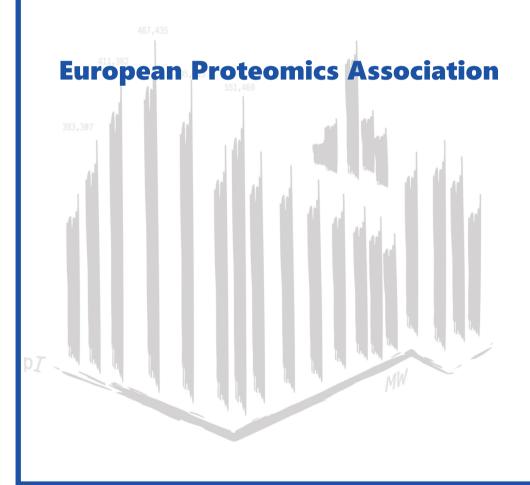


IX Annual Congress - EuPA 23rd - 28th JUNE 2015



UNDER THE AUSPICES OF







UNIVERSITÀ DEGLI STUDI DI MILANO DIPARTIMENTO DI SCIENZE VETERINARIE E SANITÀ PUBBLICA







Under the Patronage of



WELCOME

The ItPA, Italian proteomics Association, has been particularly focused in the last years in providing a common framework of exchange between the fast advancing challenges in the Human Proteomics field and the non-Human - Comparative Proteome investigations. The interaction between these two different worlds has alreadv produced the first actual Proteomics CE-IVD products for the health-care market, the MALDI-Biotyper and its twin products. We have followed several initiatives in this light since 2011 organizing several events dedicated to Proteomics in global health. In particular in collaboration with different European Commission of Science and Technologies (COST) actions the perspective of novel Proteomics technological advances have been explored in this field. The COST BM1403 co-organized scientific sessions and educational programs are a clear example of integration of the challenging field of Native Mass Spectrometry with the Proteomics community at large. Moreover the Imaging Mass Spectrometry session will present the work of the COST BM 1104 advancement in this highly innovative field on the verge of the clinical health-care application. With this Congress we openly aim to provide an agora for clinical proteomics investigations and non-human proteome studies, bringing into the discussion the

role of Proteomics in the One-Health vision. This will be the leitmotiv of the EuPA scientific program which will be following the C-HPP workshop inside the EXPO2015. This unique condition will open to the proteomics community an unprecedented window to possibly communicate to the society the fundamental advancements of Proteomics research.

So, we are greatly honored and pleased to welcome you in the prestigiuos location of University of Milano, and hope that you will enjoy the Congress.

Luigi Bonizzi President of Congress



Paola Roncada Chair of Organizing Committee



Andrea Urbani President of the Italian Proteomics Association



IX Annual Congress - EuPA



President of the Congress

Luigi Bonizzi

Scientific Committee

Emoke Bendixen Luca Bini Luigi Bonizzi Massimo Castagnola Garry Corthals Mauro Fasano Gyorgy Marko-Varga Alessandra Modesti Paola Roncada Anna Maria Timperio Andrea Urbani Peter Verhaert

Organising Committee

Paola Roncada Luigi Bonizzi Gabriella Tedeschi Armando Negri Tiziana Alberio Isabella Alloggio Mauro Fasano Viviana Greco Cristian Piras Alessio Soggiu

COMMITTEES

IX ANNUAL CONGRESS - EUPA

INVITED SPEAKERS

Adriano Aguzzi Alexander Archakov Alison Ashcroft Mohan Babu Mark Baker Perdita Barran Bernd Bodenmiller Sarah Cianferani Garry Corthals Jürgen Cox Karin Hoffmann-Sommergruber Peter L. Horvatovich Christian Huber Lisa Jones Jesús Jorrín Novo Oleg Krokhin Joshua LaBaer Lydie Lane Alexander Leitner Kathryn Lilley Gyorgy Marko Varga Lennart Martens Gabriel Mazzucchelli Liam A. McDonnell Giampaolo Merlini Alexey I. Nesvizhskii Gilbert S. Omenn Chris M. Overall Young-Ki Paik Paola Picotti Kasper Rand Jean Charles Sanchez Frank Sobott Giulio Superti-Furga Andreas Tholey Mathias Uhlèn Henning Urlaub Marc Vaudel Hans Westerhoff Pengyuan Yang Jong Shin Yoo

IX ANNUAL CONGRESS - EUPA

CONGRESS VENUE

The "IX Annual Congress - EuPA - European Proteomics Association" will be held at Università degli Studi di Milano Via Festa del Perdono, 7, 20122 Milano www.unimi.it

HOW TO REACH US

The fastest and cheaper way to move around the city is by **underground** (Metropolitana). The two metro lines which stop near Via Festa del Perdono are: the **red line** (DUOMO station) and the **yellow line** (MISSORI station). From these stops you can simply walk to the Congress site.

If you need **Taxi:** +39 02 8585 - +39 02 6969 - +39 02 4040

CATERING SERVICES



Coffee breaks are provided as scheduled in the scientific program. Breakfast, lunch and coffee simposia have been organised by some Companies. The participation in those sessions is reserved to delegates who have made the pre-reservation (upon presentation of a ticket).

CERTIFICATE OF ATTENDANCE

Certificate of attendance has to be picked up at the Registration Desk before departure.

NAME BADGE

All participants will receive a name badge when they check in at the registration desk. The badge must be worn at all times because only registered participants will be admitted to the scientific sessions.

GENERAL INFORMATION

OFFICIAL LANGUAGE

The official language of the Congress is English. Simultaneous translation is not provided.

OPEN WIFI MILANO

Open wifi Milano is a free wifi service provided by the Municipality of Milano in several city areas. For further information: info.openwifimilano.it

WIRELESS CONNECTION

Complimentary internet access is available at **EDUROAM** if you are already registered as professor or student. In addition to the above, you can connect through wireless open "**unimi-convegni**" from 24th to 27th June.

ORGANISING SECRETARIAT

MZ Congressi srl via Carlo Farini 81 20159 Milano Phone: +39 02 66802323 www.mzcongressi.com info@eupa2015.org



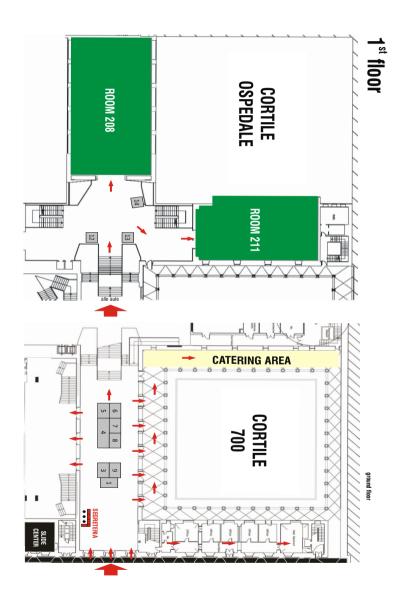
At the congress venue, from Tuesday 23 June to Friday 26 June: +39 339 727553

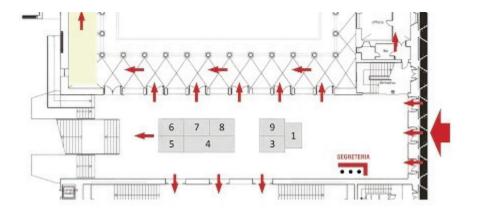
REGISTRATION DESK

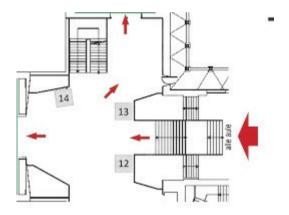
The registration desk, located in the exhibition area, is open as follows:Tuesday, 23 June05:00 pm - 06:00 pmWednesday, 24 June07:30 am - 07:00 pmThursday, 25 June08:30 am - 07:00 pmFriday, 26 June08:30 am - 07:00 pm

INDUSTRY EXHIBITION

All major international companies active in the field of proteomics are represented. The Exhibition Area is open at the same schedule time of the Registration Desk.







Exhibitors:

- 1) Sciex
- 3) Waters
- 4) Thermo Fisher
- 5) Bruker
- 6) Cambridge Isotope
- Laboratories
- 7) Elsevier
- 8) Agilent Technologies
- 9) Sigma Aldrich

12) Istanbul EuPA 2016 Organising Committee 13) Edises

14) Denator

IX ANNUAL CONGRESS - EUPA

SOCIAL PROGRAM

SOCIAL AND CULTURAL EVENING

Thursday, June 25th at 8:30 pm Loggiato del Rettorato Via Festa del Perdono, 7 University of Milan

All delegates and their accompanying person are invited to attend the Social Dinner that will take place in the nice Loggiato del Rettorato at 8:30 pm.

Tickets are purchasable onsite at Registration Desk but with limited seats availability.

Fee: € 50,00 (vat not included)

MUMAC MUSEUM - HOW TO MAKE A REAL ESPRESSO



Sunday, June 28th at 10:30 am welcome coffee.

Visit to Mumac Museum.

Coffee Lesson: how to make a real espresso.

Fee: free for regular delegate Please, register at Social Events Desk

WALKING TOUR IN LEONARDO DA VINCI'S FOOTSTEPS



Sunday, June 28th Departure at 2 pm from University of Milan.

