UNIVERSITY OF OREGON

Physical Chemistry Seminar Series

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Chemistry & Biochemistry

November 12, 2018 ~ 2:00-3:00 Klamath Hall 331

Tandem-trapped ion mobility spectromerty / mass spectrometry for structural biology applications

Differentially modified proteins (proteoforms) can differ significantly in their biological activity. Proteoforms originate from the same gene, but differ in their amino acid sequences and/or post-translational modifications. Because activity of a protein is intimately linked to its structural heterogeneity, a key question is thus how sequence variations and post-translational modifications of a protein influence its structural heterogeneity.

This contribution will discuss progress made in my lab towards experimental and computational ion mobility spectrometry – mass spectrometry methods. Specifically, we will discuss our newly-developed tandem-trapped ion mobility spectrometry – mass spectrometry (TIMS/TIMS-MS) instrument and its ability to characterize structure and sequence of proteins and protein complexes. We describe computational methods to quantitatively predict ion mobility spectra and how these methods are used to reveal which aspects of the native structure of a protein are retained in the gas phase. Case studies include the proteins ubiquitin, alpha-synuclein, CCL5/RANTES, and the tetrameric protein complex avidin.

Refreshments served at 1:45 pm, 331 Klamath Hall

Hosted by Jim Prell