Proteins act as the molecular effectors of cells and catalyse virtually all biological processes. In this regard, proteomics aims to characterise the complete repertoire of proteins in order to better understand, at the proteome level, how cells function at the molecular level. Global analysis of proteins is challenging, owing to the high complexity (>12,000 genes transcriptionally active at any given time). To tackle these analytical challenges, proteomics uses state-of-the-art MS technology coupled to quantitative multiplexing approaches enabling profiling the entire proteome across multiple biological conditions (11 in a single experiment).

In collaboration with the Hereditary Endocrine Cancer Group, the Proteomics Unit continued to implement new technologies to the catalogue of available services. Throughout 2019, we optimised protocols for the global analysis of protein methylation, including mono-, di- and tri-methylation of lysines as well as mono- and di- (symmetric and asymmetric) methylation of arginines. Furthermore, exosomes and extracellular vesicles extracted from lymphatic drainage as surrogate markers of melanoma progression. We found that seroma-derived exosomes are enriched in proteins mimicking melanoma progression. Along the same lines, in collaboration with the Genes, Development and Disease Group, we applied this strategy to perform proteomic analysis of exosomes in a mouse lung fibrosis model and found that they are enriched in collagen-related proteins secreted by macrophages. Finally, the Unit continues to implement new technologies to the catalogue of available services. In 2019, we optimised protocols for the global analysis of protein methylation, including mono-, di- and tri-methylation of lysines as well as mono- and di- (symmetric and asymmetric) methylation of arginines.