



HUPO Education and Training Programs

Among the several activities that HUPO is carrying out and supports, a particular effort has been dedicated to the creation and development of global educational programs that are capable of propagating proteomics standards and sustaining the collaborative research effort gathered under the HUPO banner.

The mission of the HUPO Education and Training Initiative is: To create educational opportunities and promote research and technology development in the field of proteomics.

In collaboration with partners selected for their excellence, HUPO offers training opportunities to cover the following topics:

- Sample preparation: pre and sub-fractionation techniques
- Protein separation: gel electrophoresis and liquid chromatography
- Mass spectrometry analysis: protein identification and quantification
- Bioinformatics (for developers): databases and softwares development
- Bioinformatics (for end-users): proteomics data management and analysis
- Experimental validation strategies: biological assays (e.g. functional and localization assays) and biological tools production (*i.e.* expression of recombinant protein and production of antibodies)

The current courses are:

Bioinformatics in Mass Spectrometry Based Proteomics

Date: June 19–21, 2007

Location: University of Southern Denmark (SDU), Odense, Denmark

Course organizer: Ole Nørregaard Jensen

Description: This hands-on course focuses on bioinformatics and data interpretation with respect to mass spectrometric analysis in the field of proteomics.

The aim of the course is to introduce different bioinformatics tools useful for interpreting of the information given in the mass spectra especially with respect to MALDI-MS analysis of peptide mixtures for protein identification and with respect to both MALDI and ESI-MS/MS analysis of peptides, including determination of post-translational modifications.

Researchers with some experience in proteomics and protein mass spectrometry will benefit from this course. Documented work/research experience in protein chemistry and biological mass spectrometry, preferably MALDI MS and/or ESI MS is required. Course participants will be accepted based on their written application and CV.

The number of participants per course is limited to 16.



Mass Spectrometry in Protein Chemistry and Proteomics: Analysis of Post Translational Modifications

Date: September 24–28, 2007

Location: University of Southern Denmark (SDU), Odense, Denmark

Course organizer: Ole Nørregaard Jensen

Description: This hands-on course focuses on the analysis of post translational modifications in protein chemistry and proteomics using advanced mass spectrometry techniques.

The course aims to provide an overview of state-of-the-art methods for enrichments of modified proteins and peptides and the characterization and quantization of modified peptides by MALDI-MS, ESI-MS and MS/MS. Techniques for the analysis of protein phosphorylation, glycosylation and acetylation will be discussed, but additional topics can be included upon request.

Researchers with some experience in proteomics and protein mass spectrometry will benefit from this course. Documented work/research experience in protein chemistry and biological mass spectrometry, preferably MALDI MS and/or ESI MS is required. Course participants will be accepted based on their written application and CV.

The number of participants per course is limited to 16.

HUPO will further develop new educational programs based on the constant assessment of the community's needs through annual surveys and course evaluations. Visit http://www.hupo.org/educational/et_survey_2005.pdf to view the results from the First Annual HUPO Education and Training Survey.