

Fiche de proposition de stage de L3 et M1 UFR Chimie et Biologie

Cochez la spécialité correspondant à ce stage:

M1C

L3C L3CB

Adresse et appartenance du laboratoire :

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

Thématique générale du laboratoire ou du groupe de recherche (par mots clés)

Mass spectrometry, intact biomolecules, protein primary sequence and post-translational modifications

Thème du stage proposé (en 10 lignes, si possible)

TITRE: 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 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".

Méthodologies et/ou techniques qui seront utilisées

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.

Personne à contacter:

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Complément d'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