**Course synopsis**

**BIOC557 - Advanced Topics in Biochemistry - Protein-based Mass Spectrometry**

**1. Introduction:**

This 12 lecture module will teach the basics of protein-based mass spectrometry and introduce a variety of related topics such as deep proteomics, quantitative mass spectrometry (e.g., SILAC), methods to study protein-protein interaction (e.g. AP-MS, BioID, protein correlation profiling), identification of post translation modifications, and structural proteomics (e.g. limited proteolysis, protein cross-linking). This course will consist of introductory lectures, student presentations of selected articles and student presentations of data analysis. Students will be graded based on their presentations (50%), project assignment (25%) and participation (25%). This course will be taught in alternative years in Fall 2020 and 2022.

Instructors:

Dr. Leonard Foster (course chair; foster@msl.ubc.ca)

Dr. Thibault Mayor ([mayor@mail.ubc.ca](mailto:mayor@mail.ubc.ca))

Ms. Abigail Chapman (abbi.a.chapman@gmail.com)

Format: 90-minute lectures (12), 1.5 credits.

Time: Tue/Thu (10:30-12pm) from September 8 to October 15, 2020.

Number of seats: 14

Location: this course will be given online on Zoom.

Zoom ID for Part I (Sep 8 to Sep 17):

Meeting ID: 665 3691 2623

Passcode: 550675

<https://ubc.zoom.us/j/66536912623?pwd=U1U5Yks0UER5UHp5U3dWMnB3aVBYQT09>

Zoom ID for Part II: TBA

**2. Course Overview:**

**Part I - Dr. Thibault Mayor**

Sep 8 - Lecture 1: Introduction to MS & Biochemical Applications

Sep 10 - Lecture 2: Papers 1-2 - Standard vs non tryptic

Sep 15 - Lecture 3: Papers 3-4 - AP-MS vs BioID

Sep 17 - Lecture 4: Papers 5-6 - Structural biology

**Part II - Dr. Leonard Foster**

Sep 22 - Lecture 5: Proteomics in Systems Biology

Sep 24 - Lecture 6: Papers 7-8 - Biomarkers I

Sep 29 - Lecture 7: Papers 9-10 - Biomarkers II

Oct 1 - Lecture 8: Papers 11-12 - Signalling

Oct 6 - Lecture 9: Papers 13-14 - Protein-Protein Interaction Networks

**Part III - Dr. Leonard Foster & Abigail Chapman**

Oct 8 - Lecture 10: Introduction to Data analysis + Tutorial part I

Oct 13 - Lecture 11: Tutorial part II and Q&A

Oct 15 - Lecture 12: Student presentations (teams of 2/3)

**3. Student Paper Presentations:**

Each student will have to present one listed article to the rest of the class. The student is expected to have carefully read the article, including supplementary information and methods, as well as additional articles if required. Presentation should be done on powerpoint or other related software, and should consist of about 15-20 slides. The presentation should include an introduction to provide some background information (typically 2-5 slides) and a conclusion (1-2 slides).  In most cases, the student will have to select a subset of the results to present and should avoid too many figure panels within one slide. Particularly, the student should emphasize the mass spectrometry methods used in the presented article. Discussion during the presentation is encouraged. To do so, students are asked to include a blank slide every 3-4 slides to interrupt their presentation and discuss the presented results. If required the student will have to adapt their presentation to respect the time limit (35 minutes).

Students will select which paper they want to present in a first-come first-served basis in a [shared online form](https://docs.google.com/spreadsheets/d/1diUqtSGQY7FQNFDxP2kBOVuD9Q8vt4cvPO_WfxLaRCI/edit?usp=sharing). Students with experience in mass spectrometry will be strongly encouraged to select a paper in lecture 2. Presentations will be graded by the course instructor (50%) and by peer evaluation (50%). Each student will be required to fill a [peer evaluation form](https://docs.google.com/document/d/1rpPl1dr2Zcm7ySSEBhyPwbMOVpAqZYB0opsJXdwfOLg/edit?usp=sharing) to be sent by email to the course instructor after each presentation (within 24 hours). The course instructor will provide direct feedback to the presenter after the lecture. Grades and (anonymous) peer evaluations will be provided once all presentations are completed.

**4. Final Student Presentation:**

The final presentations will be short (10 min each) and done in teams of 2 to 3. Each team will be responsible for presenting what they did with their data analysis and what their findings were.

