

General Information
Proteomics course 138018

Spring 2025: Lectures Wednesday 14:30-16:30 in Biology Computer Farm (Biology Building, 2nd Floor) *

A short Zoom meeting will be coordinated at the beginning of the Semester to provide information required for course.

Lectures will begin in May 2025 and will commence weekly until the end of the semester

Lab dates Aug 17, 2025, to Aug 21, 2025*

Teaching Staff:

Instructor:

Associate Prof. Oded Kleifeld, Biology Building room 433-4, Tel 073-3871453

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Office Hours: by appointment

TA:

Noam Cohen (Kleifeld lab) Biology Building room 433-4, Tel 073-3871452

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Course Goals and Description

The course aims to introduce and familiarize the students with the modern technologies of bottom-up proteomics. The students will learn and practice some of the methodologies and their uses and gain sufficient knowledge to design basic proteomics experiments using the technologies.

The course will include frontal lectures and the equivalent of one week of hands-on lab and bioinformatics exercises.

If possible, the practical part of the course will be a study of a relevant scientific question selected by the students.

The theoretical part of the course will cover the subjects of mass spectrometry, proteins, and peptides characterization and quantification, posttranslational modifications, affinity enrichment of posttranslational modifications, analysis of interactions between proteins and their ligands, use of stable isotopes labeling, protein chips, and bioinformatics, identification of sites of proteolysis, proteins as biomarkers, deciphering signaling cascades by use of proteomics. The lectures will be given during the second part of the semester and the lab part.

Learning Outcomes

The student will become familiar with the technologies, methodologies, instrumentations, and bioinformatics analytical tools of modern proteomics technologies and will be able to design, perform and analyze proteomics experiments on their own, and to critically read articles describing advanced proteomics analyses.

The students are expected to perform protein extraction, proteolysis, to prepare disposable chromatography columns, to perform gel electrophoresis and in-gel-digest, mass spectrometry, and analysis of the resulting data with the dedicated software and other analysis and bioinformatics tools.

Course Content/Topics

1. Introduction about proteins and separation of proteins and peptides based on physical properties by chromatography and their use in proteomics.
2. Liquid chromatography separation for proteomics
3. Sample preparation for proteomics study with emphasis on bottom up proteomics.
4. Mass spectroscopy including basic features of a mass spectrometer, sample introduction, analyzers, Fragmentation methods. Peptide mass fingerprinting.
5. Data Dependent Acquisition (DDA), use of MS and MS-MS for identification and de novo sequencing of peptides and proteins, computational tools for automated analysis of MS-MS data.
6. Data Independent Acquisition (DIA/SWATH) and targeted proteomics
7. Post-translational modifications and their analysis by MS
8. Quantitative proteomics: relative and absolute quantification using label-based and label-free approaches
9. MS-based analysis of protein-protein and protein-ligand interactions.
10. Hands-on experience in sample preparation and data analysis of bottom-up proteomics experiment.
11. Bioinformatics and statistics for bottom-up proteomics data analysis (DDA-based).

Assignments and Grading Procedures

Presence and active participation in all classes and labs are required.

The grade will be based on 2-3 assignments* and the teacher+TA evolution:

- Short presentation of selected proteomic method assigned by the teachers 20%
- Proteomic data Analysis of published results - a critical review of an article including re-analysis of the MS data. Alternatively, participation in data analysis and manuscript writing 20%
- Analysis of experiments performed in the lab part followed by a short report and presentation of the results 30%

Teacher evaluation: 30%

*If we will not be able to complete all 3 assignments within the course timeframe, the relative part of each element/assignment will be re-calculated based on the parts that were completed

Course Requirements& Course Policies

The students are expected to participate actively in the course by attending the lectures and lab classes, being involved with the discussion in the class room, preparing themselves to the lab part, planning the proteomics experiment, presenting a proteomic method and explaining the advantages and difficulties in the presented experimental approach.

The students will perform 2-3 proteomics experiments, in the lab part based on samples provided by the teachers. Students are expected to participate actively in the lab part the entire time. The students are expected to plan their part in the lab experiments and understand the logic behind their design and not just perform the experiments in a 'cookbook' style. The students are expected to display, explain and criticize the results of their experiments in a formal presentation to the teachers. Students are expected to be critical of

their results and the results of their peers and to reach a level of knowledge that will enable them to design new experiments based on the use of proteomics methodologies in their future research.