

## BIOENG-517

## Lab methods : proteomics

| Cursus                    | Sem.     | Type |
|---------------------------|----------|------|
| Bioengineering            | MA3      | Opt. |
| Life Sciences Engineering | MA1, MA3 | Opt. |
| Sciences du vivant        | MA3      | Opt. |

|                      |                     |
|----------------------|---------------------|
| Language of teaching | English             |
| Credits              | 2                   |
| Withdrawal           | Unauthorized        |
| Session              | Winter              |
| Semester             | Fall                |
| Exam                 | During the semester |
| Workload             | 60h                 |
| Weeks                | 14                  |
| Hours                | 2 weekly            |
| Project              | 2 weekly            |
| Number of positions  | 12                  |

**Il n'est pas autorisé de se retirer de cette matière après le délai d'inscription.**

## Remark

Pas donné en 2020-2021. Inscriptions sur dossier auprès du responsable de cours, présence aux cours obligatoire

## Summary

Introduction to several mass spectrometry techniques and their application to the proteomics field. Description of bioinformatics tools used to analyze proteomics data. The goal of the course is to provide an overview of main proteomics strategies and their applications in the Life Science context

## Content

The course is structured so as to alternate theory and illustrative practical exercise periods in the laboratory.

## Day 1:

## Morning (theory)

- Introduction to proteomics analysis principles:
- Define what Proteomics is
- Introduction to the Platform
- Mass spectrometry: sample ionization and mass analysis principles (MALDI, electrospray, m/z, resolution, isotopic distribution)
- Liquid chromatography: sample separation principles.
- Instrumentation and methods used in proteomics:
- Distribution and presentation of a selection of representative articles and lab visit

## Noon (practical)

- Illustration of what was presented in the morning
  - Sample preparation (protein digestion)
  - ESI-MS molecular weight measurement: infusion of diverse samples on Orbitrap instrument (single peptide, several peptides mix, single protein, several proteins mix, show resolution, monoisotopic mass)

- MALDI-MS molecular weight measurement: sample preparation and measurements on MALDI-TOF/TOF (same samples as infusion)

**Day 2:***Morning (theory)*

- Simple Proteomics Workflows
  - Intact mass measurements
  - Protein identification principles

*Noon (practical)*

- Illustration of what was presented in the morning
  - Sample preparation (protein digestion finalization and sample desalting)
  - Quality control check on MALDI-MS (MW measurements)
  - Infusion-MS/MS to illustrate tandem MS fragmentation principles
  - Presentation of LC-MS/MS principles for peptide separation and protein identification in front of instruments.

**Day 3:***Morning (theory)*

- More complex Proteomics Workflows
  - Increasing the depth of analysis: typical workflows for protein and peptide fractionations
  - Increasing the complexity: typical workflows for Post Translational Modifications analysis
  - Increasing the information content: Protein quantification strategies (SILAC, Dimethyl labeling, iTRAQ-TMT, SRM/MRM)

*Noon (practical)*

- Illustration of what was presented in the morning
- - SRM quantification: Triple Quadrupole instrument presentation
  - Hands on introduction on representative bioinformatics tools for MS based protein identification and quantification
- Debriefing about the practical session, Q&A and conclusions

**Day 4:**

- Presentation of selected Papers (morning or noon, to be defined)

**Learning Prerequisites****Required courses**

First year of master in Life Sciences & Technology or Bioengineering program.

**Learning Outcomes**

By the end of the course, the student must be able to:

- Integrate the basic theoretical and technical concepts of mass spectrometry
- Apply these concepts to the analysis of proteins and to the proteomics field
- Describe and explain the different methods and tools presented during the course
- Perform sample preparation for mass spectrometry related experiments
- Analyze and interpret data coming from mass spectrometry and simple proteomics experiments
- Select appropriately approaches and sample preparation methods adapted to the nature of the biological sample analyzed
- Decide between the different methods and tools presented during the course which one could be used in different contexts
- Systematize useful information from a paper and summarize its content

### Transversal skills

- Collect data.
- Summarize an article or a technical report.

### Teaching methods

Shortex-cathedra lectures to introduce the concepts followed by hands on practical sessions in the laboratory including sample preparation, analysis by mass spectrometry and data interpretation. Deepening of knowledge acquired in practical sessions by personal work on selected papers representative of the technique used in proteomics

### Expected student activities

**This block course will take place from November 26th to November 29th, 2019, full time.**

Practical part will take place in the proteomics core facility.

### Assessment methods

Written exam during the semester.

### Supervision

|              |                                                                               |
|--------------|-------------------------------------------------------------------------------|
| Office hours | Yes                                                                           |
| Assistants   | Yes                                                                           |
| Others       | Office hours : 8h30-18h<br>Assistants: Jonathan Paz Montoya and Adrien Schmid |

### Resources

#### Websites

- <http://pcf-ptp.epfl.ch/>

#### Moodle Link

- <http://moodle.epfl.ch/enrol/index.php?id=13401>