

INTERNSHIP PROPOSAL

Institute and Group: IBS, Viral Infection and Cancer group

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Research project title: Mass spectrometry-based sequencing of proteins using a MALDI-TOF/TOF instrument

Keywords: mass spectrometry (MS), Matrix Assisted Laser Desorption Ionisation (MALDI), sequencing, post-translational modifications (PTMs)

Description of the project

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 team 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 2017 we plan 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”.

Aims and recommended background

This project aims to set up the use of novel mass spectrometer to perform top-down investigation of proteins. It should appeal to students with a background in nanoscience or physics, who are interested in biological applications.

Experimental techniques

Using a 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.

Relevant publications of the team:

1. **Boeri Erba E**, Klein PA, Signor L.

Combining a NHS ester and glutaraldehyde improves crosslinking prior to MALDI MS analysis of intact protein complexes. *J Mass Spectrom.* 2015, 50(10):1114-9. doi: 10.1002/jms.3626

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

3. 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, (79). doi: 10.3791/50635