Proteomics

Autumn 2018 CHEM 8199 MWF, 1:50-2:45 McPherson 1005 Instructor: Amanda B. Hummon hummon.1@osu.edu; 614-688-2580 Office Hours: By Appt (414 Biomedical Research Tower)

Course Description

This course will cover the basic analytical methods that make the study of proteomes feasible. Proteomics is a rapidly moving field and we will touch on historical background as well as discuss current developments. Some of the topics to be covered include: separations, fundamentals of mass spectrometry, protein versus peptide mass spec, imaging mass spectrometry, ion mobility and studying post-translational modifications.

Course Goals:

- 1) Identify challenges in analyzing proteomes (size, complexity, dynamic range, repetitive nature, etc)
- 2) Evaluate the analytical tools used to sequence, annotate and quantify proteins
- 3) Acquire the ability to critically assess the primary literature

Reading

The main course material is the primary literature, with the individual research articles assigned for each lecture indicated in the syllabus. For students wishing to read additional background material, the book *"Introducing Proteomics"* edited by Josip Lovric (Wiley-Blackwell) is suggested. It can be purchased through Amazon.

Course Philosophy

This is a graduate course intended to introduce advanced students to cutting-edge research. Any information covered in the lectures or the readings is fair game for exams. Therefore, attendance in class is strongly encouraged.

Grading: 1000 points Total

400 pts per Exam (400 for Midterm + 400 for Final = 800 pts) 200 pts Critical Report

Exams

There will be 2 non-cumulative, equal-weighted exams in class. Accommodations may be made *only in advance* of missed exams.

Critical Report

Manuscripts will be selected by the students. Paper selections are due to ABH for approval by November 1st. The report should be 2 pgs and be a *critical review* of a recent manuscript. The manuscript can be published in scientific journal and peer-reviewed or it can be from a preprint server.

The <u>goal of this assignment</u> is for you **to evaluate**, **not just accept**, a manuscript and determine if it is of sufficient quality to be published.

<u>Critical reports are due to ABH on Fri, Nov 30th in class.</u>

As you evaluate the primary literature, please consider the following questions:

- 1) What is the hypothesis tested?
- 2) What previous experiments/information provide the background for this work?
- 3) What experimental system(s) have the authors selected to test their hypothesis?
- 4) What results were obtained in the experiments presented? Briefly describe the results that you consider of primary importance in their study.
 - a. Are the experiments scientifically sound?
 - b. Did they include the correct controls? (If not, what should have been included?)
 - c. Are the results correctly interpreted?
- 5) What conclusions do the authors draw from their results?
 - a. Do the conclusions follow logically from the results? If not, what conclusions should have been made?
 - b. Are there any gaps between the experimental results and the conclusions presented?
- 6) Do the results support or disprove the scientific hypothesis?
- 7) Do the results lead to conflict with respect to the current paradigms?
- 8) Do the results provide any insight into the scientific problem under investigation?
- 9) What experiments should be done to clarify any confusion concerning their interpretation or to provide additional support for their hypothesis?
- 10) If you were a reviewer for a journal and this manuscript was submitted, would you accept it as is? Would you suggest revisions? Reject it?

Syllabus (Will evolve during semester)

Lecture	Date	Торіс	Reading*
1	10/15	Separations: Chromatography	Wolters, Anal Chem, 2001 , 73, 5683.
2	10/17	Liquid Chromatography	
3	10/19	Capillary Electrophoresis	Jorgenson, <i>Science</i> 1983 ; 222. 266. Dovichi, <i>Angrew Chem Int Ed</i> , 2000 , 39, 4463.
4	10/22	Ion Mobility	Zheng, Smith, Baker. <i>Curr Opin Chem Biol.</i> 2018 , 42:111-118.
5	10/24	Mass Spectrometry: Ionization Sources	Aebersold & Mann, <i>Nature</i> 422 , 198 (2003). Peng <i>Analyst</i> , 2014 , 139, 3507.
6	10/26	Mass Spectrometry: Ionization and Mass Analyzers	Trimpin, <i>JASMS</i> . 2016 , 27, 4.
7	10/29	Mass Spectrometry: Mass Analyzers	Aebersold & Mann, <i>Nature</i> 422 , 198 (2003).
8	10/31	MS/MS Sequencing	Steen & Mann <i>, Nat Rev</i> 5 , 699 (2004).
9	11/2	MS/MS Sequencing	
10	11/5	Post-translational Modifications	Mann, Nat Biotechnol 2003 , 21, 255.; Cesnik, Journal Proteome Res 2016, 15 (3), 800–8.
11	11/7	Midterm in Class	
12	11/9	Imaging MS	Gessel, J. Proteomics 2014, 107, 71-82.
13	11/14	Top Down versus Bottom Up	Ebhardt, <i>Proteomics</i> 2015 , 15, 3193-3208. Kelleher, <i>Expert Reviews Proteomics</i> 2014 , 11, 649.
14	11/16	Quantifying with Labels	Schulze, AnnuRevPlantBiol. 2010 , 61, 491. Ong, NatChemBio 2005, 1, 252.
15	11/19	Quantifying with Labels	
16	11/26	Quantifying without labels	Picotti and Aebersold, <i>Nature Methods</i> 2012 , 9, 555-566.
17	11/28	Quantifying without labels	
18	11/30	Structural Biology Approaches: FPOP, etc.	Zhang, Cheng, Rempel, Gross. <i>Methods</i> . 2018 . doi: 10.1016/j.ymeth.2018.05.016.
19	12/3	Metabolomics	Gowda and Djukovic. <i>Methods Mol Biol</i> . 2014 ; 1198:3-12.
20	12/5		Final in Class