

Hands-On Course on Protein Identification by Mass Spectrometry

Bring your own samples!!!

2nd - 4th November 2011

**Organized by Mass Spectrometry Laboratory
ITQB-UNL/IBET**



"During the past two decades, mass spectrometry (MS) has become established as the primary method for protein identification from complex mixtures of biological origin. This is largely attributable to the fortunate coincidence of instrumental advances that allow routine analysis of minute amounts of involatile, polar compounds such as peptides in complex mixtures, with the rapid growth in genomic databases that are amenable to searching with MS data. Like many other developing fields in science, the creation of techniques and software tools and the initial generation and interpretation of data have been the domain of experts, people who are cognizant not only of the benefits of the methods but also of their actual and potential weaknesses. Now, as MS techniques and proteomic tools become increasingly available and accessible, a much broader range of researchers is applying the same methodology, often with substantially less understanding of the major limitations that critically affect the reliability and significance of the results."

M A Baldwin *Molecular & Cellular Proteomics* 3:1-9, 2004

This Hands-On Training Course, to be held at ITQB-UNL, is dedicated to researchers using or planning to use mass spectrometry methodologies for protein identification. Participants will have the opportunity to bring their own samples for protein identification.

Main objectives

- to give practical insight into the mostly used MS strategies for protein identification
- to provide hands-on experience on crucial areas, sample preparation and data evaluation
- to present major methods advantages and limitations
- to supply information on the preparation of protein identification data for publication

Course Schedule

Wednesday, 2nd November

Program

8H30	Registration
9:00-9:45	<u>Seminar:</u> Protein identification and characterization using MS data: a general overview Ana V Coelho (ITQB) <i>Room 2.13</i>
9:45-10:30	<u>Seminar:</u> Fundamentals on Soft Ionization and MS Instrumentation Catarina Franco (ITQB) <i>Room 2.13</i>
10:30-11:00	Coffee break
11:00-11:50	<u>Seminar:</u> New mass analysers and their applications Michaela Scigelova (Thermo/ABSciex) <i>Auditorium</i>
12:00-13:00	<u>Seminar:</u> LC-ESI-MS/MS and MALDI-TOF-TOF data acquisition, processing and database search Renata Soares (ITQB) <i>Room 2.13</i>
13:00-14:00	Lunch
14:00-18:30	<u>Hands-on Protein digestion</u> Luis Domingos (ITQB), Miguel Ventosa (ITQB), Filipa Blasco (ITQB), André Almeida (IICT, ITQB) <i>Teaching Lab</i>

Thursday, 3th November

Program

9:00-9:45	<u>Hands-on Protein digestion (Conclusion)</u> Luis Domingos (ITQB), Miguel Ventosa (ITQB), Filipa Blasco (ITQB), André Almeida (IICT, ITQB) <i>Teaching Lab</i>
9:45-13:00 GROUP A	LC-ESI-MS/MS data acquisition Kamila Koci (ITQB) MALDI-TOF-TOF data acquisition Elisabete Pires (ITQB) NanoLC separation and spotting Guenes Barka (Sunchrom) <i>Lab MS</i>
9:45-13:00 GROUP B	<u>Supervised training</u> Data processing and database search <i>De novo</i> sequencing Renata Soares (ITQB) and Miguel Ventosa (IBET) <i>Bioinformatic Room at IGC</i>
13:00-14:00	Lunch
14:00-14:45	<u>Seminar:</u> protein identification data for publication Ana V Coelho (ITQB) <i>Room 2.13</i>
14:45-18:00 GROUP B	LC-ESI-MS/MS data acquisition Kamila Koci (ITQB) MALDI-TOF-TOF data acquisition Elisabete Pires (ITQB) NanoLC separation and spotting Guenes Barka (Sunchrom) <i>Lab MS</i>
14:45-18:00 GROUP A	<u>Supervised training</u> Data processing and database search <i>De novo</i> sequencing Renata Soares (ITQB) and Miguel Ventosa (IBET) <i>Bioinformatic Room at IGC</i>

Friday, 4th November

Program

9:00-11:00 Grupo A	<u>Supervised training</u> Identificação das proteínas Elisabete Pires (ITQB), Miguel Ventosa (ITQB) <i>Lab MS</i>
9:00-11:00 Grupo B	<u>Supervised training</u> Preparing data for publication Ana V Coelho (ITQB) e Isabel Marcelino (IBET) <i>Bioinformatic Room at IGC</i>
11:00-11:15	Coffee break
11:15-13:15 Grupo B	<u>Supervised training</u> Identificação das proteínas Elisabete Pires (ITQB), Miguel Ventosa (ITQB) <i>Lab MS</i>
11:15-13:15 Grupo A	<u>Supervised training</u> Preparing data for publication Ana V Coelho (ITQB) e Isabel Marcelino (IBET) <i>Bioinformatic Room at IGC</i>
13:15-14:30	Lunch
14:30-15:30	<u>Seminar:</u> Ion mobility, ETD and HDX Robert Tonge (Waters) <i>Auditorium</i>
15:30-17:00	<u>Seminar:</u> Proteomics in regeneration processes Catarina Franco (ITQB) <i>Room 2.13</i>

Sponsors:

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