

# Internship project Master 2 Year 2018-2019

Laboratory/Institute: Institute of Structural Biology (IBS) Director: Winfried Weissenhorn Team: Mass spectrometry laboratory Head of the team: Elisabetta Boeri Erba

Name and status of the scientist in charge of the project: Elisabetta Boeri ErbaHDR: noAddress: 71 Avenue des Martyrs, 38044 Grenoble cedex 9e-mail: elisabetta.boeri-erba@ibs.frHDR: no

# Program of the Master's degree in Biology:

□ Neurosciences and Neurobiology X□ Integrative Structural Biology □ Immunology, Microbiology, Infectious Diseases

 $\hfill\square$  Physiology, Epigenetics, Differentiation, Cancer

# Title of the project:

# Mass spectrometry-based sequencing of proteins using a MALDI-TOF/TOF instrument

## Objectives (up to 3 lines):

This project aims to set up the use of a novel mass spectrometer to perform sequencing of proteins and their "top-down" investigation (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. We obtain funding to acquire 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".

#### Methods (up to 3 lines):

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.

#### Up to 3 relevant publications of the team:

Boeri Erba E. Investigating macromolecular complexes using top-down mass spectrometry. Proteomics. 2014 May;14(10):1259-70. doi: 10.1002/pmic.201300333 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, biochemistry, mass spectrometry