

## **All round description of the human parasite Giardia by mass spectrometry**

Serena Camerini

Mass spectrometry is a powerful and versatile instrumental technique applicable to a variety of inorganic, organic, and biological molecules. When applied to proteins, it can uncover a large number of features, ranging from protein identification, also in complex mixtures, and study of protein-protein interactions to characterization of post-translational modifications (PTMs) and adduct formation.

To illustrate the power and flexibility of protein mass spectrometry, we have chosen the studies conducted in our laboratory on the human parasite *Giardia duodenalis*, from a small to a large scale. We will start from the particular description of a single *Giardia* protein, (g14-3-3), its characterization in terms of peculiar PTMs and interactions with other proteins, getting to the comprehension of its role in the *Giardia* life cycle and infection capacity. Expanding further the view on this parasite, we will present the characterization of the proteome secreted by *Giardia* inside particles (exosomes and microparticles) or as secretoma. Then we will move to the study of new drugs against *Giardia* and the identification on protein drug targets. Lastly, the sequence of a virus infecting the parasite will close this presentation, which intends to illustrate how mass spectrometry can be applied to obtain an all round description of the human parasite *Giardia* and, more generally, provide a plethora of information that cannot be directly obtained with other techniques, without any preliminary hypothesis.