Fee: free for regular delegate Please, register at Social Events Desk

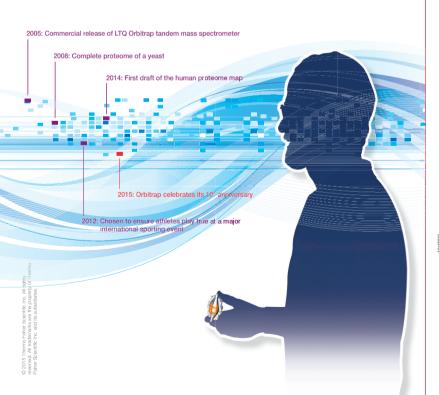


Happy 10.0000th

For 10 years, you've never stood still. Neither have we. Celebrate 10 years of Orbitrap MS with us at EUPA and see what the future holds.

Transform your science.

thermoscientific.com/proteomics

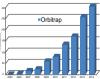




The Orbitrap: A novel high-performance electrostatic trap introduced 10 years ago.



Thermo Scientific[™] Orbitrap[™] Q Exactive[™] MS system: Unmatched Quan/Qual performance introduced 4 years ago.



Published papers from Nature Family and Science citing the Orbitrap mass analyzer significantly increase.

c-HPP SHOWCASE MEETING EXPO 2015 - PADIGLIONE ITALIA

10:30	Y. K. Paik, P. Roncada, A. Urbani		Welcome address and Congress Opening
10:45	M. Uhlén		Deciphering Mitochondrial Proteome
11:15	M. Fasano	mt	Mitochondrial Proteome in Neurodegenerative Disorders
11:30	Y. K. Paik	13	Expression Landscape of the Hepatocellular Carcinona-Associated Mitochondrial Proteins
11:45	G. Omenn	17	Chromosome 17: Analyses of Splice Variance and Biological Pathways related to ERBB2 (Her2/neu) in Breast Cancers
12:00	C. Overall	6	Protein TAILS tell remarkable tails in the HPP
12:15	M. Baker	7	Finding the Human Proteome Project's Missing Proteins and Sharing a Common Language
12:30	J. LaBaer	10	IVTT-coupled proteomic identification of missing proteins
10.15	E. Lundberg		Detecting missing proteins in the Human Protein Atlas
12:45			project
13:00	Lunch Break		
	-		
13:00	Lunch Break	2	project
13:00 14:30	Lunch Break BioInformatics Session	2 11	project Nesvizhskii, Martens, Cox, Vaudel
13:00 14:30 15:00	Lunch Break BioInformatics Session <i>L. Lane</i>	_	project <i>Nesvizhskii, Martens, Cox, Vaudel</i> The uncharted human proteome Bioinformatic pipeline using proteomics search engines with proteogenomic databases for CHPP
13:00 14:30 15:00 15:15	Lunch Break BioInformatics Session <i>L. Lane</i> <i>J. S. Yoo</i>	11	project <i>Nesvizhskii, Martens, Cox, Vaudel</i> The uncharted human proteome Bioinformatic pipeline using proteomics search engines with proteogenomic databases for CHPP The first master proteom of singol chromosome: example of human chromosome 18 Human testis and spermatozoa as models to search for missing proteins in the context of the
13:00 14:30 15:00 15:15 15:30	Lunch Break BioInformatics Session <i>L. Lane</i> <i>J. S. Yoo</i> <i>A. Archakov</i>	11 18	project <i>Nesvizhskii, Martens, Cox, Vaudel</i> The uncharted human proteome Bioinformatic pipeline using proteomics search engines with proteogenomic databases for CHPP The first master proteom of singol chromosome: example of human chromosome 18 Human testis and spermatozoa as models to search
13:00 14:30 15:00 15:15 15:30 15:45	Lunch Break BioInformatics Session <i>L. Lane</i> <i>J. S. Yoo</i> <i>A. Archakov</i> <i>C. Pineau</i>	11 18 14	project Nesvizhskii, Martens, Cox, Vaudel The uncharted human proteome Bioinformatic pipeline using proteomics search engines with proteogenomic databases for CHPP The first master proteom of singol chromosome: example of human chromosome 18 Human testis and spermatozoa as models to search for missing proteins in the context of the chromosome-centric Human Proteme Project HPP Disease pathology and Proteoinforms: Bioninformatics - The bio-diversity of proteomes
13:00 14:30 15:00 15:15 15:30 15:45 16:00	Lunch Break BioInformatics Session L. Lane J. S. Yoo A. Archakov C. Pineau P. Horvatovich	11 18 14 5 19	project Nesvizhskii, Martens, Cox, Vaudel The uncharted human proteome Bioinformatic pipeline using proteomics search engines with proteogenomic databases for CHPP The first master proteom of singol chromosome: example of human chromosome 18 Human testis and spermatozoa as models to search for missing proteins in the context of the chromosome-centric Human Proteme Project HPP Disease pathology and Proteoinforms: Bioninformatics - The bio-diversity of proteomes Disease Pathology and Biobanking: Discovering New
13:00 14:30 15:00 15:15 15:30 15:45 16:00 16:15	Lunch Break BioInformatics Session L. Lane J. S. Yoo A. Archakov C. Pineau P. Horvatovich G. Marko-Varga	11 18 14 5 19	project Nesvizhskii, Martens, Cox, Vaudel The uncharted human proteome Bioinformatic pipeline using proteomics search engines with proteogenomic databases for CHPP The first master proteom of singol chromosome: example of human chromosome 18 Human testis and spermatozoa as models to search for missing proteins in the context of the chromosome-centric Human Proteme Project HPP Disease pathology and Proteoinforms: Bioninformatics - The bio-diversity of proteomes Disease Pathology and Biobanking: Discovering New Biomarksers C-HPP in Spain. One step beyond the understanding

VISIT EXPO

08:00 amBreakfast SeminarSponsored by Thermo Fisher ScientificB. DomonAdvances in Targeted Proteomics Analyses:
Parallel Reaction Monitoring Version 2.0



09:00 am PLENARY SESSION Aula Magna

MICROBIAL AND VIRAL

Chair: P. Roncada and L. Bonizzi

9:00 - A. Aguzzi - Molecular Biology of Prions

9:35 - *C. Overall* - Proteogenomics Reveals intracellular and nuclear activity of a secreted macrophage metalloproteinase in viral infection is essential to invoke the IFN α secretion by regulating gene transcription

10:15 am Coffee Break and POSTER SESSIONS

10:45 am PARALLEL SESSIONS

Microbial and Infectious Proteomics - Aula Magna Chair: P. Roncada and C. Overall

10:45 - *F. Schmidt* - A combined proteomics approach for the characterization of the human adaptive immune response to s. Aureus antigens

11:20 - *T. Chaze* - Modulation of the human neuronal proteome upon west nile and japanese encephalitis virus infection

11:40 - *J. Malmström* - Probing plasma proteome homeostasis in severe infectious disease using tissue specific spectral libraries and dia-ms

12:00 - *E. Milani* - AP-MS and BioID analysis of the HBx Viral-Host interactome 12:20 - *R. C. Rodrigues* - A proteomic approach to decipher the oxidative stress response of an atypical aerotolerant strain of Campylobacter jejuni

Integrated OMICS - Aula 208

Chair: P. Verhaert and A. Negri

10:45 - O. Krokhin - Separation science in the proteomics era: an abundance of data impacts our understanding of chromatography

11:20 - V. Matafora - Exploring mitosis dynamics by combining dia and dda strategies

11:40 - A. Gagliardi - Functional proteomics in dominant and recessive forms of osteogenesis imperfecta

12:00 - *R. P. Zahedi* - Simplex - a multimolecular omics approach for systems biology

12:20 - *I. Edwards* - Microfluidics coupled mass spectrometry for multiomics/targeted assays in translational research

Plant Proteomics- Aula 211

Chair: A. Scaloni

10:45 - *J. Jorrín Novo* - Why and how to move from the descriptive stage in plant proteomics research?

11:20 - *B. M. Alexandre* - New phosphorylation sites in key proteins of C4 photosynthesis in Maize: uncovering the signaling events in the activation of key enzymes

11:40 - *I. M. Luís* - Optimizing the protein extraction method for phosphoproteome analysis in a C4-photosynthetic plant

01:00 pmLuncheon Seminar
Sponsored by WatersWaters
WatersI. EdwardsMulti-Omics MS Technology UpdateTHE SCIENCE OF WHAT'S POSSEBLE."A. CorbinProgenesis QI for Multi-Omics Studies
Large Scale Quantitation of Stable Isotope Labelled Proteomes
using Retention Time and Drift Time Profiling

03:00 pm PLENARY SESSION Aula Magna

BIOINFORMATICS

Chair: P. Horvatovic and K. Mechtler

03:00 - *A. Nesvizhskii* - Computational advancements and challenges in MS-based proteomics 03:35 - *L. Martens* - Small microbes, big problems: metaproteomics tools and challenges

04:15 pm Coffee Break and POSTER SESSIONS

04:45 pm PARALLEL SESSIONS

ProteoInformatics - Aula Magna

Chair: A. Jones and G. Omenn

04:45 - *J. Cox* - Controlling false discovery rates (FDRS) in genome-wide proteomics data sets

05:20 - *M. Vaudel* - Proteomics for high resolution medicine: from science fiction to the clinics

05:55 - *K. Mechtler* - A novel software suite for accurate label free quantification of protein complexes

