Activity

The Institut Curie Mass Spectrometry and Proteomics facility (LSMP) was established in 2001 to answer a request in proteomics. This service consists of personnel with specialized know-how and expertise in the proteomics field as well as state-of-the-art proteomics equipment (MS, LC, softwares, etc.).

New collaborators are met to discuss the most appropriate way forward in their project. Altogether, we design the experiment so as to answer their questions. Some biological and biomedical questions will apply existing technologies. Others are technically more challenging and require the development of new techniques, reagents or software in order to solve pressing problems.

Aims

The LSMP facility aims to provide researchers with technical services enabling them to analyze proteins (identification of proteins, comparison of proteomes, analysis of post-translational modifications, identification of partners interacting with the protein of interest etc.) by mass spectrometry. One of the most promising approaches is combining qualitative and quantitative analysis in a single analytical run (adapted to research samples, which means high sensitivity and low-level quantitation). The goal is to provide our collaborators with scientific hypotheses more quickly and to functionally validate our quantified candidates.

Networking

The LSMP facility is an “Ile-de-France Proteomics facility” for cancer research labeled IBiSA, which is part of the “Proteomics @ PSL Research University” Montagne Sainte Geneviève Proteomic Facility. The LSMP is a founding member of Paris proteomics platforms network, is
Mass Spectrometry and Proteomics Facility

Platforms

associated to the French Society for electrophoresis and proteomic analysis and to the French Society of Mass Spectrometry part of EuPA and HUPO.

Services

In practical terms, the facility carries out two distinct modes: collaborative or service. Fees are billed on an hourly basis for instruments usage.

- Collaborative research requires advanced experiments by working closely in a true collaborative effort: a person of the research team is trained at the facility to prepare the samples and to interpret the data. The fees stand for machines maintenance contracts and consumables. Institut Curie subsidizes the rest.
- Service: on each project, a service mode can be chosen if the co-signature is not wished. The analysis fees include people salary, structure costs and investments renewal.

The services provided:

- Definition of optimal experimental design
- Advice concerning the setting up
- Advice and assistance in preparation of samples/quality control
- Protein and peptide identification
- Comparison of proteomes
- Accurate mass measurements
- Analysis of post-translational modifications (localization and characterization).
- Targeted proteomics
- Quantitative proteomics
- MS processing
- Bioinformatics and statistical analysis

Equipment

- Thermo Scientific™ Q Exactive™ HF-X Hybrid Quadrupole-Orbitrap™ MS
- Thermo Scientific™ Q Exactive™ Exploris 480 Quadrupole-Orbitrap™ MS
- Thermo Scientific™ Orbitrap Fusion™ Tribrid™ MS
- Thermo Scientific™ Ultimate™ 3000 RSLCnano LC system
- Thermo Scientific™ Dionex™ Ultimate™ 3000 AFC Automated Fraction collector
- myProMS web server
- Thermo Scientific™ Proteome Discoverer™ 2.4 software
- Database search algorithms (SEQUEST HT, Matrix Science Mascot Server and Daemon 2.5, ...)

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Mass Spectrometry and Proteomics Facility
Platforms

- Trans-Proteomic Pipeline (TPP 4.8) tools

Training and methodological expertise

The LSMP Facility aims at providing to its users three types of expertise: 1-personalized training to realize a part of analyses; 2-advanced training about all aspects of Proteomics (from helping in defining questions and experimental design, to sample preparation, through MS analysis, to MS processing and analysis); 3-development of MS processing and analysis tools.

The LSMP develops in-house solutions, in collaboration with the Bioinformatics platform (U900), to provide the community with bioinformatical tools for management, mining, curation or mass spectrometry-based (MS) data sharing. The web server myProMS was designed to handle projects and curate databank-search results from multiple MS runs while optimizing data sharing between users with complementary competences. It is improved continuously so as to be up-to-date with the quality standards. myProMS is a freely distributed tool, GPL license, already implemented in 4 institutes (ESPCI, Institut Cochin, IGF de Montpellier and IC).

