ORIGINAL COURSE IMPLEMENTATION DATE: September 2026

REVISED COURSE IMPLEMENTATION DATE:

COURSE TO BE REVIEWED (six years after UEC approval)**:** April 2032

Course outline form version: 29/08/2024

OFFICIAL UNDERGRADUATE COURSE OUTLINE FORM

Note: The University reserves the right to amend course outlines as needed without notice.

Course Code and Number: BIOC 442	**Number of Credits:** 3 Course credit policy (105)
Course Full Title: Analytical Proteomics **Course Short Title:** Analytical Proteomics	
Faculty: Faculty of Science	**Department/School:** Chemistry

Calendar Description:

Analytical proteomics is a rapidly expanding area bridging chemistry and biology. This course focuses on learning the structure of proteins and peptides, using analytical techniques to separate and identify them, and using protein data bases to analyze the obtained data.

Note: This course is offered as BIOC 442 and CHEM 442. Students may take only one of these for credit.

Note: Students with credit for CHEM 412H cannot take this course for further credit.

Prerequisites (or NONE):	None.
Corequisites (if applicable, or NONE):	None.
Pre/corequisites (if applicable, or NONE):	CHEM 341 or BIO 320/BIOC 320.

Antirequisite Courses *(Cannot be taken for additional credit.)*

Former course code/number: **CHEM 412H**

Cross-listed with: **CHEM 442**

Equivalent course(s):

(If offered in the previous five years, antirequisite course(s) will be included in the calendar description as a note that students with credit for the antirequisite course(s) cannot take this course for further credit.)

Typical Structure of Instructional Hours

Lecture/seminar	45
Total hours	**45**

Scheduled Laboratory Hours

Labs to be scheduled independent of lecture hours: **No**

Course Details

Special Topics course: **No**

(If yes, the course will be offered under different letter designations representing different topics.)

Directed Study course: **No**

(See policy 207 for more information.)

Grading System: **Letter grades**

Delivery Mode: **May be offered in multiple delivery modes**

Expected frequency: **Every other year**

Maximum enrolment (for information only)**: 24**

Prior Learning Assessment and Recognition (PLAR)

PLAR is available for this course.

Transfer Credit *(See **bctransferguide.ca**.)*

Transfer credit already exists: **No**

Submit outline for (re)articulation: **No**

(If yes, fill in transfer credit form.)

Department approval	**Date of meeting:**	December 11, 2025
Faculty Council approval	**Date of meeting:**	February 6, 2026
Undergraduate Education Committee (UEC) approval	**Date of meeting:**	April 24, 2026

Learning Outcomes *(These should contribute to students' ability to meet program outcomes and thus Institutional Learning Outcomes.)*

Upon successful completion of this course, students will be able to:

1. Analyze the molecular structure of different proteins.
2. Explain the common separation techniques to separate proteins.
3. Articulate the reasons protein digestion might be necessary as a preliminary step before protein identification.
4. Identify the differences between bottom-up and top-down proteomics.
5. Use online and open sources software such as UniProt and Expassy to run a protein digestion and obtain the peptide sequence of the protein and other related information.
6. Explain the integration of proteomics with genomics, transcriptomics, and metabolomics in systems biology approaches.
7. Explain how post-translational modifications (PTMs) influence protein function, interactions, and disease development.
8. Explain the role of target identification, mechanism-of-action studies, and biomarker discovery in the context of proteomics.
9. Explain as proteomics advances in clinical applications, what ethical considerations must be addressed, and how proteomics data from biomarker discovery or patient samples should be handled responsibly.

Recommended Evaluation Methods and Weighting *(Evaluation should align to learning outcomes.)*

Project:	30%	Assignments:	50%	Quizzes/tests/midterm:	20%
	%		%		%

Details:

NOTE: The following sections may vary by instructor. Please see course syllabus available from the instructor.

Typical Instructional Methods *(Guest lecturers, presentations, online instruction, field trips, etc.)*

The presentation of the course will be by interrelated theory classes ("lectures"), and discussion periods ("seminars"). Audio visual aids will be used where appropriate, and students will be expected to use the UFV library for literature research. Students may be required to present seminars or research papers. Guest lecturers will be invited to share their knowledge on the field of proteomics with students.

Texts and Resource Materials *(Include online resources and Indigenous knowledge sources. Open Educational Resources (OER) should be included whenever possible. If more space is required, use the Supplemental Texts and Resource Materials form.)*

	Type	Author or description	Title and publication/access details	Year
1.	Textbook	Donald Voet, Judith G. Voet; Charlotte W. Pratt;	Fundamentals of Biochemistry	Current
2.	Textbook	Douglas A. Skoog, F. James Holler, Stanley R. Crouch, Brooks Cole	Principles of Instrumental Analysis	Current
3.	Book	Daniel C. Liebler	Introduction to Proteomics: Tools for the New Biology	Current
4.	Book	Nawin C. Mishra	Introduction to Proteomics: Principles and Applications	Current
5.				

Required Additional Supplies and Materials *(Software, hardware, tools, specialized clothing, etc.)*

Course Content and Topics

- What is proteomic?
- Amino acids and proteins
- The role of proteomics in systems biology (class discussion)
- Protein digestion
- Post-translational modifications (PTMs) and their biological significance (class discussion)
- Extracting proteins from biological samples
- Proteomics in drug discovery and development (class discussion)
- Ethical considerations in clinical proteomics (class discussion)
- Methodology of separation and identification of proteins
- Proteomics in personalized medicine (class discussion)
- Methodology of separation and identification of proteins
- Proteomics data analysis: handling big data and bioinformatics challenges (class discussion)
- The future of proteomics: integrating with other "omics" fields (class discussion)