



Proteomics at AgResearch

# Proteome profiling

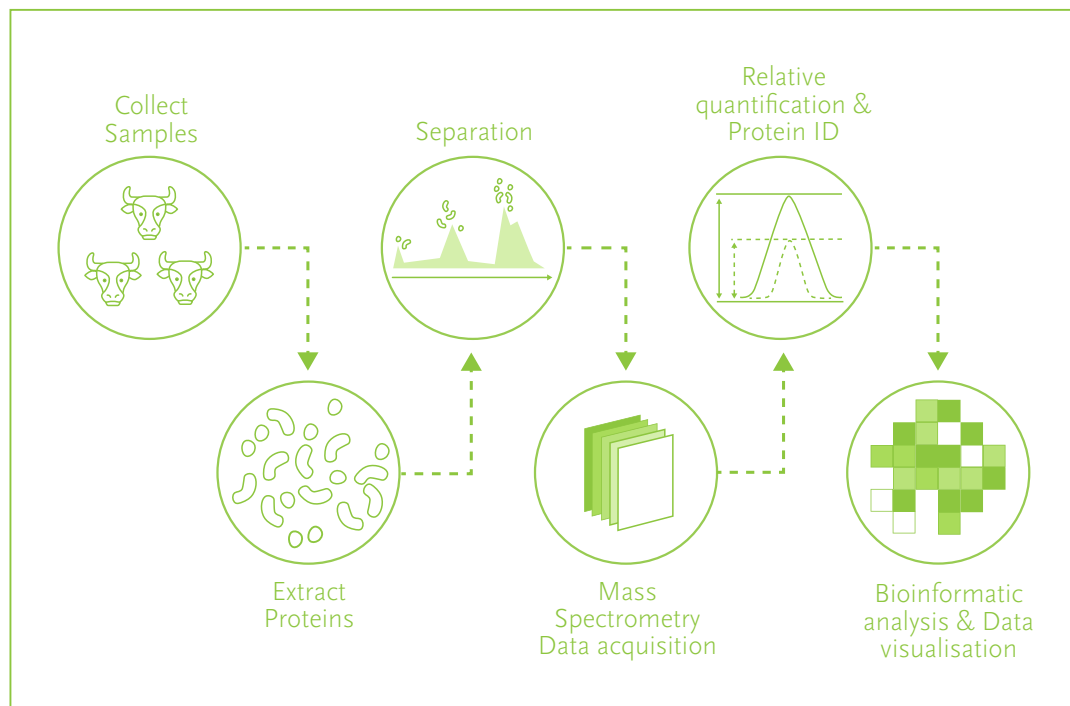
# Analysing entire sets of proteins at one time.

Rather than just analysing a few proteins of interest as is typically achieved in traditional biochemistry approaches, proteomics technologies allow the comprehensive analysis of hundreds or thousands of proteins in a given cell, tissue or fluid at a given time point.

This proteome analysis comprises the identification of the entire set of proteins of an organism or system, i.e. a proteome, with techniques that include protein extraction, purification and mass spectrometry.

At AgResearch, we have experience in the processing and the mass spectrometric analysis of a broad range of biological sample types. We tailor our proteomics work according to the type of sample and aims of the work.

In many research questions, a comparison between different proteomes (e.g. different time points, different treatments) is requested. In proteome profiling, the abundance levels of a wide range of proteins in different samples is compared get an overview of what is happening to a biological system, and thus develop hypotheses about the underlying biological mechanisms.



Above: Overview of proteome profiling workflow. Proteins will be extracted from samples, followed by sample preparation including reduction, alkylation, and digestion of the proteins in peptides. The resulting peptide mixtures are separated via reversed phase liquid chromatography and analysed via high resolution mass spectrometry. Identification and/or relative quantification is performed by both commercial and in-house developed bio-informatics tools.