

**ONE-DAY COURSE, Sunday only**  
**20 Top-down Proteomics**

**Instructors**



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Top-down mass spectrometry (MS)-based proteomics is arguably a disruptive technology for the comprehensive characterization of proteoforms by providing a “bird’s eye” view of all proteoforms to decipher the post-translational modification codes together with genetic variations that regulate cellular signaling in healthy and diseased states. In the recent years, significant strides have been made to advance top-down MS and bring it to the mainstream in a way that is accessible to the scientific community. As a result, interest in top-down MS has grown considerably with numerous studies demonstrating the potential of top-down proteomics for the unraveling of disease mechanisms and discovery of new biomarkers. Recently, the burgeoning top-down proteomics field has gained momentum through the creation of the Consortium for Top-down Proteomics (<http://www.topdownproteomics.org/>). CTDP provides the fostering ground for education, collaboration and technology development to further advance top-down proteomics towards comprehensive analysis of proteoforms and to realize its impact in biomedical research and pharmaceutical industry.

Each tutorial lecture will be aimed at beginners/newcomers to the top-down proteomics field, and will conclude with a dynamic moderated discussion/quiz session.

**Topics:**

- 1) Introduction
  - a) History of top-down proteomics
  - b) Concept of proteoforms
  - c) Measurement of Proteoforms and their complexes
  - d) Denatured vs. native mode
- 2) Sample preparation
- 3) Intact protein separation
- 4) Instrumentation, activation and dissociation methods for top-down MS
- 5) Comparison of bottom-up and top-down – pros and cons
- 6) Data interpretation and software tools for top-down proteomics
- 7) Top-down quantitative proteomics – including experimental design
- 8) Biomedical and biopharmaceutical applications of top-down MS
- 9) Future outlook

**Prerequisites:** Basic knowledge of mass spectrometry, including familiarity with ESI and mass analyzers, basic knowledge of protein structure