06:20 - *E. Ponomarenko* - Estimation of protein species number based on consolidation of postgenomic data in gene-centric knowledgebase

06:45 - *E. Kontopodis* - Insights of the Human Proteome based on unique peptide analysis

Biobanking, standardization and targeted approaches - Aula 208 *Chair: G. Marko-Varga and C. Pineau*

04.45 - *G. Marko-Varga* - Semi-automated biobank sample processing with a 384 high density sample tube robot used in cancer and cardiovascular studies 05:20 - *T. Alm* - Affinity Binder Knock-Down Initiative

05:40 - F. Canals - A Multi-Centric Study To Evaluate the Use of Relative Retention Times in Targeted Proteomics

06:00 - *S. Fraselle* - A urinary protein biomarkers panel to discriminate progressive from non-progressive chronic kidney disease using a targeted proteomics method. 06:20 - *M. Manfredi* - Application of SWATH-MS to different biological matrices for fast and quantitative proteomics analysis

Functional Proteomics - Aula 211

Chair: L. Bini and F. J. Corrales

04:45 - *H. Clausen* - Precise gene editing technologies - a revolution for glycomics 05.20 - *G. Palmisano* - Protein glycosylation analysis of Trypanosoma cruzi in different life stages

05:45 - *G. Grande* - Proteomic characterization of the qualitative and quantitative differences in cervical mucus composition during the menstrual cycle 06:05 *C. Cattaneo* - The secret(e)s of Cellulomonas fimi interacting with cellulose

09:00 am PLENARY SESSION Aula Magna

NON HUMAN PROTEOMICS

Chair: P. Roncada and A. Tholey

09:00 - *L. J. Foster* - Guiding selective breeding in honey bees using protein biomarkers

09:35 - *A. Gonzalez-Bulnes* - The use of large animal models in proteomics of metabolic disordes.

10:15 am Coffee Break and POSTER SESSIONS

10:45 am PARALLEL SESSIONS

Proteomics of Metabolic and Cardiovascular Disorders - Aula Magna *Chair: A. Modesti and P. Ping*

10:45 - *F. J. Corrales Izquierdo* - Changes on the proteom and methyl proteom triggered buy a deficiency on Mtap in liver cells.

11:20 - *A. Sickmann* - Moving from inventory to personalized medicine: reducing cardiovascular mortality

11:55 - *U. Eckhard* - The human heart N-terminome: A new strategy to identify Human Proteome Project "missing proteins" using N-terminal peptides.

12:20 - *K. Kratochwill* - Equalizer technology and TMT-based proteomics for detection of cellular proteins in clinical peritoneal dialysis effluents

Mitochondria & Metabolism - Aula 208

Chair: M. Fasano and A. Urbani

10:45 - *M. Babu* - Network analyses of mitochondria reveal new components associated with neurodegenerative disordes

11:20 - E. Lundberg - Towards a complete Subcellular Protein Atlas

11:55 - *M. Ronci* - High Density Proteome Coverage of Enriched Mitochondria Fractions from Human Cell Lines

12:15 - *F. Ciregia* - Palmitate treatment promotes protein lysine acetylation in rat INS-1E mitochondria

12:35 - *A. Soggiu* - In depth mitochondrial proteome profiling of the monocytic cell line THP-1

iMOP Initiative on Multi-Organisme Proteomics - Aula 211 Chair: L. Bonizzi and M. Montedoro

10:45 - *A. Tholey* - Interaction of species - a versatile playground for proteomics 11:20 - *I. Miller* - Characterization of pig saliva proteins and identification of lipocalin-1 as a marker of transport stress

11:40 - *A. Katsafadou* - Proteomic analysis of blood and milk of ewes with experimental mastitis induced by Mannheimia haemolytica

12:00 - *A. Bassols* - PBMC proteins involved in cell migration and immunomodulation identified as potential pig welfare markers by DIGE 12:20 - *C. Kondethimmanahalli* - Proteomic Changes Associated with Successive Reproductive Periods in Male Polychaetous Neanthes arenaceodentata 12:40 - *V. Grieco* - Network for the Evaluation of One Health (NEOH)

01:00 pm	Luncheon Seminar Sponsored by Sciex	SCIEX
J. Dojhan	SWATH [™] Acquisition and the OneOmics [™] Project: from MS Data Acquisition to Biological Answers	
C. Pineau	Combining Next Generation Proteomics and NGS the OneOmics™ to gain new insights into human sperm	•
02:00 pm	Coffee & Cake Seminar Sponsored by Thermo FIsher Scientific	Thermo
C. Overall	Using the 10-Plex TMT Quantitative TAILS N- Terminomics with Thermo Scientific Orbitrap	A Thermo Fisher Scientific Brand
	Fusion MS to Understand the Mechanism for NFkB Autoimmunity	Deficiency in

03:00 pm PLENARY SESSION Aula Magna

HUMAN PROTEOMICS

Chair: A. R. Pitt and P. Mocarelli

03:00 - *G. Superti-Furga* - Medical systems biology and the mechanism of action of drugs

03:35 - *G. Merlini* - Proteomics in the understanding and management of systemic amyloidoses

04:15 pm Coffee Break and POSTER SESSIONS

04:45 pm PARALLEL SESSIONS

Cancer - Aula Magna

Chair: C. Gelfi and A. Sickmann

04:45 - Y. K. Paik - Multiple functions of the human carboxylesterase 1 in hepatocarcinogenesis

05.20 - *B. Domon* - Towards a "Load and Play" Solution for Parallel Reaction Monitoring Assays

05:40 - *M. J. Castillo* - Targeted quantitative proteomics for cancer biomarker validation via high sample throughput N-in-1 uMS

06:00 - *I. Pucci-Minafra* - Large scale 2d-gel based proteomics of breast cancer tissues to detect putative tumour markers

06:20 - D. Scumaci - Plasma Proteomic Profiling in Hereditary Breast Cancer

Protein Post Translational Modifications- Aula 208

Chair: G. Corthals and M. Castagnola

04:45 - *G. Corthals* - Phosphorylation analysis: knowledge beyond comparison? 05:20 - *K. Gallardo* - Quantitative Profiling of Post-translational Modifications of Histones by LC-MS/MS

05:40 - *G. Sigismondo* - Dynamic profiling of chromatome at enhancers of inflammatory genes

06:00 - *A. Cuomo* - An Integrate HRMS-Based Proteomics Approch to Identify and Quantify Histone Modifications

EuPA INITIATIVES & COMPANY CLUB - Aula 211

Chair: A. Lisitsa

04:45 - *A. Lisitsa* - Flagship Program for EuPA Initiatives: Opportunities for Company Club

04:55 - *F. J. Corrales* - Standardization Initiative. Integrating proteomic strengths across Europe

05.10 - T. Alm - Affinity Binder Knock-Down Initiative

05:25 - *A. Wheelock* - Improving productivity&quality in Biobanking: the need for synergy between industry, academia and the public sectore.

05:40 - Utility of EuPA Initiatives for established corporation (Presentations of CC members):

K. Ray (Sigma Aldrich) - Sigma-Aldrich Product Development and Future Directions in Support of Proteomics Standarization; Biobanking and Validation using CRISPR Knockout Technology

S. Pellenz (Antibodies-online.com) - Independent Validation Initiative 06:10 - Utility of EuPA Initiatives for SME and start-ups - Round table discussion

X Annual Congress - EuPA

09:00 am PLENARY SESSION Aula Magna

DIAGNOSTICS and TRANSLATIONAL

Chair: Y. K. Paik and A. Lucacchini

09:00 - *M. Baker* - Translational signatures of colorectal cancer 09:35 - *J. C. Sanchez* - Discovery of brain biomarkers and their translation to clinical settings.

10:15 am Coffee Break and POSTER SESSIONS

10:45 am PARALLEL SESSIONS

Native MS and biopharmaceutical COST BM 1403 - Aula Magna *Chair: F. Sobott*

10:45 - F. Sobott - Native MS and structural proteomics - the state of the art
11:20 - H. Urlaub - Cross-linking in macromolecular assemblies
11:50 - P. Barran - Molecular Insights to the Thermal Stability of Protein
Complexes with Variable Temperature Ion Mobility Mass Spectrometry
12:20 - G. Mazzucchelli - De Novo sequencing using MELD proteolysis coupled to
a "Sequence Assembly" Algorithm

Allergy and foodomics - Aula 208

Chair: P. Roncada and G. Tsangaris

10:45 - *K. Hoffmann-Sommergruber* - How proteomics can improve diagnosis of allergy

11:20 - *C. Huber* - Proteomic and secretomic responses of antigen-presenting cells to stimulation with birch pollen allergen

11:55 - *T. Cirkovic Velickovic* - Immunoproteomics of Tilia cordata pollen reveals novel and known homologues of respiratory allergens

12:15 - *C. Piras* - Molecular mechanisms of biofilm formation of S. aureus food isolates: new insights for food safety

12:35 - *A. Cerquone* - Probiotic-containing chewing-gum production: purification and proteomic characterization of bacteriocins of Lactobacillus salivarius

Neuroproteomics - Aula 211

Chair: M. Fasano and G. Tedeschi

10:45 - *P. Picotti* - Probing protein structural changes in health and disease 11:20 - *A. Armirotti* - Peroxide-dependent mgl sulfenylation regulates 2-ag-mediated endocannabinoid signaling in brain neurons

11:45 - C. Fania - CSF maldi profiling for the identification of novel biomarkers in dementia patients

12:10 - V. Greco - Mitochondria protein repertoire adaptation in animal models of Amiotrophic Lateral Sclerosis

01:00 pm	Luncheon Seminar	BRUKER		
	Sponsored by Bruker	$\langle \times \rangle$		
	"Proteomics on a time-of-flight instrument"			
L. Foster	Where genomics can't go: practical application agriculture and medicine.	ns of proteomics in		
M. Barret	Evaluation of quadruple time-of-flight mass sp	ectrometry for		
Andersen	qualitative and quantitative proteomics.			
02:00 pm	Coffee & Cake Seminar	Waters		
	Sponsored by Waters - Waters Food Research			
S. Stead	Research: REIMS Research System with iknit	Evaporative Ionization Mass Spectometry for Food rch: REIMS Research System with iknife Sampling for Direct alyses of Food for Authenticity, Quality, Profiling and Marker cation		

03:00 pm **PLENARY SESSION Aula Magna**

CELLULAR and SYSTEMS BIOLOGY

Chair: I. Messana and A. Ozpinar

03:00 - K. Lilley - Spatial proteomics on a cell-wide scale 03:35 - H. Westerhoff - Proteomics for Individualized Medicin: yes, but how?

