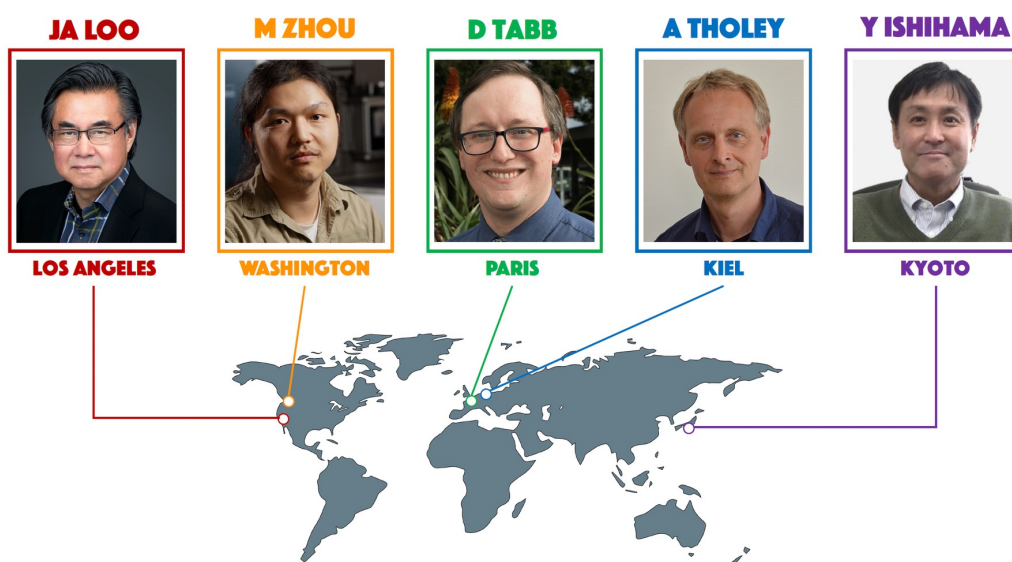


# August 7, 2022 JPrOS Pre-Congress Webinar

English Japanese

JPrOS 2022 Annual Meeting – 20th Anniversary Project –  
at 9:30 PM JST / 2:30 PM CEST / 5:30 AM PDT

## Top-Down Proteomics



### Speakers

**Joseph A. Loo**  
(University of California, Los Angeles, U.S.A.)

**Mowei Zhou**  
(Pacific Northwest National Laboratory, U.S.A.)

**David Tabb**  
(Pasteur Institute, France)

**Andreas Tholey**  
(Christian-Albrechts-Universität zu Kiel, Germany)

**Yasushi Ishihama**  
(Kyoto University, Japan)

### About the Webinar

**Nobuaki Takemori, organizer**  
(Ehime University, Japan)

Top-down proteomics, which enables large-scale analysis of proteoforms, is rapidly attracting interest among researchers in various life science fields. In this webinar, world-leading researchers in top-down proteomics and proteoform research will introduce their latest findings and discuss how top-down proteomics will be promoted in Japan.



#### What is proteoform analysis? Can't bottom-up proteomics alone be used for analysis?



**Dr. Ishihama (Kyoto University)** will introduce proteoform research from the perspective of bottom-up proteomics and explain the importance of top-down proteomics in comprehensive proteoform analysis.

#### What technologies are needed to conduct top-down proteomics studies?

**Dr. Tholey (CAU)** will explain state-of-the-art mass spectrometry and intact protein separation techniques that enable top-down proteomics and present examples of in-depth proteoform analysis using top-down proteomics techniques.



#### How are proteoforms identified from top-down mass spectrometry data?



**Dr. Tabb (Pasteur Institute)** will introduce the principles of and required resources for top-down MS data analysis and will present examples of actual data analysis and explain how proteoforms are identified in an easy-to-understand manner.

#### What about analysis of entire protein complexes?

Top-down proteomics can even be combined with native mass spectrometry to analyze the entire structure of a protein complex. **Dr. Zhou (PNNL)** will present the principles of this newest technique, called native top-down proteomics, and its application to plant research.



#### What are the future prospects for this new and powerful proteomics research in the field of medicine?



Attempts to use top-down proteomics for human disease research have also begun. **Dr. Loo (UCLA)**, a pioneer in this field, will tell us what top-down proteomics research has accomplished so far and what challenges lie ahead.

### Time Table

Time (JST)	Speaker	Title
21:30	<b>Nobuaki Takemori</b> Ehime Univ	Opening Remarks
21:40	<b>Yasushi Ishihama</b> Kyoto Univ	Protein terminome-centric proteoform analysis – is a xeel train ride really a good deal?
22:05	<b>Andreas Tholey</b> CAU	Top-down proteomics: an (exciting) challenge for bioanalytical chemistry!
22:30	<b>David Tabb</b> Pasteur Institute	Identifying proteoforms from top-down MS/MS: is one search enough?
22:55	<b>Mowei Zhou</b> PNNL	Dissecting unknown and heterogenous plant proteins by native top-down mass spectrometry
23:20	<b>Joseph A Loo</b> UCLA	Applying native top-down mass spectrometry in structural biology and neurodegenerative disease research