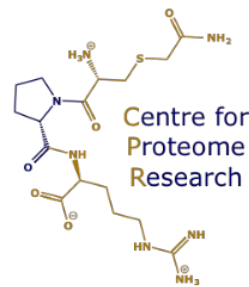


# Centre for Proteome Research

part of the

## NERC Environmental 'Omics Facility



**NEOF**  
NERC ENVIRONMENTAL  
OMICS FACILITY

*We are a specialist protein mass spectrometry facility, experienced in analysing an extensive range of sample types using state-of-the art instrumentation and methodologies to get the best information from your sample.*

### What we do

- Quantify global protein-level changes arising due to e.g. infection, environmental factors, or defined treatments
- Targeted identification and quantification of proteins and peptides of interest
- Analysis of protein binding partners (interaction networks)
- Signalling changes in post translation modifications, including phosphorylation
- 'Single cell' proteomics analysis for small sample amounts
- Sample discrimination (e.g. of faecal pellets by species, gender, age etc.) based on pattern matching
- Training users in experimental design, sample preparation and analysis of proteomics studies.

### FAQ:

#### ***How much material do we need?***

Typically 25-100  $\mu$ g. However with new single cell analysis capabilities, and depending on the question asked of the sample, smaller amounts are possible.

#### ***Is this a destructive technique?***

Yes, for analysis we need to break open the cells/tissues to extract the proteins, which we then typically digest for analysis.

#### ***Do we need a genome sequence?***

No, but it helps a lot! If there isn't a genome we are in a good position to obtain a genome sequence relatively easily working with the Centre for Genomic Research. We can also use cross species matching, and de-novo sequencing where this is not feasible.

#### ***How many replicates?***

At least 3 for model lab systems, for field based samples you will need more depending on biological variability.

#### ***Is my sample suitable for mass spectrometry analysis?***

There are many ways to make samples suitable for analysis by mass spectrometry. We have a variety of validated strategies in-house for preparing difficult samples to get rid of unwanted material for optimal proteome analysis.