



***Ph.D. School in Chemical Sciences
Cycle XXXVIII***

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Research project title: Development of high throughput methodologies for the analysis of proteins post-translational modifications in complex matrices

Key words: Glycosylation, phosphorylation, mass spectrometry, proteins, natural matrices

Research project abstract: The analysis of post-translational modifications (PTMs) of proteins in natural matrices is an area of ongoing development due to the various connections between PTMs and the macroscopic properties of the matrices themselves. Numerous factors complicate this characterisation, as many of them are in sub-stoichiometric quantities (e.g. phosphorylation) and lead to huge molecular heterogeneity (e.g. glycosylation). A further aspect that complicates the extensive characterisation of PTMs is the complexity of the natural matrix (due to the co-presence of molecules with different chemical-physical properties) in which they are present. The aim of this project is to develop a sensitive and reproducible analytical platform, based on state-of-the-art biomolecular mass spectrometry methodologies, for the detailed analysis of PTMs in natural matrices. In recent years, the development of these methodologies allowed to achieve a considerable speed of analysis without compromising the quality of the results produced. In this scenario the application of the developed methodologies to characterize proteins PTMs in different complex matrices (vegetal and animal origin of biological and food interest), represent a promising application field