

# 1<sup>st</sup> Greek Orbitrap Users Workshop

9<sup>th</sup> October 2010

## Program

9:00 Welcome to ProFI, (*T. Economou*)

9:10 ProFI presentation (*part I*)

9:45 ProFI presentation (*part II*)

10:25 ProFI presentation (*part III*)

(*M. Papanastasiou, N. Kountourakis, M. Aivaliotis. See page 2 for detailed description*)

11:00 Coffee break

11:30 *E. Denisov*, “Orbitrap Mass Spectrometry of Intact Proteins”  
Thermo Scientific

12:05 *M. Filiou*, “Biomarker discovery using <sup>15</sup>N metabolic labelling and an Orbitrap mass spectrometer”  
Max Planck Institute of Psychiatry

12:40 *M. Samiotaki*, “Proteomic Approaches in Cancer Research”  
BSRC Al. Fleming

13:15 Lunch break

14:00 *M. Halabalaki*, “Application of LC-MS & LC-MS<sup>n</sup> techniques in natural products chemistry”  
University of Athens

14:35 *E. Gikas*, “Metabolite identification through MS/MS data mining”  
University of Athens

15:10 Round table discussion

Tour in ProFI will follow

**Presentations' duration: maximum 30 minutes plus discussion.**

ProFI presentation:

**5 minutes Intro:** Overview of ProFI setup (Experimental workflows, Bioinformatics)

**I. HIGH THROUGHPUT PROTEOMICS**

**1. Protein isolation/separation**

- Gel-based (2DE, Native PAGE, SDS-PAGE)
- Gel-free (Sucrose gradient, OFFGEL, SCX, Gel Filtration)

**2. Protein identification/characterization**

- nLC-ESI-MS/MS
- Data processing (Mascot, Sequest, Proteome Discoverer, X!tandem, Scaffold)
- Characterization of protein PTMs

**3. Protein annotation/curation**

- GO annotation (OBO)
- Data mining

**II. INTACT PROTEIN ANALYSIS**

- Mass determination (Ion trap, Orbitrap)
- Characterization of protein PTMs with Top-Down analysis (CID, ETD, HCD)
- Data processing/validation (Xcalibur-Xtract, ProMass, ProSight, manual validation)

**III. PROTEIN INTERACTIONS**

- 1. Protein-protein interactions**
- 2. Protein-DNA interactions**