



## **Chemistry and Cultural Heritage: Deciphering Natural Polymers by Bottom up and Top down Mass Spectrometry Analysis**

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The study of organic biomolecules in Cultural Heritage is key to deciphering ancient materials in order to reveal new historical insights or help in preservation issues. Mass spectrometry-based techniques, such as proteomics has become the mainstream method but it remains challenging due to the limited sample amount available for analysis, the complexity of the composite material and its degradation state. This presentation will describe the currently most robust and sensitive methods to analyze trace amounts of proteins, lipids and polysaccharides from artworks and archaeological objects and their main achievements; i.e. accurate identification, identification of biological origins, identification of chemical modifications related to ageing or reaction with other components within the sample or external.

This presentation will also show how the top down methodology addresses the current challenges, such as structural elucidation of biopolymers with unknown structures and/or their chemical modifications (e.g. historic art paintings, watercolors, archaeological ceramics). For example, protein lactosylation, a Maillard reaction signaling the potential heating processing of milk was identified in 1st century nursing bottles. Another example is the combination of soft depolymerization experiments and high resolution mass spectrometry to unravel the 3D networks formed by insoluble lipidic films (e.g. historic oil-paintings). First analytical evidence of protein crosslinkings in historic artworks will be also presented (e.g. tempera, painted leather).

Finally, the combination of the omics approaches with DNA analysis or with immuno-based techniques will be introduced. In particular epitope mapping using proteomics for a better understanding of ELISA detection in artworks will be presented. Another example dealing with proteins from non-sequenced species will show the importance to pair DNA and proteomics analysis. These examples will be illustrated by various cases of study from the Metropolitan Museum of Art collection.