



Basic course: Mass Spectrometry for Proteomics

Organisers: EuPA Education Committee with CREATE Health

Course dates: **December 10 – 14, 2012**

One-week full time at the Department of Immunotechnology, Lund, Sweden.

Course objectives

In accordance with the HUPO/EuPA guidelines, we aim to

- Provide a theoretical basis for understanding mass spectrometry instrumentation
- Illustrate how the techniques are being applied in modern proteomics studies
- Help students to design their own experiments
- Provide practical instruction in laboratory techniques
- Provide extensive tutorial/discussion sessions

Course description

The course is part of a series designed to give researchers a thorough basis to understand the new trends in protein expression analysis. The aim is to give an of mass spectrometry techniques and how to apply them effectively in their research.

Course outline

Theoretical lectures

- Sample ionization techniques
- Mass, isotopes and resolution and separation principles
- Automated protein and peptide identification methods
- Peptide fragmentation interpretation
- Peptide quantitation by chemical and in vivo labeling

Practical classes

- Protein digestion, MS sample preparation and column preparation
- Protein and Peptide fingerprinting
- Data dependent MS programming
- HPLC comparison software
- *De novo* searching and manual MS/MS interpretation.

Deadline for registrations: October 15, 2012

Minimum number of students: 5 (if not the course will be cancelled). Maximum 16

Fee: 350 € (not including food, accommodation and travel) payable upon confirmation of participation.

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