04:15 pm Coffee Break and POSTER SESSIONS

PARALLEL SESSIONS 04:45 pm

Structural proteomics COST BM 1403 - Aula Magna

Chair: A. Ashcroft and T. Janaky

04:45 - A. Ashcroft - Using ion mobility-mass spectrometry for protein structural studies

05:20 - L. Jones - In Cell Footprinting for the Structural Analysis of Proteins 05:50 - S. Cianferani - Native MS and Ion Mobility for the analysis of mAbs and related products

06:20 - K. Rand - H/D exchange and mass spectrometry to characterize the conformation and interactions of complex proteins of therapeutic interest



Imaging Mass Spectrometry - Aula 208

Chair: F. Magni and L. McDonnell

04:45 - *L. McDonnell COST BM 1104* - De novo discovery of tumor clones linked to metastasis and poor prognosis using maldi mass sprectrometry imaging 05:20 - *B. Bodenmiller* - Simultaneous and targetered imaging of 100 biomarkers on tissues with subcellular resolution by mass cytometry 05:55 - *M. Marchetti-Deschmann* - From Proteomics to Mass Spectrometry Imaging – The Study of Mycoparasitic Interactions 06:10 - *Y. Sugihara* - A Personalized Medicine Distribution in Malignant Melanoma Tissue with MALDI-MS Imaging 06:25 - *M. Vasso* - Sphingolipids in cystic fibrosis lung infection and inflammation: a MALDI Imaging approach

EuPA Young Investigators POSTER PRIZE

Closing Remarks

P. Roncada and A. Urbani

EuPA General Council Meeting

from 09:00 am to 05:00 pm - Aula 102

EDUCATIONAL PROGRAM

Morning Sessions

Protein crosslinking track A. Leitner; H. Urlaub

Liquid Chromatographic separation for MS analysis *C. Huber*

Proteome BioInformatics *M. Vaudel*

Afternoon Sessions

Protein HDX / covalent labeling track *K. Rand; L. Jones*

Experimental design in proteomics research *K. Lilley*

Proteome BioInformatics *M. Vaudel*

All Posters will be display from June, 24th 8.00 am until June, 26th at 16.30 pm, At last coffee break on June, 26th afternoon all posters must to be removed.

EuPA intends to promote young scientists in the field of Proteomics by establishing poster awards for the EuPA2015 Congress, Milano, June 24-26th, 2015 (www.eupa2015.org).

The two following categories will be considered:

Bachelor and Master Proteomics Award: open to all students and young scientists who have held a Bachelor or a Master degree for less than one year. Up to five candidates will be identified by the Educational Committee from all of the eligible presenting authors of posters. Oral presenters who wish to be considered must also provide a poster presentation for the evaluation procedure. Three awardees will be acknowledge with the following prizes:

- 1. 500.- €
- 2. 350.- €
- 3. 250.-€

POSTERS

YPI Award: open to all Ph.D. students and scientists who are Early Stage Researcher according to EU regulations (researchers of any nationality with up to 7 years of experience since completion of PhD or equivalent degree). Up to five candidates will be identified by the Educational Committee from all of the eligible presenting authors of posters. Oral presenters who wish to be considered must also provide a poster presentation for the evaluation procedure. The winner will be nominated EuPA2015 Young Proteomics Investigator and invited to submit a paper to EuPA Open Proteomics which will be recognized with an honorarium of 1000.- €. The second and third placed researchers will be awarded a prize of 500.- € and 350.-€ respectively.

The shortlist for this award (maximum 10) will be announced on the evening of June 25th and candidates will be required to deliver a 5 minute talk in front of the Award Committee on the afternoon of June 26th in the dedicated poster prize session.

Applicants for either of these awards have been previously registered by e-mail to : milanoeupa2015@gmail.com providing the following information: category of participation, title of the contribution they are presenting and the year and Institution in which the relevant Academic degrees were achieved.

001

LABEL-FREE MASS SPECTROMETRY-BASED VS 2D GEL-BASED QUANTITATIVE APPROACH TO IDENTIFY THE PROTEOMIC CHANGES THAT OCCUR IN CACO-2 CELLS EXPOSED TO GOLD NANOPARTICLES (AUNPS) Chassaigne, Hajduch, Gioria, Lobo Vicente, Barboro, Kinsner-Ovaskainen, Rossi

002

GLOBAL INVESTIGATION OF METABONOMIC AND PROTEOMIC RESPONSES TO HYPEROSMOTIC STRESS REVEALED NOVEL MOLECULAR MECHANISMS OF DRY EYE Zhou, Chen, Li, Guo, Koh, Aebersold, Chan, Beuerman

003

ORGANIC MATRIX PROTEINS OF OYSTER SHELLS AND BIO-MINERALIZATION Upadhyay

004

DEVELOPMENT FOR PLASMA BIOMARKER FOR DETECTION OF EARLY STAGE PANCREATIC CANCER USING ANTIBODIES FOR APOLIPOPROTEIN-AII ISOFORMS

Honda, Kobayashi, Okusaka, Nakamori, Shimahara, Ueno, Tsuchida, Sata, Ioka, Yasunami, Kosuge, Jung, Yamada

005

QUANTITATIVE ANALYSIS OF CEREBROSPINAL FLUID PROTEOME IDENTIFIES CHITINASE 3-LIKE PROTEINS AS CANDIDATE BIOMARKERS FOR MULTIPLE SCLEROSIS DIAGNOSIS AND PROGNOSIS Hinsinger, Urbach, Vigy, Lehmann, Thouvenot, Séveno, Marin

006

THE INTERACTOME OF RAR-ALPHA IN A NOVEL SUBTYPE OF BREAST CANCER REVEALED BY SILAC Brunelli, Garattini, Pastorelli, Terao

007

THE PROGNOSTIC VALUE AND BIOLOGICAL EFFECTS OF GLYCOPROTEIN QSOX1 ON RECURRENCE AND METASTASIS OF HEPATOCELLULAR CARCINOMA Zhou, Qin

008

PROTEOMIC ANALYSIS OF THE MODEL METHANOARCHAEA METHANOSARCINA MAZEI Cassidy, Prasse, Schmitz-Streit, Tholey

009

PERSONALIZED PROTEOGENOMICS OF HUMAN CANCER CELL LINES

Karpov, Ivanov, Karpova, Kuznetsova, Levitsky, Kopylov, Zgoda, Gorshkov, Moshkovskii

010

A MALDI-TOF-MS PLATFORM FOR INTEGRATED PROTEOMIC AND PEPTIDOMIC PROFILING OF MILK SAMPLES ALLOWS RAPID DETECTION OF ILLEGAL FOOD ADULTERATIONS

Sassi, Arena, Scaloni

011

UP-REGULATED TRANSGELIN INCREASES THE INVASIVENESS OF CANCER STEM CELLS Kim*, Song , Han, Lee, Jeong

012

PROTEOMIC ALTERATIONS IN HUMAN RENAL EPITHELIAL CELLS EXPOSED TO NEPHROTOXINS Kollipara, Limonciel, Zahedi, Sickmann, Jennings

013

PROCAINAMIDE LABELING ENABLES SENSITIVE AND EFFICIENT GLYCOPROFILING BY HILIC-FLR-MS Rav. Gau

014

COMPARATIVE PROFILING BETWEEN STROMAL FIBROBLAST-LIKE STEM CELLS (F-LSCS) AND ADULT HUMAN FIBROBLASTS.

Musso, Di Cara, Cancemi, Tomasello , Cillino, Giordano, Pucci-Minafra

015

LIPIDOMICS STUDY OF SERUM EXOSOMES IN MULTIPLE SCLEROSIS PATIENTS

D'Alessandro, Raimondo, Cicalini, Pieragostino, Di Ioia, Lugaresi, Sacchetta, Pitto, Del Boccio

016

IMPACT OF CONVENTIONAL CIGARETTE SMOKING AND CESSATION ON THE LUNG PROTEOME OF ApoE-/-MICE QUANTIFIED BY TANDEM MASS TAG (TMT) LC MS/MS APPROACH.

