



Contribution ID: 21

Type: **Invited**

X-ray footprinting of proteins: using hydroxyl radical damage to infer structural conformation

Wednesday, 14 October 2020 16:40 (20 minutes)

The method of X-ray footprinting mass spectrometry (XFMS) is used to investigate structural features and conformational changes of macromolecules in the solution state. XFMS is an in situ hydroxyl radical ($\bullet\text{OH}$) labeling method; X-ray irradiation dissociates solvent water to produce hydroxyl radicals, which covalently modify side chains which are solvent accessible. More specifically, residues which are in proximity to water molecules (either bulk or bound) are modified to a greater extent than residues which are not in proximity to water. Because liquid chromatography-mass spectrometry is then used to analyze the stable covalent modifications produced, the data provide a “water map” at the single residue level, which is then used to determine sample conformation. In this talk, I will describe the XFMS method, its advantages and disadvantages relative to other methods, some recent examples of structural information obtained on protein systems using the method, and some recent instrumentation advances and plans for future improvements to the method.

Primary author: RALSTON, Corie (Lawrence Berkeley National Laboratory)

Presenter: RALSTON, Corie (Lawrence Berkeley National Laboratory)

Session Classification: Session 1 - Biological Studies Affected by Radiation Damage