

## **PROTEOMICS WORKSHOP 1**

**16-18 FEB 2010 PROGRAM**

### **DAY 1**

***(Open to public) Seminar Room III -Orfanoudakis***

#### **9.00 -10.00: INTRODUCTION TO PROTEOMICS**

- Brief history (Proteomics and Mass Spec-based proteomics)
- State-of-the-art proteomics

#### **10.00 -12.00: HIGH THROUGHPUT PROTEOMICS -Gel-free**

- (MudPIT, OFFGEL, microrotofor etc) -Gel-based (2DE, Native, SDS-PAGE) -Introduction to LC-MS/MS

#### **12.00 -13.30 LUNCH BREAK**

#### **13.30 -16:30: BIOINFORMATICS I**

***(For ProFI users only) ProFI-Lab***

##### ***In silico analysis***

- Expasy Tools
- In silico* digestion (proteolysis, parameters, etc)
- Protein/peptide properties (GRAVY score, pI, MW etc)
- Prediction tools (PTMs, function, structure etc)

#### **16:30 – 17:00: HOMEWORK I (Bioinformatics I)**

## **DAY 2**

*(For ProFI users only) Seminar Room III -Orfanoudakis*

**9.00 -12.00: MS-BASED STRUCTURAL AND FUNCTIONAL**

**CHARACTERIZATION OF PROTEINS**

-MS (Ion trap, Orbitrap, FT)

-MS/MS -Peptide fragmentation (CID, ETD, HCD, b-&y-ions etc)

-Data analysis (Xcalibur – familiarity with MS & MS/MS spectra)

**12.00 -13.30 LUNCH BREAK**

**13.30 – 16.30: BIOINFORMATICS II ProFI Lab**

**Data processing**

-**2DE:** Delta 2D

-**LC-MS/MS I:** Proteome Discoverer, Sequest, Mascot

**16.30 – 17.00: HOMEWORK II (Bioinformatics II)**

## **DAY 3**

***(For ProFI users only) ProFI Lab***

**9.00 -12.00: BIOINFORMATICS III (ProFI)**

### **Data processing**

-**LC-MS/MS II:** Proteome Discoverer, Sequest, Mascot

-**Intact Protein** (runs + deconvolution example)

### **Protein annotation**

-**Introduction to GO annotations** (DAVID, Blast2Go)

-**PTMs** (example spectra + databases)

**12.00 -13.30 LUNCH BREAK**

**13.30 -15.00: CASE STUDIES**

**15.00 – 16.30: ROUND TABLE DISCUSSION -CONCLUDING REMARKS**