IPD Project Details

Project ID: IPD7996

Project Title: Vibrio cholerae (p)ppGpp and DksA mutants SWATH

Description: This study elucidates the whole proteome changes in the wild type and gnetically modified strains of Vibrio cholerae. Label-free SWATH-MS is used for protein quantitation following genetic modifications in alarmone (p)ppGpp metabolizing genes and transcription factor DksA.

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Sample Preparation: Total extracted proteins from the differetn strains 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 differetn strains 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: Different DDA runs were performed and searched using ProteinPilot v5 to generate spectral library of Vibrio cholerae 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: Unknown No Data

Instrument Details: Data in instrument_details Data in instrument_details

Protein Modifications: No PTMs

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