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Editorial Note on Biomarker Identification and Quantification

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Editorial

The development of new disease-related biomarkers by proteome analysis of commonly accessible bio-fluids like plasma utilising liquid chromatography (LC)-coupled mass spectrometry (MS)-based technologies is a promising possibility for better patient care. Clinical proteomics main goal is to use these highly specific disease/pathology-related signatures to improve current clinical practise by allowing for accurate early diagnosis, appropriate therapeutic strategy selection, and patient-by-patient monitoring of disease progression and/or possible side effects.

Clinically effective novel biomarkers must have high sensitivity (indicate a positive test for patients who are positive for the disease), high specificity (indicate a negative test for patients who do not have the disease), and be sufficiently robust to operate in a variety of settings in order for MS-based proteomics to be successful. It's also essential that the transition from preclinical discoveries to regulatory-approved biomarkers be carried out as efficiently and realistically as feasible, with an understanding of the numerous hurdles that this entails.

Due to the ethical situation surrounding biopsies, as well as the convenience and expense of patient sample as compared to established procedures such as biopsy, much attention has been focused on the development of new blood borne biomarkers.

The determination of the mass of proteins and peptides as defined by their mass: charge ratio (m/z) is the basis for biomarker discovery utilising mass spectrometry to identify and quantify the protein components of bio-fluids such as plasma. The necessity for accurate quantification from MS or MS/MS spectra, as well as protein/peptide identification, is essential. Biomarker data must be thoroughly checked and verified, as well as statistical approaches that are acceptable.

Recent advancements in MS technology have resulted in the creation of equipment with increased sensitivity and specificity, allowing for the comprehensive investigation of complicated biological fluids like plasma. It is critical to thoroughly evaluate novel biomarker profiles, and it is probable that routine application will be carried out via immunoassays, which can create major hurdles.

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