Dijon, Nury, Schneider, Titz, Elamin, Martin, Philips , Vanscheeuwijck, Ivanov, Peitsch, Hoeng

017

ONLINE MULTIPHASE CHIP LC FRACTIONATION TO ENHANCE MELANOMA CELL PROFILING BY SWATH DATA INDEPENDENT MASS SPECTROMETRY Krisp, Parker, van Soest, Yang, Molloy

018

CLUSTERING AND IDENTIFICATION OF COMMON FOODBORNE PATHOGENS FROM MALDI-TOF MASS SPECTRA USING SELF-ORGANISING MAP Seah, Liang, Liew, Kong, Mesbahi, Lau

019

PLASMA PROTEOMIC ANALYSIS OF PATIENTS WITH CORONARY ARTERY DISEASE WITH DIFFERENT LEVELS OF APOLIPOPROTEIN CIII

Chiariello, Castagna, Manfredi , Ranzato, Martinotti, Marengo, Cecconi, Olivieri

020

THE NORMAL VARIATION OF CANCER ASSOCIATED PROTEINS IN BLOOD PLASMA Stenemo, Teleman, Sjöström, Grubb, Malmström, Malmström, Niméus

021

DECIPHERING MOLECULAR CONSEQUENCES OF THE PROHORMONE CONVERTASE 1/3 INHIBITION IN MACROPHAGES FOR APPLICATION IN IMMUNOTHERAPY Duhamel, Rodet, Delhem, Vanden Abeele, Kobeissy, Day, Wisztorski, Fournier, Salzet

022

SECRETOME ANALYSIS OF PANCREATIC CANCER STEM CELLS BY ITRAQ-BASED SHOTGUN PROTEOMICS REVEALS CERULOPLASMIN AS A PROMISING PUTATIVE DIAGNOSTIC BIOMARKER Brandi, Dalla Pozza, Dando, Biondani, Robotti, Jenkins, Elliott, Park, Costello, Scarpa, Palmieri, Cecconi

023

PEPTIDOMIC PROFILING OF GINGIVAL CREVICULAR FLUID BY MALDI-TOF MASS SPECTROMETRY: ASSESSMENT OF COLLECTION AND STORAGE CONDITIONS Preianò, Maggisano, Falcone, Paduano, Savino, Terracciano

024

PHOSPHOPROTEOME CHARACTERIZATION OF HEK 293 CELL LINE EXPRESSING THE ATYPICAL CHEMOKINE D6 RECEPTOR

Nonnis, Borroni, Maffioli, Santagata, Negri, Locati, Tedeschi

025

PROTEOMIC ANALYSIS OF THE HUMAN MESENCHYMAL STEM CELLS SECRETOME USING A LABEL-FREE APPROACH

Nonnis, Zanotti, Maffioli, Santagata, Negri, Viola, Tedeschi

026

ORANGE PROTEOMIC FINGERPRINTING: FROM FRUIT TO COMMERCIAL JUICES

Lerma-García, D'Amato, Simó-Alfonso, Righetti, Fasoli

027

PROTEOMIC PROFILE CONFIRMS NANOSTRUCTURE-INDUCED NEURITOGENESIS AND REFLECTS ALTERATIONS OF THE MECHANOTRANSDUCTIVE PROCESSES IN PC12 CELLS Maffioli, Schulte, Nonnis, Negri, Puricelli, Borghi, Sogne, Piazzoni, Santagata, Podestà, Lenardi, Milani, Tedeschi

028

SUBTILISIN - AN ALTERNATIVE ENZYME FOR PTM RESEARCH

Gonczarowska-Jorge, Dell'Aica, Dickhut, Zahedi

029

PROTEOME DISSECTION OF THE ATHEROSCLEROTIC PLAQUE: A DEEP IMMERSION INTO THE EXTRACELLULAR MATRIX OCEAN

Ucciferri, Cecchettini, Comelli, Pelosi, Terreni, Marconi, Ferrari, Rocchiccioli

030

A PNEUMOCOCCAL PROTEIN ARRAY AS A PLATFORM TO DISCOVER SERODIAGNOSTIC ANTIGENS AGAINST INFECTION

Olaya-Abril, Jiménez-Munguía, Obando, Rodríguez-Ortega

031

PROTEOMICS APPROACH AS A TOOL FOR SALIVARY FINGERPRINT CHARACTERIZATION ABLE TO DISCRIMINATE DIFFERENT SJÖGREN'S SYNDROME PHENOTYPES

Rocchiccioli, Martini, Ucciferri, Baldini, Sernissi, Mosca, Lorenzini, Cecchettini

032

PEPTIDOME CHARACTERIZATION OF PLASMA SAMPLES FROM HEALTHY AND HEMORRHAGIC-SHOCK RATS Maffioli, Santagata, Aletti, Nonnis, Schmid-Schoenbein, Negri, Tedeschi

033

BIOCOMPATIBILITY ASSESSMENT OF HAEMODIALYSIS MEMBRANE MATERIALS BY PROTEOMIC INVESTIGATIONS

Pieroni, Levi Mortera, Greco, Ronci, Sirolli, Fucci, Bernardini , Di Daniele, Bonomini, Urbani

034

IMPROVED SELECTIVITY FOR THE QUANTITATION OF PROTEINS IN COMPLEX BIOLOGICAL SAMPLES BY THE USE OF THE SelexION TM TECHNOLOGY

Merkel, Dojahn, Macht

035

BALANCING SPEED, SAMPLE COMPLEXITY AND DATA QUALITY IN PROTEOMICS APPLICATIONS ON A BENCH TOP QUADRUPOLE ORBITRAP MASS SPECTROMETER Arrey, Damoc, Xuan, Strupat, Lai, Moerhing, Kellmann

036

VARIABLE STOICHIOMETRY AMONG CORE RIBOSOMAL PROTEINS Slavov, van Oudenaarden, Budnik

037

THE OXIDIZED PROTEOME OF PERIPHERAL BLOOD MONONUCLEAR CELLS: A VALUABLE REPOSITORY FOR CLINICAL PROTEOMICS

Xie, Jiang, Lopez-Ferrer, Dauly, Huhmer

038

THE USE OF CAPILLARY ELECTROSPRAY IONIZATION (CESI) FOR THE CHARACTERIZATION OF PROTEINS BY NATIVE MS. THE SEPARATION OF INTACT PROTEINS BY CAPILLARY ZONE ELECTROPHORESIS AND IT USE IN THE ANALYSIS OF TRYPTIC DIGESTS OF BIOPHARMACEUTICALS Lock

039

A PROTEOMIC ANALYSIS OF GLYCOPROTEIN VI SIGNALING REVEALS THIS PLATELET RECEPTOR AS A PROMISING DRUG TARGET IN ST-SEGMENT ELEVATION ACUTE MYOCARDIAL INFARCTION Vélez, Ocaranza-Sánchez, López-Otero, Grigorian-Shamagian, Izquierdo, Rosa, González-Juanatey, García

040

SPATIAL AND TEMPORAL 3D MSI AND PROTEOMIC STUDIES OF RAT SPINAL CORD INJURY: EVIDENCE OF CAUDAL SEGMENT FOR POSSIBLE THERAPY TARGET

Devaux, Cizkova, Quanico, Franck, Hauberg-Lotte, Mass, Wisztorski, Slovinska, Blasko, Fournier, Salzet

0/1

THE FIRST MASTER PROTEOME OF SINGLE CHROMOSOME: EXAMPLE OF HUMAN CHROMOSOME 18 Archakov, Ponomarenko, Poverennava, Lisitsa, Kopylov, Zgoda

042

THE MZQLIBRARY/MZQVIEWER -- AN OPEN SOURCE JAVA LIBRARY FOR SUPPORTING QUANTITATIVE **PROTEOMICS STANDARD**

Qi, Zhang, Fan, Simpson, Pisconti, Perkins, Bessant, Hubbard, Jones

043

PANCREATIC CANCER ASSOCIATED POTENTIAL BIOMARKER MINING BY MASS SPECTROMETRY BASED-CLINICAL VALIDATION

Lee, Park, Lee

044

SHOTGUN LABEL-FREE PROTEOMIC ANALYSIS OF THE BRAIN EXTRACELLULAR MATRIX IN THE EARLY STAGE OF 5XFAD ALZHEIMER'S DISEASE MOUSE MODEL Gurel, Sevinc, Cansev, Baykal

045

LABEL-FREE SHOTGUN PROTEOMICS ANALYSIS OF HUMAN MEDULLOBLASTOMA CANCER STEM-LIKE CELLS: INSIGHTS INTO THE QUIESCENT STATE

Ronci, Catanzaro, Pieroni, Po, Ferretti, Urbani

046

LIPIDOMICS-TLC-MALDI-IMAGING APPROACH REVEALS LOW LEVELS OF SPHINGOMYELINS IN CEREBROSPINAL FLUID OF MULTIPLE SCLEROSIS PATIENTS Pieragostino, Cicalini, D'Alessandro, di Ioia, Lugaresi, Urbani, Sacchetta, Del Boccio

047

ANALYSIS OF OXYSTEROLS-MEDIATED ANTIVIRAL ACTIVITY BY QUANTITATIVE PROTEOMICS Colzani, Civra, Cagno, Aldini, Lembo, Poli

