

IPD Project Details

Project ID: IPD2486

Project Title: Mass spectral Analysis of Synthetic Peptides: Implications in Proteomics

Description: Tryptic synthetic peptides generated in silico from human proteome are used as standards to evaluate the performance of MS and algorithm used to identify the proteins.

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Sample Preparation: Sample preparation steps: 599 synthetic peptides were dissolved in suitable solvents (Acetonitrile and water with different ratios) and mixed (equimolar and different concentrations).

Peptide Separation: Trypsin digestion was carried out in silico with 1 or 2 missed cleavages, and peptides were selected from a mass range of 616–3169 Da. Solvent A: 5% ACN in water containing 0.1% formic acid, Solvent B: 95% ACN in water containing 0.1% formic acid LC runs were carried out using pepmapRSLC C18 column, 3 μ m, 100A0, 75 μ m X 15cms with different time gradient and the mass spectral data was combined in the final analysis.

Protein Characterization: Proteins and peptides were identified using SEQUEST algorithm supplied by the manufacturer. Using no enzyme provided maximum results by setting precursor ion mass tolerance to 5ppm and MS/MS mass tolerance at 0.02Da. Human proteome database from Uniprot was used to analyse the results: UniProt human curated fasta.

Experiment Type: Shotgun proteomics

Species: Data in species_details No Data

Tissue: Unknown No Data

Cell Type: Unknown No Data

Disease: Disease free No Data

Instrument Details: Data in instrument_details Data in instrument_details

Protein Modifications: monohydroxylated residue

PubMed ID: [33953644](#)