**One-Day Course, Saturday Only**
Top-down Proteomics

People attending this course might also be interested in attending Mass Spectrometry Data Analysis and Visualization, so we bundled these two one-day courses as a two-day course (there is a cost savings in purchasing one two-day course versus two one-day courses). The bundled two-day course is listed as *Top-Down Proteomics AND Mass Spectrometry Data Analysis and Visualization* under the two-day course section.

Instructors
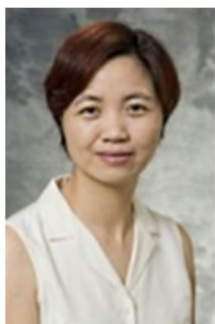
Ying Ge
University of
Wisconsin, Madison

Joseph Loo
University of
California,
Los Angeles

Neil Kelleher
Northwestern
University

Ljiljana Pasa-Tolic
Pacific Northwest
National Laboratory

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