

Title: Is your sample MS-Proteomics ready? It is just matter of one tip, tube or gel away!

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Summary:

Mass Spectrometry (MS) based proteomics relies heavily on sample preparation, an essential part for a successful experiment. In order to select the preparation technique, it is required a profound understanding of the biological samples to be analyzed. Depending on the experiment, biological samples often contain components in the buffer like salts, detergents or polyethylene glycols, and intrinsically lipids, chromatins, antibodies, and other contaminants like BSA or human keratin, that are not necessarily compatible with the LC-MS-MS analysis and irrelevant to the protein analysis. Although, these components are irrelevant, they have an enormous negative impact on the final result. Thus, successful sample preparation starts with a proper experimental design, with emphasis on selected buffers and enrichment/purification procedures. On this technical IAS seminar a brief summary of successful sample preparation strategies will be presented, including tips and a method selection criteria based on each sample attributes.

