IPD Project Details

Project ID: IPD5599

Project Title: Detection of mutated peptides of SARS-CoV-2 from COVID-19-infected patients

Description: This project involves the identification of mutated peptides from swab and plasma samples using an in-house developed Mutant Peptide Database (MPD)

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Sample Preparation: Heat-inactivated swabs and plasma samples were used.

Peptide Separation: Proteins present in the sample were extracted, of which 30 microgram was quantified and digested using trypsin. Digested peptides were desalted using C-18 material before taking samples forward for MS analysis.

Protein Characterization: Raw datasets obtained from the MS were processed with MaxQuant (Tyanova, Temu, and Cox 2016) (v 2.0.0.) against the Human Swiss-Prot Database (downloaded on 13.8.2021). Raw files were processed using Label-Free-Quantification (LFQ) parameters and setting label type as "standard" with a multiplicity of 1. The Orbitrap was set to Orbitrap Fusion mode. Trypsin was used for digestion with a maximum missed cleavage of 2 for Human and COVID. Carbamido-methylation of Cysteine was set as the fixed modification, whereas oxidation of Methionine was set as the variable modification. The False-Discovery-Rate (FDR) was set to 0.01 for the protein and peptide levels to ensure high reliability of the protein detection.

Experiment Type: Shotgun proteomics

Species: Homo sapiens - 9606

Tissue: Blood plasma (bto:0000131)

Cell Type:

Disease: Unknown

Instrument Details: Orbitrap Fusion (MS:1002416)

Protein Modifications: monohydroxylated residue, iodoacetamide derivatized residue

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