

Protein Identification

SAMPLE SUBMISSION FORM

THIS INFORMATION MUST BE SUPPLIED BEFORE ANALYSIS:

Name: **Please circle:** PhD student / Post Doc /
Phone/Ext.: PI / External / other
Email: Date:
Grant holder name: Account code (or PO):
Number of samples:

Aim of submission:

- Localising post translational modifications (please email sequence and residue site information)
- Confirming protein ID (please email sequence information)
- Identifying unknown proteins

Name of protein + species (from UniProt) Species used to express protein

If the expected protein sequence differs from the wild type (e.g inclusion of His tag or presence of TEV cleavage site) or if it is not present in the Uniprot database please email the sequence in single letter amino acid format to mass-spec@leeds.ac.uk.

Gel box/ Sample vial labels: Stain used: Advised- Expedeon InstantBlue Coomassie stain Approximate molecular mass of bands: **Specify amount of protein submitted:**

Requirements- Gel submissions: Ideally between 1-5µg protein loaded

In-solution: vol= 50-100 µL, single protein= 0.1-1 mg mL⁻¹, simple mixture (few tens of proteins)= 20-50 µg of total protein, complex mixture (100+ proteins)= >300 µg of total protein**Specify solvent/buffer composition (In-solution samples only):**

Requirements- Avoid where possible glycerol and very high salt concentration (0.2M+)

Please attach picture of gel (with bands of interest clearly marked) to this form and store samples at 4 °C

By submitting samples you agree to be bound by our 'Conditions of Service' which can be found at: <https://biologicalsciences.leeds.ac.uk/biophysical-techniques/doc/mass-spectrometry/page/4>