Manager and Team

The LSMP facility is managed by Damarys Loew and has a team specialized in the field of 1) Mass spectrometry and proteomics 2) Biology and 3) Bioinformatics

- Dr Damarys Loew, mass spectrometry specialist and facility manager contact: Tél. : +33 (0)1 56 24 65 22 (spectro@curie.fr)
- Bérangère Lombard, MS engineer
- Florent Dingli, Proteomic engineer
- Vanessa Masson, Biology engineer
- Valentin Sabatet, Bioinformatics engineer
- Victor Laigle, Bioinformatics engineer

Key publications

Year of publication 2020

**Germline Elongator mutations in Sonic Hedgehog medulloblastoma.**

Year of publication 2019

CAMPAGNE Antoine, LEE Ming-Kang, ZIELINSKI Dina, MICHAUD Audrey, LE CORRE Stéphanie, DINGLI Florent, CHEN Hong, SHAHIDIAN Lara Z, SERVANT Nicolas, LOEW Damarys, PASMANT Eric, PISTEL-VINAY Sophie, WASSEF Michel, MARGUERON Raphaël (2019 Jan 21)

**BAP1 complex promotes transcription by opposing PRC1-mediated H2A ubiquitylation**
*Nature Communications*: 10 : 1-15 : [DOI: 10.1038/s41467-018-08255-x]

Year of publication 2018


**The Implication of Early Chromatin Changes in X Chromosome Inactivation**

Antoine Forget, Loredana Martignetti, Stéphanie Puget, Laurence Calzone, Sebastian Brabetz, Daniel Picard, Arnaud Montagud, Stéphane Liva, Alexandre Sta, Florent Dingli, Guillaume Arras, Jaime Rivera, Damarys Loew, Aurore Besens, Joëlle Lacombe, Mélanie Pagés, Pascale Varlet, Christelle Dufour, Hua Yu, Audrey L Mercier, Emilie Indersie, Anaïs Chivet, Sophie Leboucher, Laura Sieber, Kevin Beccaria, Michael Gombert, Frauke D Meyer, Nan Qin, Jasmin Bartl, Lukas Chavez, Konstantin Okonechnikov, Tanvi Sharma, Venu Thatikonda, Franck Bourdeaut, Célio Pouponnot, Vijay Ramaswamy, Andrey Korshunov, Arndt Borkhardt, Guido Reifenberger, Patrick Poullet, Michael D Taylor, Marcel Kool, Stefan M Pfister, Daisuke Kawauchi, Emmanuel Barillot,
Marc Remke, Olivier Ayrault (2018 Sep 12)

**Aberrant ERBB4-SRC Signaling as a Hallmark of Group 4 Medulloblastoma Revealed by Integrative Phosphoproteomic Profiling.**

*Cancer cell*: 379-395.e7 : [DOI: S1535-6108(18)30356-8](https://doi.org/S1535-6108(18)30356-8)

Year of publication 2017

Alexandros Glentis, Philipp Oertle, Pascale Mariani, Aleksandra Chikina, Fatima El Marjou, Youmna Attieh, Francois Zaccarini, Marick Lae, Damarys Loew, Florent Dingli, Philemon Sirven, Marie Schoumacher, Basile Gurchenkov, Marija Plodinec, Danijela Matic Vignjevic (2017 Oct 15)

**Cancer-associated fibroblasts induce metalloprotease-independent cancer cell invasion of the basement membrane.**

*Nature communications*: 924 : [DOI: 10.1038/s41467-017-00985-8](https://doi.org/10.1038/s41467-017-00985-8)

Gheghiani Lilia , Loew Damarys, Lombard Bérangère, Mansfeld Jörg, Gavet Olivier (2017 Jun 6)

**PLK1 Activation in Late G2 Sets Up Commitment to Mitosis**

*Cell Reports*: 19 : 2060-2073 : [DOI: 10.1016/j.celrep.2017.05.031](https://doi.org/10.1016/j.celrep.2017.05.031)