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CBM - UPR4301

Center for Molecular Biophysics

MASS SPECTROMETRY FACILITY

The Mass Spectrometry and Proteomics facility handles high resolution UHR-QTOF, MALDI-TOF/TOF and nanoLC-MS/MS analyses.

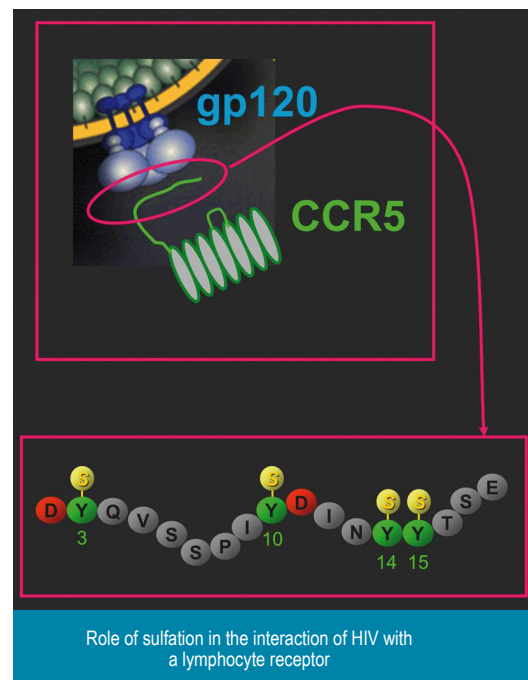
These services are open to research communities both public (state organizations, academia) and private at the local, national and international level.

The facility specializes in the analysis of biomolecules (whole proteins, peptides, oligonucleotides, glycans, lipids, and small organic molecules) in pure form or directly from complex mixtures.

Analyses can be performed with the aim to:

- Monitor the quality of a product obtained by organic synthesis, by purification from cells or tissues, or by biotech engineering
- Determine the exact molecular formula of a compound
- Identify unknown molecules (metabolites, impurities...)
- Identify and localize post-translational or artificial modifications of proteins
- Identify and de novo sequence proteins (proteomics).

The research team associated with the facility has collaborations in the fields of membrane protein characterization and protein-ligand interactions.



Contacts

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Experimental facilities

3 mass spectrometers:

- 1 MALDI-TOF/TOF UltraFlex I (Bruker),
- 1 HCT Ultra-ETD Ion Trap (Bruker),
- 1 UHR-Q-TOF MaXis-ETD (Bruker) shared within the FR2708 federation.

These spectrometers can be coupled to one of 3 types of liquid chromatography :

CapLC (Waters),
 UHPLC U3000 and nanoUHPLC U3000 (Dionex).

Keywords : mass spectrometry, high resolution, nanoUHPLC-MS/MS, proteomics, structural characterization, interactions, biomolecules.

High Resolution Mass Spectrometry for antibody characterization

