

**Master 2 internship project
Year 2020-2021**

Laboratory/Institute: Institute of Structural Biology (IBS) **Director:** Winfried Weissenhorn
Team: Viral and cancer group, Mass spectrometry laboratory **Head of the team:** Carlo Petosa

Name and status of the scientist in charge of the project: Elisabetta Boeri Erba, **HDR: yes**
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Program of the Master's degree in Biology:

Integrative Structural Biology

Title of the project:

Mass spectrometry-based sequencing of soluble and membrane proteins

Objectives (up to 3 lines):

This project aims to compare two different mass spectrometers used to perform sequencing of soluble and membrane proteins (see below).

Abstract (up to 10 lines): The primary sequence and post-translational modifications (PTMs) of proteins influence their structure and function, tuning their actions in key cellular processes. The IBS MS laboratory aims to characterise proteins and their PTMs using mass spectrometry (MS). MS can assess the mass of biomolecules with high accuracy, sensitivity and rapidity. In the lab there are two mass spectrometers which allow the student to sequence intact proteins and to determine type, number and position of their PTMs.

Methods (up to 3 lines):

The student will use a Matrix Assisted Laser Desorption Ionisation (MALDI) time-of-flight (TOF)/TOF, and an electrospray-orbitrap to sequence soluble and membrane proteins. She/he will assess the performances of the two different instruments in terms of sensitivity, resolution, m/z range and sequence coverage.

Up to 3 relevant publications of the team:

Boeri Erba E, Signor L, Petosa C. Exploring the structure and dynamics of macromolecular complexes by native mass spectrometry. *J Proteomics*. 2020 Apr 29;222:103799. doi: 10.1016/j.jprot.2020.103799

Puglisi R, Boeri Erba E, Pastore A. A Guide to Native Mass Spectrometry to determine complex interactomes of molecular machines. *FEBS J*. 2020 Mar 6. doi: 10.1111/febs.15281

Signor L, Boeri Erba E. Matrix-assisted laser desorption/ionization time of flight (MALDI-TOF) mass spectrometric analysis of intact proteins larger than 100 kDa. *J Vis Exp*. 2013 Sep 9;(79). doi: 10.3791/50635.

Requested domains of expertise (up to 5 keywords):

Structural biology and biochemistry