048

PERFORMANCE EVALUATION OF THE Q EXACTIVE™ HF HYBRID QUADRUPOLE-ORBITRAP MASS SPECTROMETER FOR HIGH-THROUGHPUT TOP-DOWN PROTEOMICS Eugen, Ping, Leena, Alexander, Bernard, Eduard, Oksana, Helene, Jason, Alexander, Jim

049

RENAL CELL CARCINOMA BIOMARKERS: A LABEL-FREE PROTEOMIC STRATEGY BASED ON URINARY **EXOSOMES**

Corbetta, Raimondo, Cerra, Chinello, Cazzaniga, Magni, Pitto

050 CHLOROPLAST PROTEOME RESPONSE TO WATER DEFICIT IN TOMATO

Tamburino, Vitale, Ruggiero, Sassi, Sannino, Arena, Costa, Batelli, Scaloni, Grillo, Scotti

051

PROTEOMICS OF URINARY EXOSOMES FOR THE DIFFERENTIAL DIAGNOSIS OF SALT-LOSING TUBULOPATHIES

Cerra, Corbetta, Raimondo, Cazzaniga , Chinello, Magni, Pitto

052

PROTEOMICS EXPRESSION IN HEALTHY AND OSTEOPOROTIC-LIKE CONDITIONS DURING EARLY AND LATE STAGES OF BONE REGENERATION

Calciolari, Mardas, Dereka, Anagnostopoulos, Papadopoulou, Lelovas, Kostomitsopoulos, Tsangaris, Donos

053

DIFFERENTIAL PROTEIN EXPRESSION AND CHANGES IN THE PHOSPHOPROTEOME OF BROWN ADIPOSE TISSUE IN HIBERNATING GROUND SQUIRRELS

Vertommen, Herinckx, Hussain, Opperdoes, Storey, Rider

054

IDENTIFICATION OF OVER-EXPRESSED PROTEINS IN PROSTATE CANCER STEM

Aikins, Cho, Kim, Kim

055

DING PROTEINS INVOLVED IN ALZHEIMER'S DISEASE IDENTIFIED BY PROTEOMIC ANALYSIS Andreadou, Pantazaki, Papadopoulou, Tsangaris, Tsolaki

056

PROTEOMICS STUDIES OF PEDIATRIC EPENDYMOMA TUMORS Anagnostopoulos, Teangaris

057

LARGE SCALE QUANTITATION OF STABLE ISOTOPE LABELLED PROTEOMES USING RETENTION AND DRIFT TIME PROFILING

Collins, McCabe, Morns, Vissers, Jones

058

A PROTEOMIC APPROACH TO EXPLORE PROTEIN PROFILE CHANGES IN PLASMA FROM WOMEN WITH CHRONIC WIDESPREAD PAIN

Wåhlén, Carlsson, Olausson, Ghafouri, Gerdle, Ghafouri

059

DO SPECIFIC PROTEINS CORRELATE WITH PAIN SENSITIVITY AND INTENSITY? - A MULTIVARIATE PROTEOMIC STUDY OF THE TRAPEZIUS MUSCLE IN WOMEN WITH CHRONIC WIDESPREAD PAIN Olausson, Ghafouri, Ghafouri, Gerdle

060

N-TERMINOMICS AS A NOVEL TOOL FOR A BETTER UNDERSTANDING OF PROTEIN TRAFFICKING OF PLASMODIUM FALCIPARUM

Westermann, Bertaccini, Sanchez, Lanzer, Van Dorsselaer, Schaeffer-Reiss

061

DIFFERENTIAL PROTEOMICS UNVEILS METABOLIC PATHWAYS AND REGULATORY NETWORKS IN MICROBISPORA SP. ATCC-PTA-5024 ASSOCIATED TO NAI-107 LANTIBIOTIC PRODUCTION Gallo, Renzone , Palazzotto, Monciardini, Arena, Faddetta, Giardina, Alduina, Weber, Spinelli, Sosio, Scaloni, Puglia

062

PROBING THE PROTEIN EXPRESSION PROFILE DIFFERENCES IN ERYTHROCYTES OF ALCOHOL USE DISORDER PATIENTS

Boşgelmez, Güvendik, Dilbaz, Esen

063

BIOMARKERS OF EXPOSURE TO DIOXIN-LIKE COMPOUNDS IN CONTAMINATED CATTLE: A PROTEOMIC APPROACH

Renzone, Girolami, Spalenza, Manzini, Badino, Rychen, Feidt, Salzano, Dal Piaz, Scaloni, Nebbia

064

MEGAPIXEL TISSUE IMAGING AT HIGH-SPEED: EVALUATION OF A MALDI-TOF PROTOTYPE Becker, Schaefer, Beckmann, Fütterer, Holle, Höhndorf

065

HOW PROTEOMICS CAN PROVIDE USEFUL INFORMATION FOR METABOLIC ENGINEERING PURPOSES Ferro, Berny, Bestel-Corre, Bournais, Bruley, Brun, De Jong, Curien, Finazzi, Gloaguen, Jaquinod, Rolland, Tardif, Tomizioli, Vandenbrouck, Trauchessec

066

IDENTIFICATION OF FBXO7 INTERACTORS: THE ROLE OF UBL DOMAIN IN PARKINSON'S DISEASE Zilocchi, Alberio, Mandemakers, Peroni, Pieroni, Urbani, Bonifati, Fasano

067

QUANTITATIVE PROTEOMICS OF WEIGHTLESSNESS AFTER A 30-DAY SPACE FLIGHT IN MICE VS. PHYSICAL INACTIVITY AFTER 5 MONTHS OF HIBERNATION IN BROWN BEARS

Tascher, Ziemianin, Evans, Arnemo, Swenson, Van Dorsselaer, Gauquelin-Koch, Blanc, Bertile

068

THYROID-ASSOCIATED ORBITOPATHY: BIOMARKERS DISCOVERY IN TEARS BY QUANTITATIVE PROTEOMICS

Graciá, Eperon, Fouda, Hainard, Salvisberg, Hamedani, Turck

069

TOWARDS A GENERIC PROTEOMICS METHOD

Kaspar, Lubeck, Michalski, Andersen, Schmit

070

MASS SPECTROMETRY IDENTIFICATION OF PEPTIDES AND PROTEINS FROM NAJA NAJA VENOM Inserra, Vincenzoni , Marzano , Iavarone, Castagnola, Petruzzelli, Patamia

071

A SYSTEMATIC INVESTIGATION OF CID QTOF COLLISION ENERGIES TO ALLOW THE IDENTIFICATION OF COMPLETE N- AND O-GLYCOPEPTIDE

Hinneburg, Stavenhagen, Pengelley, Seeberger, Silva, Wuhrer, Kolarich

072

PROTEOMIC ANALYSIS OF RAT PERIPHERAL NERVES IMPLANTED WITH MICRO-PATTERNED COLLAGEN SCAFFOLD

Rizzello, Vergara, Franck, Gimeno, Mosticchio, Romano, Cerri, Storelli, Fournier, Salzet, Quattrini, Maffia

073

EPITHELIAL MESENCHYMAL TRANSITION INDUCES ALTERATIONS OF LIPID METABOLISM

Vergara, Giudetti, Simeone, Gimeno, Franck, De Nuccio , Lunetti , Rizzello, Fournier , Capobianco, Salzet, Maffia

074

TRAUMA PROTEOME: PROTEOME CHANGES IN INDIVIDUAL SUBJECTS AFTER MICRODIALYS CATHETER TRAUMA

Turkina, Ghafouri, Gerdle, Ghafouri

075

LARGE SCALE METABOLIC EXPLORATION OF HUMAN CSF PROTEINS USING SILAV Lehmann, Schmit, Gabelle, GRAS COMBE, Tall, Hanon, Hirtz

076

PROTEOMIC AND METABOLOMIC CHARACTERIZATION OF STREPTOZOTOCIN-INDUCED DIABETIC NEPHROPATHY IN TIMP3 DEFICIENT MICE

Rossi, Marzano, Zucchelli, Consalvo, Levi Mortera, Menghini, Casagrande, Mavilio, Sacchetta, Federici, Urbani, Ciavardelli

077

TOP-DOWN CHARACTERIZATION OF PUTATIVE BIOACTIVE PEPTIDES OF BEER

Granieri , Nobile , Iavarone, Vincenzoni, Marzano, Messana, Castagnola, Palmerini, Vitali

078

HIGH PH REVERSED-PHASE PEPTIDE FRACTIONATION IN A CONVENIENT SPIN-COLUMN FORMAT. Snovida, Jiang, Ganapathy, Hou, Bomgarden, Haney, Viner, Hornshaw, Rogers

079

OVERCOMING THE CHALLENGES IN DATA INDEPENDENT ACQUISITION (DIA) VIA HIGH RESOLUTION ACCURATE MASS ORBITRAP BASED MASS SPECTROMETER.

