

The Proteomics Team (Bioinformatics)

Patrick Poulet: Team leader, dev, data analysis

Stéphane Liva: dev, data analysis

Isabel Brito (50%): statistics

Lieng Taing: dev, workflow/NGS

Bioinformatics platform

Valentin Sabatet: dev, data management

Victor Laigle: dev, data analysis

Mass spectrometry facility

Missions:

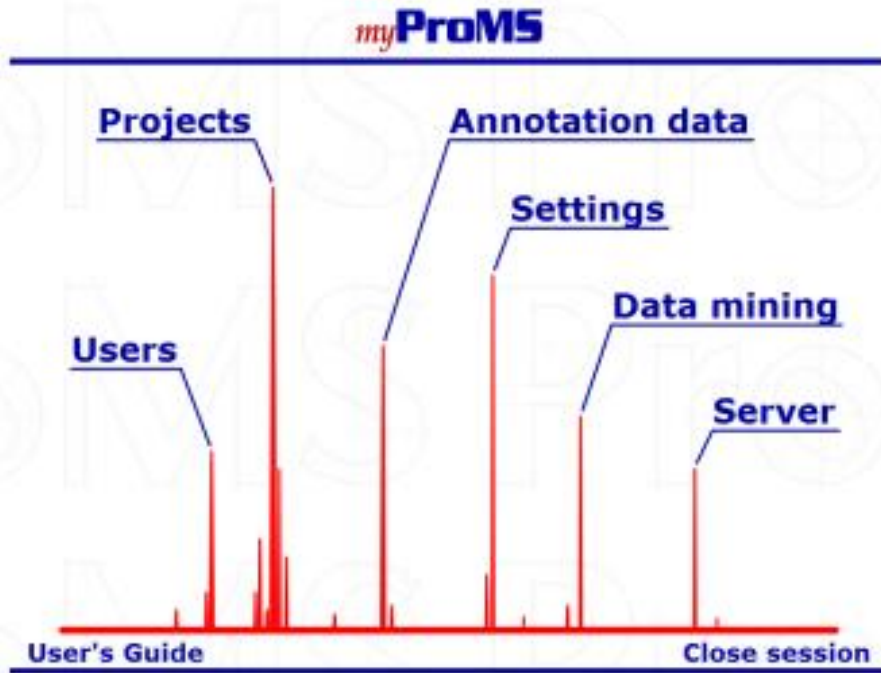
- Bioinformatics support for IC proteomics facilities (Mass Spec, RPPA)
- Contribute large-scale proteomics-based projects
- Assist end-users (project design, training, ...)
- Methodological development

Support to proteomics facilities

Implement comprehensive solutions for user-friendly data access, management and analysis (both **facilities** and **collaborators**).

2 web-based applications

myProMS: Mass Spectrometry



myProMS: Poulet et al. Proteomics 7, 2007
<https://github.com/bioinfo-pf-curie/myproms>

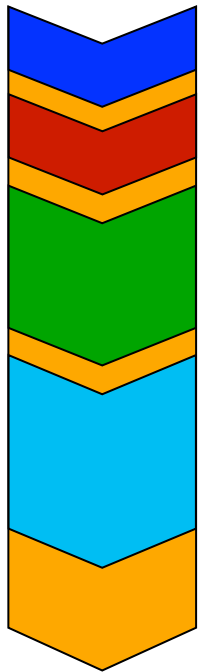
PARYS: Reverse-Phase Protein Array



The interface for **PARYS Home** features a list of menu items: **Projects**, **Antibodies**, **Micro-Arrays**, **Biological Samples**, **Proteins and Pathways**, **Tools**, **Users**, and **Leave Server**. To the right of the interface is a photograph of the PARYS hardware, a tall, light-colored cabinet with a door and a control panel.

myProMS main functionalities

myProMS



- Experimental design
- Sample annotation
- Search results import & curation
- Identification analyses
- Peptide/transition quantification
- Protein/PTM differential analyses
- Analyses:
 - PCA, Clustering, ...
 - GO, Pathway, ...
 - Sequence motifs
- Data centralization, accessibility, mining & traceability



Client side

Server side



Update since 03/2019

myProMS:

- PTMs quantification (DDA/DIA):
 - Multi-PTMs
 - Protein FC correction
 - IPF workflow (OpenMS)
- Native support for Skyline (PRM/DIA)
- Improved support to MaxQuant (multi-parameter groups, latest version)
- Proteomic Ruler (absolute quantification)

- Improved computation throughput (300 tumour samples in DIA)
- MySQL database optimization: 250Go to 150Go
- Migration from Perl (2003!) to Python (initiated)

Proteogenomic:

- Proteome generator
- CustomProDB
- In-house workflow