IPD Project Details

Project ID: IPD8604

Project Title: MDR K. penumoniae, A. baumannii, E. coli, and P. aeruginiosa SWATH

Description: This study elucidates the whole proteome changes in the MDR isolates of K. penumoniae, A. baumannii, E. coli, and P. aeruginiosa in the presence of Ampicillin, Kanamycin, and Nalidixic acid. Label-free SWATH-MS is used for protein quantitation of antibiotics treated and untreated samples.

Principal Investigator: Prof.Bhabatosh Das

PI Affiliation: Translational Health Science and Technology Institute, India.

Sample Preparation: Total extracted proteins from the isolates were digested using trypsin and desalted by C18 solid phase extraction before being analyzed by reverse phase microLC (Eksigent) connected to a TripleTOF 5600 (Sciex) mass spectrometer.

Peptide Separation: Total extracted proteins from the isolates were digested using trypsin and desalted by C18 solid phase extraction before being analyzed by reverse phase microLC (Eksigent) connected to a TripleTOF 5600 (Sciex) mass spectrometer.

Protein Characterization: All the DDA data were first searched in ProteinPilot v5 with Paragon algorithm for library generation with the following settings: sample type - identification, cysteine alkylation - iodoacetamide, digestion - trypsin, instrument - TripleTOF 5600, species - none, search effort - thorough ID, result quality - 0.05. SWATH data was search with the library and peptide level quantitation were performed using SWATH microapp in the Peakview software v2 (Sciex) and Markerview v1.2. Intrinsic peptides were chosen for RT shift alignment between in-house library and SWATH data before exporting for quantitation.

Experiment Type: SWATH MS

Species: Data in species_details No Data

Tissue: Unknown No Data

Cell Type: Unknown No Data

Disease: Data in disease_details No Data

Instrument Details: Data in instrument_details Data in instrument_details

Protein Modifications: No PTMs

PubMed ID: