IPD Project Details

Project ID: IPD3121

Project Title: Proteomic characterization of the Plasmodium falciparum PCNA2 interactome

Description: This project investigates the PCNA2 interactome in *Plasmodium falciparum* using LC-MS/MS. Samples were analysed using a Thermo Scientific Orbitrap Velos Pro mass spectrometer with data-dependent acquisition (DDA) and collision-induced dissociation (CID). Protein identification was performed using Proteome Discoverer 1.4 with SEQUEST HT against a *P. falciparum* protein database downloaded from PlasmoDB. Trypsin was used as the protease, with precursor and fragment ion mass tolerances of 20 ppm and 0.6 Da, respectively. Percolator was used for post-search validation.

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Sample Preparation: Anti-PCNA2 antibody was first immobilised on Protein A/G beads and covalently crosslinked using dimethyl pimelimidate (DMP). The antibody-coupled beads were then incubated with Plasmodium falciparum parasite lysate. The captured proteins were subsequently eluted from the beads.

Peptide Separation: The eluted proteins were digested with trypsin, and the resulting peptides were separated by liquid chromatography and analysed by tandem mass spectrometry (LC-MS/MS) using a Thermo Scientific Orbitrap Velos Pro mass spectrometer. Data were acquired using data-dependent acquisition (DDA) with collision-induced dissociation (CID).

Protein Characterization: MS/MS data were analysed using Thermo Scientific Proteome Discoverer 1.4 with SEQUEST HT as the search engine. Spectra were searched against Plasmodium falciparum 3D7 protein databases obtained from PlasmoDB, using trypsin as the protease. Percolator was used for post-search validation.

Experiment Type: Bottom-up

Species: Data in species_details No Data

Tissue: Data in tissue_details No Data

Cell Type: Data in cell_details No Data

Disease: Data in disease_details No Data

Instrument Details: Data in instrument_details Data in instrument_details

Protein Modifications:

PubMed ID: