Master 2 research internship in Integrated Structural & Cell Biology in Grenoble

Supervisor(s):
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Host laboratory:
IBS, EPIGEN group
https://www.ibs.fr/spip.php?lang=en

Title of the M2 research internship:
Sequencing soluble and membrane proteins using mass spectrometry

Project summary:
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 characterises soluble and membrane proteins and their PTMs using mass spectrometry (MS). MS can assess the mass of biomolecules with high accuracy, sensitivity and rapidity. One of our mass spectrometers allows us to sequence intact proteins. Sequencing shed light on identity, sequences [e.g., loss of first amino acid (often a Met), annotation errors, mutations], identity, truncations, PTMs, and key structural knowledge (such as position of disulfide bridges to distinguish conformational isomers of a protein). To our knowledge, many purified proteins do not have the theoretical mass calculated from the amino acid sequences.
The student will analyse interesting samples (both soluble and membrane proteins) purified in collaboration with our colleagues at the IBS, LPCV (Laboratoire de physiologie cellulaire végétale) and Grenoble-Institut des neurosciences (GIN). Using a MALDI time-of-flight (TOF)/TOF, the student will optimise sample preparation conditions to sequence these proteins. She/he will assess different types of matrices, sample deposition and matrix crystallisation. She/he tests distinct types and concentration of samples and laser intensity. The student will aim to maximise mass resolution, accuracy, sensitivity and sequence coverage.
Overall, this project aims to enhance our MS-based ability of sequencing soluble and membrane proteins. It should appeal to students with a background in biology, nanoscience or physics, who are interested in innovative approaches.

Keywords:
mass spectrometry, sequencing, soluble and membrane proteins

Relevant publications of the team:
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

Boeri Erba E. et al. Characterizing Intact Macromolecular Complexes Using Native Mass Spectrometry. Methods Mol Biol 2018, 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, (79). doi: 10.3791/50635