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""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 TECHNOLOGIES IN PROTEOMIC ANALYSIS""; ""2.1. 2D-DIGE""; ""2.2. Protein Chip ArrayA®""; ""2.3. ClinProtA®""; ""2.4. Shotgun Proteomics Using LC""; ""3. MASS SPECTROMETRY""; ""3.1. Fundamentals of MS""; ""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""