



## Title

**PRACTICAL COURSE IN BIOLOGICAL DATA-BASE MANGEMENT AND IN BIOINFORMATIC TOOLS FOR PROTEIN IDENTIFICATION BY TANDEM MASS SPECTROMETRY**

## Description

The aim of the course is to introduce participants into the main bioinformatics tools currently used in proteomics for protein identification, like databases and search engines. The course will comprise three modules:

- 1) Databases management and manipulation
- 2) Protein identification by MSMS: use of search and *de novo* peptide sequencing
- 3) High throughput protein identification.

**Location:** Aula Roberto Arche, Facultad de CC. Químicas, Av. Complutense s/n, 28040 Madrid, Spain.

**Number of participants:** max. 12

**Date:** September 21<sup>st</sup> to 22<sup>nd</sup>, 2006

**Duration:** 2 Days

**Organizer:** Proteored education and training group

**Contact person:** Benito Cañas

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## Contents

### Thursday, September 21<sup>st</sup>

#### **Module 1: Protein Databases. Salvador Martínez de Bartolomé.**

- I. Introduction
- II. Database management

#### **Module 2: Peptide sequencing. Benito Cañas.**

- I. Peptide fragmentation mechanisms
- II. Denovo peptide sequencing, practical training

### Friday, September 22<sup>nd</sup>

#### **Module 3: Protein identification by tandem MS. Daniel López, Benito Cañas.**

- I. Search engines: SEQUEST, MASCOT
- II. Practical training in the use of search engines

#### **Module 4: Second generation Proteomics: Bioinformatics Tools. Daniel López.**

- I. High-throughput Proteomics data analysis, theoretical introduction.
- II. Practical session on multi-LC-MS/MS data



*is acknowledged for providing the SEQUEST software license*

#### **Teaching Staff**

Dr. Benito Cañas, Departamento de Química Analítica, UCM, Madrid.

Dr. Daniel López, Unidad de Proteómica, UCM, Madrid.  
Salvador Martínez de Bartolomé. Centro Nacional de Biotecnología, CNB-CSIC, Madrid

**Course fees:** 200.00 €