Xuan, Muntel, Berger, Huhmer, Steen, Oppermann, Moehring

080

PROTEOMIC ANALYSIS OF AIRWAY EPITHELIAL CELLS EXPOSED TO CIGARETTE SMOKE EXTRACT (CSE) AND LIPOPOLYSACCHARIDE (LPS)

Cigna, D'Anna, Bruno, Di Vincenzo , Ferraro, Armini, Bianchi, Bini, Gjomarkaj, Pace

081

DEVELOPMENT OF A NOVEL NANO SEPARATION DEVICE FOR ROBUST AND ACCURATE GRADIENT DELIVERY WITH INTELLIGENT DIAGNOSTICS

Kaspar, Gebhardt, Podtelejnikov, Nielsen, Hørning

082

UNRAVELING THE ROLE OF MMP2 AND MMP12 IN PULMONARY FIBROSIS BY TAILS N-TERMINOMICS. Marino, McLeod, Eckhard, Overall

083

RAPID GENERATION OF ACCURATE INFORMATION ON PROTEOFORMS DISTRIBUTION AND RELATIVE ABUNDANCY BY UHR-QTOF MS

Schmit, Meyer, Jabs, Pengelley, Albers

084

ENRICHMENT OF NICKEL BINDING HUMAN SALIVARY PEPTIDES BY NICKEL CHARGED HIS TRAP FF COLUMNS

Delfino, Della Vecchia, Marzano, Vincenzoni, Iavarone, Cabras, Messana, Castagnola, Vitali

085

ANTIBODYPEDIA - THE WIKI OF ANTIBODIES Alm, Von Feilitzen, Uhlén

086

MALDI-MS METHOD FOR THE MEASUREMENT OF UBIQUITIN ACTIVATION

Di Natale, Pappalardo, Milardi

087

PROTEOMICS OF URINARY EXOSOMES FOR THE DIFFERENTIAL DIAGNOSIS OF SALT-LOSING TUBULOPATHIES

Cerra, Corbetta, Raimondo, Cazzaniga , Chinello, Magni, Pitto

88

LIPOSUCTION ASPIRATE FLUID (LAF): A PRELIMINARY INVESTIGATION OF ITS PROTEOME Desiderio, Inserra, Martelli, Cipollina, Rossetti, Iavarone, Vincenzoni, Castagnola, di Taranto, Barba, Lattanzi

089

LC-MS TOP-DOWN PROTEOMIC CHARACTERIZATION OF DAOY MEDULLOBLASTOMA TUMOUR CELL LINE Martelli, D'Angelo, Barba, Baranzini, Tamburrini, Massimi, Di Rocco, Caldarelli, Iavarone, Michetti, Messana, Castagnola, Lattanzi, Desiderio

090

EXPLORING DEPTH AND BREADTH OF A PROTEIN COMPLEX MIXTURE WITH TOP-DOWN DATA INDEPENDENT ACQUISITION USING A TRIBRID ORBITRAP MASS SPECTROMETER Bailey, Horn, Sharma, Huguet, Dauly, Zabrouskov

091

CELLULAR DIFFERENTIATION PROGRAM IS TRIGGERED BY TRYPTOPHAN IN THE ACTINOBACTERIUM MODEL STREPTOMYCES COELICOLOR Renzone, Palazzotto, Gallo, Fontana, Sutera, Scaloni, Puglia

092

COMPARATIVE PROTEOMIC PROFILING OF HODGKIN LYMPHOMA CELL LINES Vergara, Simeone, De Matteis, Carloni, Rizzello, Napolitano, Maffia

093

SYSTEMS BIOLOGY ANALYSIS OF THE PROTEOMIC ALTERATIONS IN PARKINSON DISEASE AND AMYOTROPHIC LATERAL SCLEROSIS: COMMON AND DISEASE-SPECIFIC PATHWAYS Monti, Lopiano, Chiò, Fasano, Alberio

094

SMALL PROTEIN SCO2038: A KEY FACTOR IN MODULATING TRYPTOPHAN BIOSYNTHESIS IN THE ACTINOBACTERIUM MODEL STREPTOMYCES COELICOLOR

Palazzotto, Renzone, Gallo, Sutera, Giardina, Silva, Vocat, Fabbretti, Scaloni, Puglia

095

COMPREHENSIVE RELATIVE QUANTIFICATION OF THE CYTOCHROMES P450 USING SWATH ACQUISITION Jenkins, Heidelberger, Knapman, Brancia, Kitteringham, Park

096

DIFFERENTIAL MOBILITY SPECTROMETRY ANALYSIS OF GLYCANS AND GLYCOPEPTIDES Chang, J.C. Yves, Larry, Catherine S., Sarah A., Joerg, Tim L.

097

HUMAN MACROPHAGES SPONTANEOUSLY DIFFERENTIATED IN VITRO ARE HETEROGENEOUS AND SHOW DIFFERENT PROTEOMIC PROFILE

Brioschi, Eligini , Fiorelli , Tremoli, Colli, Banfi

098

PROTEOMICS LED TO THE IDENTIFICATION OF A NOVEL ROLE FOR THE PROCOAGULANT TISSUE FACTOR IN THE CONTROL OF THE SPLICING MACHINERY Banfi, Brioschi, Ghilardi, Tremoli

099

QUANTITATIVE CROSS-LINKING/MASS SPECTROMETRY ILLUMINATES THE CONFORMATIONAL CHANGE-DRIVEN ACTIVATION OF COMPLEMENT

Chen, Fischer, Zou, Tahir, Bukowski-Wills, Rappsilber, Barlow

100

PROTEOMIC CHARACTERISATION OF THE HUMAN MITRAL VALVE Brioschi, Baetta, Ghilardi, Guarino, Polvani, Parolari, Tremoli, Banfi

101

SELECTED REACTION MONITORING AS A TARGETED MS APPROACH FOR THE ACCURATE QUANTITATION OF PROTEINS: AN EXAMPLE OF APPLICATION ON PRENYLCYSTEINE OXIDASE1 Gianazza, Tremoli, Banfi

102

IDENTIFICATION OF SURFACTANT PROTEIN B ISOFORMS AS MARKER OF ALVEOLAR CAPILLARY MEMBRANE DAMAGE IN PATIENTS WITH HEART FAILURE

Banfi, Ghilardi, Magrì, Salvioni, Tremoli, Agostoni

103

MICROFLOW LC-MSMS ON QqTOF MASS SPECTROMETERS FOR PROTEOMIC APPLICATIONS Nicholas, Joerg

104

PRESERVED SAMPLE INTEGRITY BY HEAT STABILIZATION

Sköld, Söderquist, Borén

105

DIFFERENTIAL PROTEOMICS OF COLORECTAL CANCER : SEARCHING FOR SENTINEL CANCER PROTEINS

Repetto, Canzonieri, Cannizzaro, De Re

106

PROLINE: AN MS DATA WORKBENCH FOR VIEWING AND ANALYZING PROTEOMICS DATASETS Bouyssié, Dupierris, Barthe-Dejean, Bodin, Burel, Carapito, Menetrey, Poisat, Walter, Yapici, Burlet-Schiltz, Vandorssaeler, Cianferani, Ferro, Bruley, Garin

107

A DEEP EXPLORATION OF GOAT MILK PROTEOME VIA COMBINATORIAL PEPTIDE LIGAND LIBRARY TECHNOLOGY AND HIGH RESOLUTION MASS SPECTROMETRY Cunsolo, Fasoli, Muccilli, Gallina, Saletti, Righetti, Foti

108

COMPARATIVE PROTEIN EXPRESSION ANALYSIS OF UTERINE LEIOMYOMA

Rizzello, Pellegrino, Francesco, Mosticchio, Giudetti, Fiore, Di Tommaso, Tinelli, Maffia, Vergara

109

OXIDATION STATES OF HUMAN RECOMBINANT AND RAT LIVER MITOCHONDRIA VDAC3 INVESTIGATED BY MASS SPECTROMETRY

Reina, Saletti, Cunsolo, Belfiore, Pittalà, Foti, De Pinto

110

EXPRESSION OF DP71Δ78-79 DYSTROPHIN MUTANT IN PC12 CELLS STIMULATES NEURITE OUTGROWTH THROUGH UPREGULATED EXPRESSION OF HspB1

Merino-Jiménez, Aragón, Ceja, Rodríguez-Martínez, Cazáres, Chardonnet, Pionneau, Rendon, Montañez

111

COMPARATIVE PROTEOMIC ANALYSIS OF DIFFERENT FRAGILE X SYNDROME CELL LINES: ROLE OF MITOCHONDRIAL SUPEROXIDE DISMUTASE IN DNA METHYLATION

Marzano, Lanni, Palumbo, Goracci, Mancano, Iavarone, Vincenzoni, Castagnola, Chiurazzi, Neri, Tabolacci, Vitali

112

PROTEIN STRUCTURE DETERMINATION IN BIOLOGICAL MATRICES USING 3D PROTEOMICS AND COMPUTATIONAL BIOLOGY

Belsom, Schneider, Zou, Fischer, Brock, Rappsilber

113

AUTOMATIZED WORKFLOW FOR BLOOD SAMPLES ALIQUOTING

Yan, Yakovleva, Sugihara, Rezeli, Erlinge, Malm, Marko-Varga

114

BIOMARKERS IDENTIFICATION IN CEREBROSPINAL FLUID PROTEOME FROM CENTRAL NERVOUS SYSTEM PEDIATRIC TUMORS

Bongarzone, Pizzamiglio, Magni, Taverna , De Bortoli, Ciniselli, Barzanò , Biassoni, Luchini , Liotta, Massimino, Verderio , Spreafico

