

**M1-Molecular and Cellular Biology (MCB)  
Internship Proposal Form  
Chemistry-Biology Department**

**Laboratory Address and Affiliation:**

Institute of Structural Biology (IBS), Mass spectrometry laboratory, 71 Avenue des Martyrs, 38044 Grenoble cedex 9

**Laboratory/Team Research area (Keyword)**

Mass spectrometry, intact biomolecules, macro molecular complexes, protein primary sequence and posttranslational modifications

**Summary of the Proposed Internship Project (10 lines)**

**Mass spectrometry-based sequencing of proteins using MALDI- and ESI-instruments**

**DESCRIPTION:**

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. We have two mass spectrometers, which allow us to sequence intact proteins and to determine type, number and position of their PTMs using the so called “top-down approach”.

**Methodologies and/or Techniques to be used**

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

**Person to contact:**

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**Additional information**

Boeri Erba E et al. Exploring the structure and dynamics of macromolecular complexes by native mass spectrometry; Journal of Proteomics. 2020. doi: 10.1016/j.jprot.2020.103799  
Boeri Erba E et al. Characterizing Intact Macromolecular Complexes Using Native Mass Spectrometry. Methods Mol Biol. 2018;1764:133-151. doi: 10.1007/978-1-4939-7759-8\_9  
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