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Approaches""; ""1.3. Mass Spectrometry in Metabolomics Research"";
""2. STAGES IN AN LC-MS BASED METABOLOMICS ANALYSIS""; ""2.1.
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between LC and MS: Focus on Matrix Effect""; ""2.5. Mass
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""2.6.1.1. Filtering""
""2.6.1.2. Feature/peak detection""""""2.6.1.3. Alignment""; ""2.6.1.4.
Normalisation""; ""2.6.2. Data analysis""; ""2.6.2.1. Principal component
analysis (PCA) ""; ""2.6.2.2 Partial least-squares projections to latens
structures (PLS)""; ""2.6.2.3. O-PLS""; ""2.7. Metabolite Identification"";
""3. CONCLUSION""; ""REFERENCES""; ""BIOMARKER DISCOVERY FOR
CANCER DIAGNOSIS USING SERUM PROTEOMIC ANALYSIS:FROM BASIC
RESEARCH TO CLINICAL APPLICATION""; ""ABSTRACT"";
""INTRODUCTION""; ""1. PROTEOMIC ANALYSIS OF SERUM/PLASMA IS
EFFECTIVE TO SEARCH FOR CANCER DIAGNOSTIC MARKERS""
""1.1. Characteristics of Global Analyses and Diagnostic Availability of
Biomarkers""""""1.2. Advantages of Proteomic Analysis in the Search for
Diagnostic Biomarkers""; ""1.3. Specimen""; ""2. SEPARATION
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""3.2. Ionization Methods""; ""3.3. Mass Analyzers""; ""3.4. Types of MS
Used in Proteomic Analysis""; ""4. IDENTIFICATION OF
PROTEINS/PEPTIDES USING MS""
""4.1. Protein Identification by Peptide Mass Fingerprinting""