



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 21st to 22nd, 2006

Duration: 2 Days

Organizer: Proteored education and training group

Contact person: Benito Cañas

Phone: 91 3944368

E-mail: bcanasmo@quim.ucm.es

Contents

Thursday, September 21st

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 22nd

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 €