PROTEOMICS

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Proteins constitute half of the cell's (dry) mass and are key functional units that actively contribute to tumour initiation, progression and metastatic spread. Proteins are also used as blood markers to determine the wellness status of an individual. Mass spectrometry (MS)-based proteomics is fundamental to unravelling the identity and function of individual proteins in the cell and body fluids. The Proteomics facility is working with cutting-edge MS proteomic technologies and innovative platforms for sample preparation and data analyses to answer fundamental questions of cancer biology, thus contributing to the progress of cancer research.

The proteomics team has an outstanding expertise in high-resolution, Orbitrap-based MS proteomics, accurate quantification approaches and MS data analysis. We work in collaboration with research groups within and outside of the Institute, and we actively develop MS-based proteomic platforms to address a variety of questions to help scientists increase their understanding of the mechanisms that regulate various aspects of cancer.
To achieve this, we are equipped with three nano liquid chromatography (nLC)-MS systems, including an Orbitrap Fusion-Lumos. All our instruments are coupled online to Easy-nLC systems, and high-resolution chromatography is achieved by packing our nano-columns in house.

We house a number of dedicated software packages, of which MaxQuant is most frequently used for highly accurate label-free or label-based quantitative analysis of data acquired in data-dependent acquisition mode. Moreover, we use Skyline for the analysis of PRM data and Spectronaut for data acquired in data-independent acquisition mode. Finally, we use Perseus for data analysis and dissemination. We have a competitive portfolio of techniques available, which span from single protein to sub-proteomes and global proteome analyses. We have strong expertise in quantitative analysis of secretomes (extracellular matrix, extracellular vesicles and conditioned media) and protein translation, and are developing approaches that allow us to study the interplay between metabolism and protein synthesis by tracing ^{13}C-labelled metabolites into newly synthesised secreted proteins (Kay EJ *et al.*, 2022, *Nature Metabolism*). We are also expert in posttranslational modifications, including cysteine oxidation. For the latter, we have developed SICyLIA, a method that enables the quantification of cysteine oxidation levels at a global scale with no enrichment steps required (van der Reest, Lilla *et al.*, 2018 *Nat Commun*) which has been fundamental to answering different biological questions (Port *et al.*, 2018, *Cancer Discov*; Hernandez-Fernaud, Ruengeler *et al.*, 2017, *Nat Commun*; Cao X *et al.*, 2020, *J Cell Sci*).

During 2022, we have worked with many of the groups at the Institute and significantly contributed to the success of their research (see publications). We are continuously striving to develop new methods using proteomics to answer more complex biological questions and to improve the methods currently in place enriching the quality of the data that the facility can provide.

News

This year, Sergio Lilla presented a recent development of the SICyLIA technology to measure cysteine oxidation at global scale at the International Mass Spectrometry Conference 2022 in Maastricht.

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