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Comparison of different serum sample extraction methods and their suitability for mass spectrometry analysis

Mohamad Aljofan
Qassim University, Saudi Arabia

Mass spectrometry has been widely used, particularly in pharmacokinetic investigations and for therapeutic drug monitoring purposes. Like any other analytical method, some difficulties exist in employing mass spectrometry, mainly when it is used to test biological samples, such as to detect drug candidates in mammalian serum, which is rich in proteins, lipids and other contents that may interfere with the investigational drug. The complexity of the serum proteome presents challenges for efficient sample preparation and adequate sensitivity for mass spectrometry analysis of drugs. Enrichment procedures prior to the drug analysis are often needed and as a result, the study of serum or plasma components usually demands either methods of purification or depletion of one or more. Selection of the best combination of sample introduction method is a crucial determinant of the sensitivity and accuracy of mass spectrometry. The aim of this study is to determine the highest serum protein precipitation activity of five commonly used sample preparation methods and test their suitability for mass spectrometry. We spiked three small molecules into rabbit serum and applied different protein precipitation methods to determine their precipitation activity and applicability as a mass spectrometry introductory tool.

mo.aljofan@monash.edu