**5. Student Participation:**

Students are expected to be present to all classes, unless excused, and participate in each lecture by either asking questions, answering questions raised by the course instructor or sharing their points of view. Following each class, students are required to fill the class [participation sheet](https://docs.google.com/spreadsheets/d/1peGqzocmSHs0cOLM9U416_5bUfNJ2Qf4Peb4JXmC5YE/edit?usp=sharing). 20% for general participation, 5% for coming up with a Zoom background related to mass spectrometry/proteomics.

**6. Lecture Themes & Selected Papers:**

**Lecture 1: Introduction to protein mass spectrometry and some standard biochemical applications.** We will review standard shotgun proteomics, ions and peptide spectra (MS1 and MS2), standard methods to study protein-protein interactions (AP-MS & BioID) and briefly discuss how mass spectrometry can be used for structural analysis (crosslinking & HDX).

**Lecture 2: Standard MS and non-tryptic approaches:**

**The proteome landscape of the kingdoms of life.**

Müller JB, Geyer PE, Colaço AR, Treit PV, Strauss MT, Oroshi M, Doll S, Virreira Winter S, Bader JM, Köhler N, Theis F, Santos A, Mann M.

Nature. 2020 Jun;582(7813):592-596. doi: 10.1038/s41586-020-2402-x. Epub 2020 Jun 17.

PMID: 32555458

**Integrated proteogenomic deep sequencing and analytics accurately identify non-canonical peptides in tumor immunopeptidomes**

Chloe Chong et al.

Nat Commun. 2020 Mar 10;11(1):1293. doi: 10.1038/s41467-020-14968-9.

PMID: 32157095

**Lecture 3: Protein-protein interactions: AP-MS vs BioID**

**A SARS-CoV-2 protein interaction map reveals targets for drug repurposing.**

Gordon DE *et al.*

Nature. 2020 Jul;583(7816):459-468. doi: 10.1038/s41586-020-2286-9. Epub 2020 Apr 30.

PMID: 32353859

**Mapping the mammalian ribosome quality control complex interactome using proximity labeling approaches**

Nathan Zuzow, Arit Ghosh, Marilyn Leonard, Jeffrey Liao, Bing Yang, Eric J Bennett

Mol Biol Cell. 2018 May 15;29(10):1258-1269. doi: 10.1091/mbc.E17-12-0714.

PMID: 29540532

**Lecture 4: Proteomics in structural biology**

**Structural dynamics of the E6AP/UBE3A-E6-p53 enzyme-substrate complex**

Carolin Sailer, Fabian Offensperger, Alexandra Julier, Kai-Michael Kammer, Ryan Walker-Gray, Matthew G Gold, Martin Scheffner, Florian Stengel

Nat Commun. 2018 Oct 25;9(1):4441. doi: 10.1038/s41467-018-06953-0.

PMID: 30361475

**Structural basis of Cullin 2 RING E3 ligase regulation by the COP9 signalosome.**

Faull SV, Lau AMC, Martens C, Ahdash Z, Hansen K, Yebenes H, Schmidt C, Beuron F, Cronin NB, Morris EP, Politis A.

Nat Commun. 2019 Aug 23;10(1):3814. doi: 10.1038/s41467-019-11772-y.

PMID: 31444342

Note: require some background in structural biology

**Lecture 5: Proteomics in systems biology**. We will look at how quantitative and qualitative approaches in proteomics compare, and at how post-translational modifications and large-scale protein interaction networks can be measured by mass spec, as well as how these and other data can be integrated into systems biology analyses

Lecture 6: Biomarker discovery I

Lecture 7: Biomarker discovery II

Lecture 8: Signalling

Lecture 9: Protein interaction networks

**Lecture 10: Tutorial on the use of proteomics software** (Abbi Chapman). Abbi is a 2nd-year BIOC graduate student. She will take us through the practical use of some proteomics software packages to prepare everyone for analyzing their own data. At the end of this class, everyone should be equipped to start the analysis.

**Lecture 11: 2nd Tutorial** (Abbi Chapman). In the second tutorial, any additional demonstrations will be done, as well as a Q&A session for everyone who is in the midst of analyzing data.

**Lecture 12: Student project presentations** (students). Order of presentations will be chosen randomly. Students will be expected to present, in teams of 2 to 3, their results from analyzing a data set.