, Warren T Corns<sup>1</sup> and Peter B Stockwell<sup>1</sup>

<sup>1</sup> P S Analytical, Arthur House, Crayfields Industrial Park, Main Road, St Pauls Cray, Orpington, Kent BR5 3HP, United Kingdom, [bc@psanalytical.com](mailto:bc@psanalytical.com)

<sup>2</sup> Environmental Health Science, School of Public Health, University of Michigan, Ann Arbor, MI, USA

Arsenic and its compounds are known to cause several adverse health effects. Urinary As metabolites were used recently in epidemiological and environmental health studies as a means of assessing exposure to arsenic from drinking water. The concentrations of urinary As methylation are often found low enough (~ ng/ml) which require sensitive analytical methods involving speciation, identification and quantification of each individual As species. Arsenobetaine (AsB), arsenite (As<sup>III</sup>), dimethylarsenic acid (DMA<sup>V</sup>), monomethylarsonic acid (MMA<sup>V</sup>) and arsenate (As<sup>V</sup>) have been separated in one single chromatogram run using ion pairing reverse phase HPLC within 10 minutes. A mobile phase of pH 9 containing 20mM ammonium phosphate, 5mM TBAH and 4% ethanol was used. The eluent was further digested using an online post column UV digestion device at 200 °C, followed by the sensitive detection of HGAFS which was able to provide detection limits of 0.4-0.8 ng/ml for all the arsenic species. The developed method provided a sensitive, robust approach for the monitoring of arsenic methylation in human urine samples.