



Title

Publishing 2-DE data

Description

Participants will learn how to deal with 2D gel image-software and how to organize the obtained information in 2D databases linked to clickable gel images.

- General overview of ImageMaster and its latest updates
- First steps in a 2-DE software (visualising gels, data navigation, spot detection, matching gels)
- Analysing populations of gels (inter and intra class analysis, statistical values)
- Annotating information on 2-DE gels
- DIGE análisis
- Introduction to 2D-DB package

Location Facultad de Farmacia, UCM, pza Ramón y Cajal s/n 28040 Madrid Spain

Number of participants max. 20

Date May 16th – 17th

Duration 2 Days

Organizer Proteored Education and Training group. Sponsored by Proteored and INB. The course is free of charge. Accommodation NOT included.

Contact person Antonio Serna Sanz

Phone 91 394 16 13

e-mail antonio.serna-sanz@farm.ucm.es

Contents and guidance

Day 1

- Target group. New comers to proteomics, from PhD student to Prof.
- Special Materials & Reagents used. None
- Equipment & Software used. ImageMaster 2D Platinum & Melanie Viewer
- Course length. 1 day
- Practical outline. 3 hours. Analysis of gels with the software ImageMaster 2D Platinum & Melanie Viewer
- Theory outline. 3 hours.
- Brief reminder of 2-DE gels. Introduction to 2-DE gel analysis, the problems, the issues, the challenges. The main steps with gel analysis software: visualization, spot detection, gel matching. Analyzing populations of gels (inter and intra class analysis, statistical values). DIGE analysis. 2-DE gel databases.

Teaching staff of this part of the course:

Patricia Palagi

Senior Scientist at the Proteome Informatics Group of the Swiss Institute of Bioinformatics. Coordinator of the Master's in Proteomics and Bioinformatics of the Geneva University. Vice-President and General-Secretary of the Swiss Proteomics Society. Member of the Education Committee of the European Proteomics Association

Day 2

- Target group. People making 2-DE gels and protein identification by mass spectrometry
- Special Materials & Reagents used. None
- Equipment & Software used. Make2D-DB (<http://www.expasy.org/ch2d/make2ddb/>)
- Course length. 1 day
- Practical outline. 3 hours. The participants are asked to come with their own gel images and list of identified spots, and by the end of the day they will have their database on-line.
- Theory outline. 3 hours.
- Introduction to database. Proteomics databases (definition, content, format, etc.) with some examples. Introduction to the Make2D-DB package

Teaching staff of this part of the course:

Christine Hoogland

Senior Scientist at the Proteome Informatics Group of the Swiss Institute of Bioinformatics. She is in charge of the maintenance and development of the SWISS-2DPAGE database, and of the EXPASy proteomics Web site. She is also involved in the HUPO Proteomics Standard Initiative, regarding the exchange and consistency of proteomics data. Member of the Executive committee of the Swiss Proteomics Society, in charge of the website. Member of the Conference and Communication Committee of the European Proteomics Association.