

Provisional Program for Proteomics Workshop, location: Hellenic Pasteur Institute

Thursday, October 6, 2011

Session 1: Mass spectrometry proteomics: the basics

Chair: George Panayotou, BSRC Alexander Fleming

- 13.00-13.40: Martina Samiotaki, Biomedical Sciences Research Center "Alexander Fleming", Athens, Greece
Sample preparation for proteomic analysis
- 13.40-14.20: Malvina Papanastasiou, Institute of Molecular Biology and Biotechnology, Heraklion, Crete
Protein identification using Mass Spectrometry
- 14.20-15.00: Michalis Aivaliotis, Institute of Molecular Biology and Biotechnology, Heraklion, Crete
Strategies in functional proteomics
- 15.00-15.45: Henning Hermjakob, European Bioinformatics Institute, Cambridge, UK
Database Submission and Reporting Requirements for Proteomics Data Publication

15.45-16.15: Coffee break

Session 2: Structural Proteomics

Chair: Tassos Economou, U. of Crete/IMBB

- 16.15-17.00: Michal Sharon, Weizmann Institute, Rehovot, Israel
The emerging role of mass spectrometry in structure elucidation of cellular complexes
- 17.00-17.45: **To be confirmed**
- 17.45-18.30: **To be confirmed**

Friday, October 7, 2011

Session 3: Transcription factor proteomics

Chair: John Strouboulis, BSRC Alexander Fleming

- 9.00-9.45: Ulf Landegren, Uppsala University, Sweden
High-performance protein detection in solution and in situ
- 9.45-10.30: Jeroen Demmers, Erasmus Medical Center, Rotterdam, the Netherlands
Quantitative mass spectrometry in transcription factor functional proteomics
- 10.30-11.00: Coffee Break
- 11.00-11.45: Raymond Poot, Erasmus Medical Center, Rotterdam, the Netherlands
Purification of transcription factors and chromatin co-factors from embryonic and neural stem cells
- 11.45-12.30: Florian Grebien, Research Center for Molecular Medicine, Vienna, Austria
Tandem Affinity purification: a versatile tool for proteomic and genomic analysis of transcription factor complexes.

Session 4: Chromatin proteomics

Chair: Iannis Talianidis, BSRC Alexander Fleming

- 12.30-13.15: Juri Rappsilber, Edinburgh University, UK
Hypothesis generation from hopeless data: chromatin proteomics
- 13.15-14.00: Jerome DeJardin, Institute of Human Genetics, Montpellier, France
Heterochromatin characterization by PICh
- 14.00-15.00: Lunch break
- 15.00-15.45: Gary LeRoy, Princeton University, USA
Systems-wide High Throughput Analysis of Epigenetic Codes
- 15.45-16.30: Teresa Barth, Adolf-Butenandt Institute, Munich, Germany
Quantification of histone modifications by mass spectrometry