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The proof of concept of a unique LC-MS/MS method for the quantitative analysis of human monoclonal antibody protein drugs and related constructs in animal studies

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Quantitative analysis of proteins by LC-MS/MS has been extensively used during the last past years in bioanalysis. Triple quadrupole operation in MRM scan mode have been the preferred options for this quantitative work because of its selectivity and sensitivity. Having a unique method for the quantitative analysis of immunoglobulins and related compounds would greatly save method development time. In this presentation, we will discuss the application of triple quadrupole mass spectrometer for the quantitative analysis of a recombinant human immunoglobulin (hIgG) in rat serum with four conserved peptides GPSVFPLAPSSK, TTPPVLDSDGSFFLYSK, VVSVLTVLHQDWLNGK and FNWYVDGVEVHNAK and heavy isotope labeled IgG internal standard. Quantitative data obtained on each peptide will be discussed along with the key roles by internal standard. Furthermore, we will demonstrate the applicability of our method to the quantitative analysis hIgG1 and hIgG4 in monkey serum and we will show how this method can be extended to the quantitation of other therapeutics antibody modalities such as bispecific and antibody drug conjugates. Through comparative results obtained on PK studies in rat and monkey, in conclusion, we will demonstrate how our unique developed method can be applied for the quantitative analysis of various types of hIgG and related modalities in preclinical studies. With the present assay only limited effort would be required for the method development when addressing the quantitative analysis. This will considerably reduce the time spend for the bioanalytical support for the PK assessment of those modalities for the preclinical studies.

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Microextraction techniques coupled to GC-MS as green analytical methods for trace level determination of toxicants in various matrices

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Gas chromatography-mass spectrometry (GC-MS) is a globally used analytical instrument for trace level determination of toxicants/pollutants in various complex matrices. However, traditional sample preparation methods such as liquid-liquid extraction and solid-phase extraction limit the sensitivity of GC-MS for trace level analysis of toxicants/pollutants as well as hazardous to environment and human health. Modern sample preparation methods such as dispersive liquid-liquid microextraction (DLLME) and solid-phase microextraction (SPME) after being coupled to GC-MS results in a sensitive, selective, economical, environmentally benign and green analytical method for analysis of various toxicants/pollutants such as bisphenol-A, alkylphenols, parabens, trichloroethylene metabolites, amino acids, polycyclic aromatic hydrocarbon metabolites, alkaloids (e.g. quinine), pesticides, pharmaceutical drugs, etc., in various complex matrices such as environmental, biological and food samples. Coupling of SPME and DLLME with GC-MS or GC-MS/MS offers highly selective and sensitive determination of aforesaid analytes after throughout optimization and validation of analytical methods which can be used for routine analysis of analytes in various analytical laboratories.

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