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| UTechS MSBio | **Pasteur Proteomics Platform****Mass Spectrometry for Biology UTechS (MSBio)** |

**Mass Spectrometry Analysis Request Form**

 !!! Warning: No samples with radioactive isotopes will be accepted!!!

**USER INFORMATION**

Date submitted:

Name:

Email:

Phone number:

Name of Lab:

Department:

Address of Lab:

Head of Lab:

**IMPORTANT RULES**

* Prior project submission, please contact proteomics@pasteur.fr
* A collaboration implies customized wet lab protocols and/or specific, advanced data analysis in order to produce a joint effort towards a significant advance in life science, often in the form of a joint publication.
* The service mode consists of a fully comprehensive service performed by the platform personnel. The charges for such a service include the cost of the full wet lab workflow and the cost of the downstream bioinformatics analysis. If you use the results provided by the platform, please acknowledge the platform in your publication.
* After discussion and acceptance of the project, a quote will be sent to the Head of the Unit for validation. This quote has to be signed and returned to the platform.
* For external collaborators, please also enclose an order form from your Institute.
* The general price scheme for collaborations is based on sharing the cost of the experiments and the work; however precise arrangements will be made on a case-by-case basis.

**QUALITY CONTROL**

* The proteomics platform follows the rules of safety and security policies defined by the Institut Pasteur.
* We do not have agreement to work on MOT and live viruses so please check your samples before they’re handle by the Proteomics Platform.

**PROJECT INFORMATION**

Project title:

Collaboration:

 YES NO

* *For collaborative projects please fill the section below*
* *For any kind of project please fill the SAMPLE INFORMATION section*

**FOR COLLABORATIVE PROJECTS**

Abstract of the project (including relevant publications) - 1 page maximum

**SAMPLE INFORMATION**

*This section is mandatory.*

Sample species:

Database available:

Sample type (short description of the sample preparation):

Number of samples submitted:

Solubility:

Concentration:

Other relevant information about the sample (presence of post-translational modifications, chemical modification…):

Type of samples:

* For protein samples in solution, specify:
* Buffer (including: detergent or protease inhibitors, other…):
* Concentration (or estimation of):
* Info on Purity (for single protein analysis):
* Purification steps:
* For gel spots or bands (\*\*Please add a picture of the gel\*\*):
* % acrylamide:
* Staining:
* Amount of protein loaded into the gel:

**SAMPLE ANALYSIS (PROTEOMICS PLATFORM)**

Type of analysis requested (to be filled by the customer and approved by the platform):

|  |  |  |
| --- | --- | --- |
| **Code** | **Mass Spectrometry Analysis** | **Number of samples** |
| 4596-4598 | Intact Mass Measurement |  |
| 4599-4601 | In-Gel Digestion/Protein identification/Quantification |  |
| 4602-4604 | In Solution Digestion/Protein Identification/Quantification (SILAC, iTRAQ, TMT…)/ PTM\* |  |
| 4605-4606-4607 | Label Free Quantification\*\* (Triplicate) |  |

*\*PTM: Post-translational modifications*

*\*\*Label- free quantification on whole proteome, sub-proteome, complexes or PTM (enriched fraction)…*

For more information regarding the platform and our prices, please visit our website: <https://research.pasteur.fr/en/team/proteomics/>

Any other information:

**Project agreement**

Good for agreement: to sign and date

 MSBio Collaborator

Closing of the project: to sign and date

 MSBio Collaborator