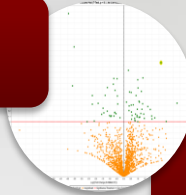
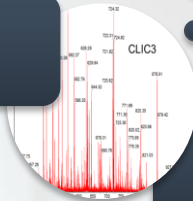


Data Analysis



Scaffold and Perseus software. Principal component analysis, sample correlation, hierarchical clustering, heat maps, Venn diagrams

Protein identification and quantification



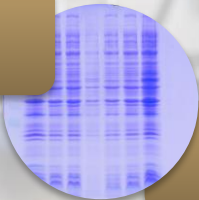
MaxQuant and Mascot software. SILAC, Label Free Quantification, TMT, PTMs

Nano LC-Mass spectrometry analysis



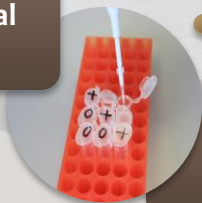
Orbitrap Fusion and TSQ Quantiva MS from ThermoScientific. Synapt G2 and Xevo MS from Waters Corp.

Sample preparation



In gel and in solution tryptic digestions, secretomes or protein fractionation and PTM enrichment

Experimental design



Label free quantification, SILAC, TMT, Immunoprecipitations, enrichments, Time courses,...

Welcome to the Proteomics Research Technology Platform at the University of Warwick. We provide service and support to academic and commercial researchers seeking to identify and quantify proteins and their modifications. The analysis of protein mixtures from gel slices, co-immunoprecipitations or enrichments is routine and we can identify several thousand proteins in complex samples. Our favorite challenges include the analysis of protein phosphorylation and post-translational modification mapping. You will find support from the proteomics team to help with scientific discussion, experimental design, sample preparation and analysis of mass spectrometry data.

Our Team:

Director: Alex Jones
Manager: Andrew Bottrill
Chief Technician: Cleidiane Zampronio
RTP Officer: Ian Hancox

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