

CH-419

Protein mass spectrometry and proteomics

Dayon Loïc

| Cursus | Sem. | Type |
|-----------------------------|----------|------|
| Chimiste | MA2, MA4 | Opt. |
| UNIL - Sciences forensiques | E | Opt. |

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| Language of teaching | English |
| Credits | 2 |
| Session | Summer |
| Semester | Spring |
| Exam | Written |
| Workload | 60h |
| Weeks | 14 |
| Hours | 2 weekly |
| Lecture | 2 weekly |
| Number of positions | |

Summary

In systems biology, proteomics represents an essential pillar. The understanding of protein function and regulation provides key information to decipher the complexity of living systems. Proteomic technology now enables deep quantitative proteome mapping via mass spectrometry.

Content

1. Introduction and mass spectrometry

Introduction to protein analysis and proteomics; Reminders in mass spectrometry; Why proteomics and mass spectrometry?; Ionization sources, analyzers, and detectors used in proteomics

2. Mass spectrometry-based proteomic strategy and workflows

Bottom-up *versus* top-down strategies; Sample preparation

3. Separations techniques in proteomics

Gel electrophoresis; Isoelectric focusing; Liquid chromatography (RP, IEX)

4. Quantitative proteomic workflows using mass spectrometry

Label-free methods; Labelling-based techniques; Other quantitative techniques

5. Proteomic bioinformatics

Databases; Identification of protein; Quantification of proteins; Bioinformatics tools; Practical examples

6. Applications to biology and clinical research

What strategy?; Experimental design; Biomarker discovery; Population proteomics; Forensics; Targeted mass spectrometry-based approaches; Other biological applications of mass spectrometry; Lab visit at Nestlé Research by group of 5-10 students

Keywords

Mass Spectrometry; Liquid Chromatography; Electrophoresis; Proteins; Peptides; Systems Biology; Bioinformatics; Human Samples; Clinics; Isotopic Labelling; Quantification

Learning Prerequisites**Recommended courses**

CH-210 Biochimie I

CH-301 Méthodes de séparation analytiques

CH-314 Structural analysis

Important concepts to start the course

Mass spectrometry; Biochemistry

Learning Outcomes

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

- Differentiate biological mass spectrometry techniques to identify and quantify proteomes
- Distinguish the main separation techniques for proteins and peptides
- Choose appropriate methodology for protein analysis
- Discuss literature related to proteomics
- Describe the field of applications of proteomics and expand those concepts beyond, e.g., to metabolomics
- Interpret some mass spectrometry data

Teaching methods

Ex-cathedra

Assessment methods

Written exam with Multiple Choice Questions (MCQ) (66-75%) & exercices (25-33%)

Supervision

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| Office hours | No |
| Assistants | No |
| Forum | No |

Resources

Ressources en bibliothèque

- [Quantitative methods in proteomics / Marcus](#)
- [LC-MS/MS in proteomics / Cutillas](#)
- [Serum/plasma proteomics / Simpson](#)

Références suggérées par la bibliothèque

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Websites

- <https://www.nature.com/nature/journal/v537/n7620/full/nature19949.html>
- <https://rd.springer.com/book/10.1007/978-1-61779-885-6/page/1>
- <https://rd.springer.com/book/10.1007/978-1-60761-780-8/page/1>
- <http://www.springer.com/gp/book/9781493970568>

Moodle Link

- <https://go.epfl.ch/CH-419>