



BIOINFORMATICS ANALYSIS FROM PROTEOMICS DATA WORKSHOP

CIC (USaI-CSIC) SALAMANCA 15th March 2010: 9:00h - 18:00h

Organizers

Juan Pablo Albar

Xosé Bustelo

Speakers

ProteoRed

Juan Pablo Albar

Montserrat Carrascal

Salvador Martínez.

Emilio Salazar

Alberto Medina

Guests

Eduardo González Couto

Kenny Helsens

Andrew Jones

Patricia Palagi

Javier De Las Rivas

Juan Antonio Vizcaíno

9:00 – 9:15	<i>Welcome Reception.</i> <i>Xosé Bustelo.</i>
9:15 – 9:45	<i>Introduction: Relevance of Proteomics Standards for ProteoRed.</i> <i>J. Pablo Albar.</i>
1st Session. MultiCenter Projects. Collaborative environment. Chairs: Alberto Medina and Andrew Jones.	
9:45 – 10:15	<i>PRIDE: current status and future plans.</i> <i>J. Antonio Vizcaino, EMBL-EBI, Cambridge, UK.</i>
10:15 - 10:45	<i>MIAPes in ProteoRed Multicentric Experiments.</i> <i>Salvador Martínez de Bartolomé, ProteoRed, CNB-CSIC, Madrid, SP.</i>
10:45 – 11:15	<i>OmicsHub Proteomics: Recent use cases.</i> <i>Eduardo González Couto, Integromics, Tres Cantos, SP.</i>
Coffee Break (30 min)	
2nd Session. Proteomics bioinformatics applications. Chairs: Juan Pablo Albar and Javier de las Rivas	
11:45 – 12:15	<i>New improvements in MIAPE generation: MIAPE API.</i> <i>Emilio Salazar, ProteoRed, CNB-CSIC, Madrid, SP.</i>
12:15 – 12:45	<i>LC/MS data processing for label-free quantitative analysis with MSight and SuperHirn and other MS stories.</i> <i>Patricia Palagi, Swiss Institute of Bioinformatics (SIB), Geneva, SW.</i>
12:45 – 13:15	<i>Data validation and annotation: PrideViewer & PIKE.</i> <i>Alberto Medina, ProteoRed, CNB-CSIC, Madrid, SP.</i>
13:15 – 13:45	<i>MS-LIMS and friends: tools to store and analyze large scale proteomics data.</i> <i>Kenny Helsens, Gent University, BEL.</i>
Lunch (1h 15min)	
3rd Session. Proteomics Standards: Current Status. Chairs: Salvador Martínez and J. Antonio Vizcaino.	
15:00 – 15:30	<i>Data standards developed by the Proteomics Standards Initiative.</i> <i>Andrew Jones, University of Liverpool, UK.</i>
15:30 – 16:00	<i>Phosphosite characterization in human T-cell proteome: Minimal Information About Sample Preparation for Phosphoproteomics (MIASPE).</i> <i>Montserrat Carrascal, ProteoRed, LP-CSIC-UAB, Barcelona, SP.</i>
16:00 – 16:30	<i>From single proteins to protein interactions and protein networks derived.</i> <i>Javier De las Rivas, CIC-USAL, Salamanca, SP</i>
Coffee Break (30 min)	
Discussion Panel Chairs: J. Pablo Albar and Xosé Bustelo.	
17:00-17:30	<i>Close</i> <i>J. Pablo Albar.</i>
Software tutorials and demos Conducted by: Miguel Ángel López García and speakers	