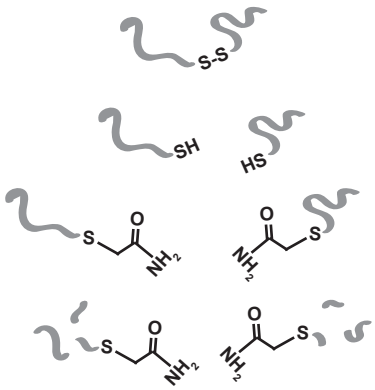
proteintech®
Antibodies | ELISA kits | Proteins

1. Sample preparation

Qualitative	*Relative Quantification*	*Absolute Quantification*
Protein identification	Metabolic labelling (SILAC)	comparison to a labelled peptide standard during mass spec (step 3)
Protein modifications	Chemical labelling (TMT)	
Kinase Assays	Unlabelled	
Immunoprecipitation		
Crosslinking/ Interaction studies		

2. Sample purification

Paramagnetic beads (e.g. SP3)



In-solution

In-gel

Reduction (Dithiothreitol=DTT)

Destaining

Alkylation (Iodocetamide=IAA)

Digest (e.g.Trypsin)

Extraction

Cleanup (C18, SP3, etc.)

3. Data analysis

Variables

Mass spectrometer (LTQ Orbitrap, Q-Exactive, LTQ Velos, etc.)

Chromatography, column length, ion source, length of run, mass analyser

Software

(MASCOT, MaxQuant, Proteome Discoverer, etc.)

Parameters (to set):	*Parameters (data analysis):*
Correct Database	Intensity, Peptide count, Coverage
Known modifications (reduction, alkylation)	Statistical significance
Sequence modifications (tags, mutations)	Normal distribution (proteomic data)
Crosslinking parameters	Correlation (Biological replicates)