CH-419

Protein mass spectrometry and proteomics

Dayon Loïc

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

Language of teaching	English
Credits	2
Session	Summer
Semester	Spring
Exam	Written
Workload	60h
Weeks	14
Hours	**2 weekly**
Courses	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, analysers, and detectors used in proteomics; Latest generation of mass spectrometers used in proteomics
2. Mass spectrometry-based proteomic strategy and workflows
Bottom-up versus top-down strategies; Data-dependent acquisition (DDA) and data-independent acquisition (DIA) approaches; 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; Industrialized and population proteomics; Forensics; Targeted mass spectrometry-based approaches; Other biological applications of mass spectrometry; Advanced innovations (single-cells, 4D proteomics, multi-omics) and emerging technologies; Limitations and ethical consideration; Lab visit by group of 5-12 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) (2/3) & exercices (1/3)

Supervision

Office hours	No
Assistant.e.s	No
Forum	No

Resources

Ressources en bibliothèque

- Find the reference at the Library

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

Videos

- https://www.youtube.com/watch?v=pJqJ1GYo0xY
- https://www.youtube.com/watch?v=m4U9bcnGtg4&t=52s
- https://www.youtube.com/watch?v=1G6jTGAfgUc