



**Master Ingénierie pour la Santé (IS)**  
**Spécialité : Chimie Médicinale et Innovation**  
**Pharmacologique (CHIP)**  
**Proposition de stage Janvier 2019 – Juin 2019**

**Directeur du laboratoire d'accueil:** Winfried Weissenhorn, Institute of Structural Biology (IBS), **Adresse:** 71 Avenue des Martyrs, 38044 Grenoble cedex 9

• **Intitulé de l'équipe :** Mass spectrometry laboratory

**Responsable de l'équipe:** Elisabetta Boeri Erba

• **Responsable de stage: Nom:** Boeri Erba, **Prénom :** Elisabetta, **HDR :** non X□

**Email:** elisabetta.boeri-erba@ibs.fr

**TITRE du travail de stage:** Mass spectrometry-based sequencing of proteins using a MALDI-TOF/TOF instrument

**DESCRIPTIF:**

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 acquired a new mass spectrometer, which allows us to sequence intact proteins and to determine type, number and position of their PTMs using the so-called "top-down approach".

First, the student will work on test proteins such as bovin serum albumin to optimise sample preparation. Then, she/he will analyse monoclonal antibodies (Ab) that represent emerging biotherapeutics in the case of inflammatory disease and cancer. The student will assess 1) Ab mass heterogeneity and primary amino acid sequence variants, 2) assignment of disulphate and 3) characterization of glycosylation. The project should appeal to students with a background in chemistry/ biology/ pharmacy, who are interested in MS and its application to answer biological questions.

**Méthodes utilisées :** Using a Matrix Assisted Laser Desorption Ionisation (MALDI) time-of-flight (TOF)/TOF, the student will optimise sample preparation conditions to sequence proteins and localise their PTMs. She/he will assess different types of matrices, sample deposition and matrix crystallisation. She/he tests distinct types and concentration of samples (both soluble and membrane proteins) and laser intensity. Overall, she/he will aim to maximise mass resolution, accuracy, sensitivity and sequence coverage.

**Additional information**

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

Boeri Erba E, Petosa C. The emerging role of native mass spectrometry in characterizing the structure and dynamics of macromolecular complexes. *Protein Sci.* 2015 Aug;24(8):1176-92. doi: 10.1002/pro.2661

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

**Keywords** Mass spectrometry, intact biomolecules, macromolecular complexes, protein primary sequence, post-translational modifications, antibodies