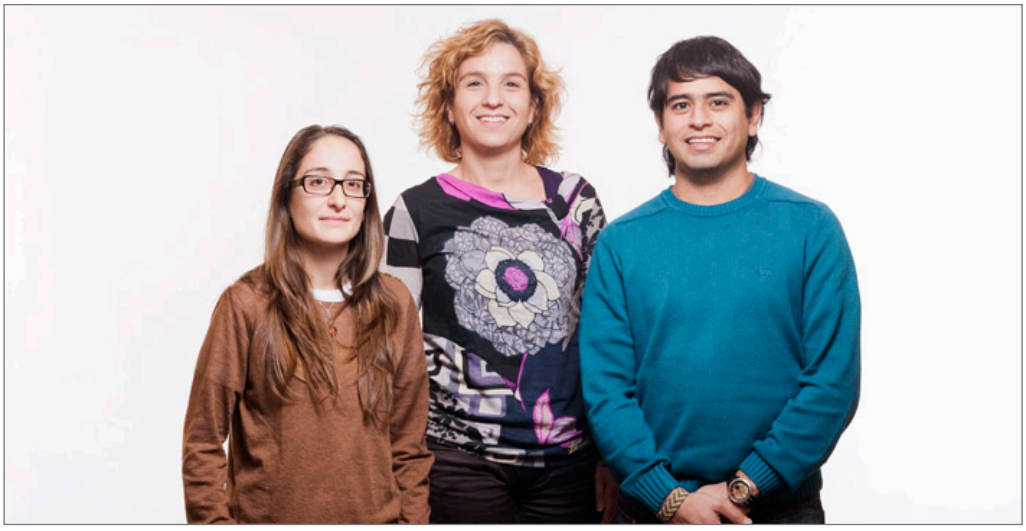
Core Facilities

Marta Vilaseca: Mass Spectrometry



Group Members

Core Facility Manager

Marta Vilaseca

Research Officers

Claudio Diema
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Highlights

- Characterization of intact proteins by top-down MS methodology is being performed in our LTQ-FT mass spectrometer. Histone 1 in *Droshophila melanogaster* has been extensively studied to provide an accurate map of its PTMs. Proteins up to 80 kDa have been analyzed by top-down or middle-down MS to determine their binding sites to covalent inhibitors or to determine catalytic mechanisms in the case of enzymes.
- β-amyloid protein oligomers and other non-covalent protein-protein and protein-ligand complexes have been studied by ion-mobility MS in our Synapt HDMS system in order to reveal structural data.
- Progress in phosphoprotein and phosphopeptide analysis has been made in collaboration with the PCB proteomics platform. Improvements of enrichment techniques and mass spectrometric methodologies have been made.

Services offered during 2010

- The services offered include MS, MS/MS and IM-MS analysis of biomolecules using atmospheric pressure ionization techniques (nanoelectrospray and electrospray) coupled to LC, nanoLC or infusion inlets.
- The Facility provides consultancy services and analytical method development for specific applications.
- Samples are analyzed either directly by the service or by researchers (previously trained by Facility members), who can use mass spectrometers through an open-access system.

Publications

- Dyachenko A, Goldflam M, Vilaseca M and Giralt E. Molecular recognition at protein surface in solution and gas phase: Five VEGF peptidic ligands show inverse affinity when studied by NMR and CID-MS. Biopolymers, 94 (6), 689-700 (2010)
- Ferrer M, Pedrosa A, Rodríguez L, Rossell O and Vilaseca M. New insights into the factors that govern the square/triangle equilibria of Pd(II) and Pt(II) supramolecules. Unexpected participation of a mononuclear species in the equilibrium. Inorg Chem, 49 (20), 9438-49 (2010)

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