

Location: Silverman Hall, Northwestern University, 2170 Campus Drive, Evanston, IL, 60208

Course Itinerary:

Monday, June 12th

8:30 – 9 AM	Coffee and Breakfast	Silverman 1510
9 AM – 12:30 PM	Module A, Part 1 (Cell Lysis and GELFrEE)	Silverman 4530
12:30 PM – 1:30 PM	Lunch	Silverman 1510
1:30 PM – 4 PM	Module A, Part 2 (GELFrEE and Cleanup Methods)	Silverman 4530
4 PM – 5 PM	Seminar – Dr. Neil Kelleher “Welcome to Top-Down Proteomics”	Silverman 1510
5 PM	Dinner with Dr. Neil Kelleher in Downtown Evanston	TBD

Tuesday, June 13th

8:30 – 9 AM	Coffee and Breakfast	Silverman 1510
9 AM – 10:30 AM	Seminar – Dr. Rich LeDuc “Experimental Design for Top-Down Proteomics”	Silverman 1510
10:30 AM – 12 PM	Seminar – Dr. Phil Compton “LC and Instrument Methods for Top-Down Proteomics”	Silverman 1510
12 PM -1 PM	Lunch	Silverman 1510
1 PM – 1:15 PM	Course Photo	TBD
1:15 PM - 5 PM	Module B: (LC/MS Setup, QC, and Data Acquisition)	Silverman B550
5 PM	Dinner	TBD

Wednesday, June 14th

8:30 – 9 AM	Coffee and Breakfast	Silverman 1510
9 AM – 10:30 AM	Seminar – Dr. Paul Thomas “Top-Down Proteomics Data Analysis, Part 1: Scoring, Single Proteins, and Simple Protein Mixtures”	Silverman 1510
10:30 AM – 12:30 PM	Module C, Part 1 (ProSight Lite and ProSight PC 4.0)	Silverman 1510
12:30 PM – 1:30 PM	Lunch	Silverman 1510
1:30 PM – 3:30 PM	Module C, Part 2 (Data Analysis Lab) (Optional) (To include analysis of data provided by course participants)	Silverman 1510
3:30 PM	Free time to explore downtown Chicago	

Thursday, June 15th

8:30 – 9 AM	Coffee and Breakfast	Silverman 1510
9 AM – 10:30 AM	Seminar – Mr. Ryan Fellers “Top-Down Proteomics Data Analysis, Part 2: High-throughput analysis (ProSight PC 4.0 and TDPortal)”	Silverman 1510
10:30 AM – 12:30 PM	Module D, Part 1 (ProSight PC 4.0 and TDPortal)	Silverman 1510
12:30 PM – 1:30 PM	Lunch	Silverman 1510
1:30 PM – 2:30 PM	Module D, Part 2 (Data Analysis Lab)	Silverman 1510
2:30 PM – 3 PM	Wrap-up and Final Questions	Silverman 1510
3 PM	End of Course	

Module A: Sample Preparation for Top-Down Proteomics

Instructors: Dr. Caroline DeHart and Mr. Timothy Toby

Topics Covered:

- Protein extraction and quantitation from biological samples
- MW-based separation of human whole-cell lysate by GELFrEE
- Special considerations and advanced methods for clinical sample preparation
- Methods to concentrate and desalt intact protein samples prior to LC/MS analysis

Module B: LC/MS Setup, Quality Control, and Data Acquisition for Top-Down Proteomics

Instructors: Dr. Philip Compton and Dr. Kristina Szrentić

Topics Covered:

- LC valve configurations and conditioning protocols for Dionex monolithic columns
- MS calibration and LC/MS method design for top-down proteomics
- Pierce Intact Protein Standard as a quality control metric for LC/MS performance

Module C: Software and Workflows for Analysis of Simple Top-Down Proteomics Data

Instructors: Dr. Paul Thomas and Mr. Joseph Greer

Topics Covered:

- Analysis of top-down MS data with ProSight Lite and ProSight PC 4.0
- Analysis of example data from the NRTDP Top-Down Standard and Pierce Intact Protein Standard
- Analysis of real-world experimental data

Module D: Software and Workflows for Analysis of High-Throughput Top-Down Proteomics Data

Instructors: Mr. Ryan Fellers and Ms. AJ VanNispen

Topics Covered:

- Analysis of high-throughput top-down proteomics data with ProSight PC 4.0, TDPortal, and TDViewer
- Analysis of example data from a well-characterized experimental dataset
- Analysis of real-world experimental data

1st Seminar: “Welcome to Top-Down Proteomics”

Presenter: Dr. Neil Kelleher

Topics Covered:

- Introduction to the field and basic principles of top-down proteomics
- Recent advances in top-down proteomics research
- Value proposition for proteoform-resolved measurements in cellular and disease biology

2nd Seminar: “Experimental Design for Top-Down Proteomics”

Presenter: Dr. Rich LeDuc

Topics Covered:

- Definitions and goals for qualitative and quantitative (label-free) top-down proteomics experiments
- Statistical considerations for a successful top-down proteomics study
- False discovery rates, data normalization, and statistical analysis for top-down proteomics data

3rd Seminar: “LC and Instrument Methods for Top-Down Proteomics”

Presenter: Dr. Phil Compton

Topics Covered:

- Strategies for chromatographic resolution of intact proteins within simple or complex mixtures
- Instrument method design for mass determination (MS1) and characterization (MS2) of intact proteins
- LC/MS strategies for targeting higher-MW proteins and increasing proteome and/or PTM coverage

4th Seminar: “Top-Down Proteomics Data Analysis, Part 1: Scoring, Single Proteins, and Simple Protein Mixtures”

Presenter: Dr. Paul Thomas

Topics Covered:

- Identity and derivation of additional scoring metrics (p -score, E-value, C-score) in top-down proteomics
- Analysis of simple protein mixtures with Xtract and ProSight Lite
- Analysis of simple protein mixtures and generation of search databases in ProSight PC 4.0

5th Seminar: “Top-Down Proteomics Data Analysis, Part 2: High-throughput analysis (ProSight PC 4.0, ProSight PD, and TDPortal)”

Presenter: Mr. Ryan Fellers

Topics Covered:

- Analysis of complex protein mixtures with ProSight PC 4.0
- Analysis of different data types (low, medium, and high-resolution) with ProSight PD 2.1
- Analysis of large and/or complex datasets with TDPortal and TDViewer