



## **Unleashing top-down mass spectrometry in study of proteinaceous materials in museum objects: Method development using paint models**

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Proteinaceous material has been extensively used by the art community for centuries as paint binders, adhesives, and varnishes. Study of these materials can give new insight into the artists' techniques (e.g. choice of materials, provenance), as well as both guide future conservation efforts and demonstrate the current state of preservation. The most common proteomics approach to the identification of protein compounds has been bottom-up proteomics, a technique where proteins are extracted from a sample and are digested into peptides using enzymes. This digestion step can often lead to loss of labile protein modifications, which in turn limits the information that these modifications can provide. We present here the direct study of intact proteins using top-down analysis, to access new valuable information on the degradation mechanisms of the organic media (e.g. protein breakdown) and protein chemical modifications such as oxidation, deamidation etc. (i.e. impact of restoration procedures and conservation conditions at molecular level).

A top-down mass spectrometry method has been developed and applied to the study of paint mock-ups based on egg protein binders. To achieve minimal invasiveness, the method had to be optimised for optimal sample extraction with minimal number of steps. Furthermore, separation and tandem mass spectrometry experiments settings had to be adapted to achieve improved sensitivity and optimal fragmentation in order to extract maximal information. Experimental details will be given during the presentation and first results on paint mock up from various composition will be discussed. In particular, the high degree of protein chemical heterogeneity will be shown and argued.