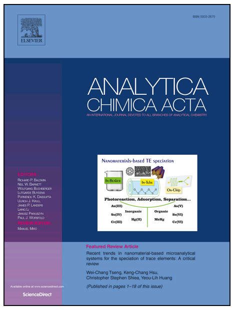

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# MASS SPECTROMETRY BASED ANALYTICAL APPROACHES AND PITFALLS FOR TOXICOMETABOLOMICS OF ARSENIC IN MAMMALS: A TUTORIAL REVIEW

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## Abstract

The present review focus on the analytical platforms and the workflow for toxicometabolomics with a special emphasis on their strengths and pitfalls presenting as a case study the toxicometabolomics of arsenic in mammals.

Although powerful analytical methods and techniques are currently available for metabolomics, the main “bottleneck” is still the absence of unified protocols for sample preparation (e.g. quenching, solvents used) as well as several important factors in toxicometabolomics, which drastically affect the metabolism (e.g. selection of model organisms, xenobiotic doses, chemical form of the xenobiotic, exposure route, biological sample). In addition, the selection of model organisms, the xenobiotic dose and administration route are of pivotal importance in toxicometabolomic studies. In this context, the applicability to complex samples, higher sensitivity, specificity and the possibility to perform quantitative analysis offered by MS is crucial to probe xenobiotic induced metabolic changes to evaluate the stress responses.