Request Form: OSR user Proteomics and Metabolomics Facility: ProMeFa

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<u>User informations:</u>		
Name:	.Phone:	e-mail:
Lab.:Division:	Internal order/Grant ID):
Signature of Group leader:		

Requested analysis:

Protein characterization

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

Protein identification: PMF and sequencing

PTM-characterization: validation by Western Blotting and 2DE +/- removal of the PTM Phosphorylation characterization by TiO₂ or IMAC enrichment and mass spectrometry Identification of a spot or band by in gel digestion and LC-MS/MS

Biomarker profiling in biological samples by 2DE, image analysis and statistical evaluation Differential protein display in control vs patient biological samples: plasma, serum, urine, tissue Six samples: control vs treated/patient in triplicates

Quantitative protein profiling by mass spectrometry and statistical analysis

Differential protein display in two or more diverse conditions using: iTRAQ or TMT labelling of peptides (run in technical duplicate) SILAC methodology (run in technical duplicate) Label-free approach (run in technical triplicate)

Metabolomics/Lipidomics by mass spectrometry and statistical analysis

Untargeted workflow for differential small molecules/lipids display in: plasma, serum, urine, tissues

Quantitative Metabolomics/Lipidomics by mass spectrometry and statistical analysis

Targeted workflow for specific small molecules/lipids display in: plasma, serum, urine, tissues

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 (€):