

**Request Form: OSR user**  
**Proteomics and Metabolomics Facility: ProMeFa**

Dibit 2, C1, 4th floor  
Via Olgettina, 60  
20132 Milan  
Phone: +39-02-26432714/2253/4928  
e-mail: [andolfo.annapaola@hsr.it](mailto:andolfo.annapaola@hsr.it)

**User informations:**

Name:.....Phone:.....e-mail:.....

Lab.:.....Division:.....Internal order/Grant ID:.....

Signature of Group leader:.....

**Requested analysis:**

***Protein characterization:***

Sample purification (zip tip or similar) and intact protein/peptide MW determination by nanospray off line MS and MS/MS.

***Proteomics:***

- Identification of a spot or a band by in gel digestion and LC-MS/MS
- PTM-characterization in several biological fluids (plasma, serum, urine, CSF), cells and conditioned media, tissues, feces:
  - glycosylation by enzymatic digestion followed by LC-MS/MS
  - acetylation by PTMScan enrichment (Cell Signaling Technologies) followed by LC-MS/MS
  - phosphorylation (Tyr/Thr/Ser) by TiO<sub>2</sub> or IMAC enrichment followed by LC-MS/MS
- Quantitative protein profiling by mass spectrometry and statistical analysis. Differential protein display in two or more diverse conditions in several biological fluids (plasma, serum, urine, CSF), cells and conditioned media, tissues, feces, using:
  - iTRAQ or TMT labelling of peptides
  - SILAC methodology
  - Label-free approach

***Metabolomics/Lipidomics:***

- Untargeted workflow for differential small molecules/lipids display in several biological fluids (plasma, serum, urine, CSF), cells and conditioned media, tissues, feces.
- Targeted workflow for specific small molecules/lipids display in several biological fluids (plasma, serum, urine, CSF), cells and conditioned media, tissues, feces.
- Tracing experiments in cell culture using stable isotope labelled (<sup>13</sup>C/<sup>15</sup>N) small molecules (glucose, glutamine, arginine)

***Data analysis***

**Sample informations (according to the wanted activity, fill in the fields):**

Sample name or gel ID number:

Buffer/solvent composition:

Quantity and volume:

Expected mass (for peptides, indicate the protecting groups):

Organism or source of protein sample:

Number of bands/spots to be identified:

**FACILITY USE ONLY:**

Date of receipt:

Analysis Performed:

N° of samples analysed:

Cost (€):