115

A PROTEOMIC LOOK AT ACTINOMYCETE PLANOBISPORA ROSEA, THE PRODUCER OF GE2270 ANTIBIOTIC Tocchetti, Bordoni, Gallo, Salzano, Scaloni, Puglia

116

SIEVING THROUGH THE CANCER SECRETOME OF MALIGNANT MESOTHELIOMA Martinotti. Manfredi. Marengo, Ranzato

117

AN INVESTIGATION INTO MULTI-MODEL TISSUE IMAGING ON A SINGLE SECTION BY DESI AND MALDI MS Edwards, Rainville, Murphy, Astarita, Wilson, Langridge

118

PROTEIN CARBOXY TERMINI ANALYSIS BY CHEMICAL DERIVATIZATION AND INDIRECT ENRICHMENT Somasundaram, Koudelka, Linke, Tholey

119

PROTEOMIC APPROACH FOR THE STUDY OF SELECTIVE DICER SUPPRESSION IN THE KIDNEY Fiumara

120

EFFECTS OF THE MITOCHONDRIAL LON PROTEASE INACTIVATION ON THE MITOCHONDRIAL ANTIOXIDANT PROTEIN PEROXIREDOXIN 3 Musicco, Cormio, Pinti, Gibellini, Cossarizza, Gadaleta

121

A CHEMICAL KNOCKOUT OF VIRULENCE REGULATOR CLPP INDUCES GLOBAL CHANGES IN THE PROTEOME AND THE TRANSCRIPTOME OF STAPHYLOCOCCUS AUREUS Wroblewski, Erhard, Csaba, Zimmer, Sieber

122

FUNCTIONAL PREDICTIVE ANALYSIS OF BIOLOGICAL PROCESSES OCCURRING IN THE ASCOMYCETES FUNGUS TUBER BORCHII VITT. DURING MYCELIAL PHASE Bianchi, Carnemolla, Landi, Gagliardi, Armini, Pierleoni, Stocchi, Bini



123

PROTEOMIC ANALYSIS OF SECRETED PROTEINS AND EXTRACELLULAR VESICLES FROM CANDIDA ALBICANS SC5314 AND THE ECM33 MUTANT STRAINS

Gil-Bona , Gil, Monteoliva

124

BACTERIAL EXTRACELLULAR PEPTIDOMES: EXTENT, SOURCES AND PRODUCTION PATHWAYS Juillard, Guillot , Boulay , Gitton, Monnet

125

AORTIC VALVE DEGENERATION: INVESTIGATING THE PROTECTIVE ROLE OF L-ARGININE Franchin, Millioni, Mortarino, Bertacco, Rattazzi, Arrigoni

126

PROTEOMIC PROFILING OF ARABIDOPSIS ROOTS TREATED WITH HUMIC SUBSTANCES Pivato, Arrigoni, Conselvan, Nardi, Roomi, Masi, Carletti

127

THE PUTATATIVE DIAGNOSTIC ROLE OF MALDI-MSI IN PRIMARY GLOMERULONEPHRITIS Smith, Pagni, Ferrario, De Sio, Galli, Chinello, Vlahou, Magni

128

PROTEOMIC AND PHOSPHOPROTEOMIC ANALYSIS OF THE HUMAN MACROPHAGES KINOME AFTER INTERACTION WITH CANDIDA ALBICANS

Vaz, Vellosillo, Hernáez, Reales - Calderón, Monteoliva, Gil

129

DIFFERENTIAL PEPTIDOMIC PROFILES BETWEEN FIORE SARDO CHEESE OBTAINED FROM RAW AND PASTEURIZED MILK

Abbondio, Pisanu, Addis, Anedda, Uzzau, Pagnozzi

130

NOVEL MILK PROTEIN BIOMARKERS FOR MASTITIS IN DAIRY ANIMALS AND THEIR IMPLEMENTATION IN DIAGNOSTIC TOOLS

Tedde, Pisanu, Puggioni, Pagnozzi, Uzzau, Dore, Cannas, Ibba, Contu, Bronzo, Moroni, Addis

131

MYCOBACTERIUM SMEGMATIS RESPONSE TO METHYLATION STRESS

Di Pasquale, Caterino, De Maria, Duilio

132

INTERKINGDOM SIGNALLING: TARGETS OF OPIOID PEPTIDES IN PATHOGENIC BACTERIA Wright, Sieber

133

MALDI-MSI AS A PUTATIVE DIAGNOSTIC TOOL IN THYROID LESIONS De Sio, Pagni, Smith, Galli, Pedretti, Chinello, Magni

134

THE IMPACT OF TEMPERATURE CHANGES ON THE LIVER METABOLISM OF GILTHEAD SEA BREAM (SPARUS AURATA)

Ghisaura, Biosa, Pagnozzi, Anedda, Bonaglini, Cappuccinelli, Slawski, Roggio, Uzzau, Addis

135

PROTEOMIC CHARACTERIZATION OF THE SEA URCHIN ROE FOR UNDERSTANDING AND MONITORING QUALITY

Ghisaura, Biosa, Pagnozzi, Anedda, Baroli, Loi, Guala, Roggio, Uzzau, Addis

136

ENHANCING THE ANALYTICAL CAPABILITIES OF DESI IMAGING USING ION MOBILITY SEPARATION Gallo, Claude, Jones, Towers, Skraskova, Langridge, Heeren

137

FINDING TARGETS OF MITOCHONDRIAL PROTEASES ACTIVATED BY DOPAMINE

Bondi, Di Pierro, Monti, Alberio, Ronci, Cilio, Pieroni, Urbani, Fasano

138

PROTEOMICS-BASED ANALYSES FOR GUT MICROBIOTA INVESTIGATIONS

Del Chierico, Vernocchi, Levi Mortera, Dallapiccola, Urbani, Putignani

139

"LABEL-FREE" DIFFERENTIAL MEMBRANE PROTEOMICS FOR THE SEARCH OF NOVEL GLIOBLASTOMA CANCER STEM CELL BIOMARKERS

Muller, Robil, Dong, Chneiweiss, Kilhoffer, Haiech, Petel, Cianferani

140

NEW PERSPECTIVES IN CANINE MYXOMATOUS MITRAL VALVE DISEASE

Alloggio, Piras, Soggiu, Brambilla, Greco, Locatelli, Minozzi, Groppetti, Riscazzi, Urbani, Bonizzi, Roncada

141

INCREASE OF HIPPOCAMPAL ALUMINUM IS LINKED TO THE OVEREXPRESSION OF MCT4 IN A TRIPLE TRANSGENIC MOUSE MODEL OF ALZHEIMER'S DISEASE Consalvo. Rossi. Sacchetta. Di Ilio . Sensi. Ciavardelli

142

MALDI-MSI ON THYROID TISSUE MICROARRAYS: PRELIMINARY RESULTS

Galli, De Sio, Pagni, Smith, Calza, Chinello, Magni

143

HMGB1 INDUCES OSTEOGENIC PHENOTYPE IN SaOS-2 CELLS Martinotti, Manfredi, Pedrazzi, Patrone, Marengo, Ranzato

144

DIFFERENCE ENERGY BALANCE IN CATTLE MODULATE ADIPOSE TISSUE PROTEOME Piras, Soggiu, Dupont, Greco , Humblot, Urbani, Roncada, Bonizzi

145

KRABBE DISEASE: PROTEOMIC INVESTIGATION AT BRAIN AND SERUM LEVEL FOR BIOMARKER'S DISCOVERY

Landi, Bianchi, Luddi, Gagliardi, Piomboni, Bini

146

PEPTIDE MRM COMPARISON USING INTEGRATED MICROFLUIDICS/NANOSCALE LC WITH HIGH/LOW RESOLUTION MS

Gallo, Hughes, Molloy, Vissers, Langridge

147

DIFFERENTIAL ANTIBIOTIC RESISTANCE TO 4TH GENERATION CEPHALOSPORIN (4GC) OF APEC ISOLATES FROM POULTRY

Soggiu, Piras, Martino, grilli, Urbani, Roncada, Bonizzi

148

LC-MS APPROACHES FOR A METAPROTEOMIC DESCRIPTION OF PERINATAL MOUSE GUT MICROBIOTA IN CORRELATION WITH GENETIC BACKGROUND AND FEEDING CONTROLS Levi Mortera, Vernocchi, Del Chierico, Rosado, Carsetti, Urbani, Putignani

149

POTENTIAL BIOMARKER PANEL FOR THE DIAGNOSIS OF MALIGNANT PLEURAL MESOTHELIOMA Giusti, Ciregia, Donadio, Bonotti, Da Valle, Foddis, Giannaccini, Mazzoni, Guglielmi, Cristaudo, Lucacchini

150

FATE OF ANTIGENS ENCODED BY SELF-AMPLIFYING RNA VACCINES

Fontana

151

TEMPERATURE OPTIMIZATION FOR MONOCLONAL ANTIBODY ANALYSIS BY REVERSED-PHASE HPLC Squillario, Brandes, Eksteen

152

OPTIMIZATION OF AN EXPERIMENTAL AND ANALYTICAL PIPELINE FOR METAPROTEOMIC CHARACTERIZATION OF THE HUMAN GUT MICROBIOTA

Palomba, Tanca, Abbondio, Addis, Pagnozzi, Manghina, Fraumene, Deligios, Pisanu, Uzzau

153

MALIGNANT MELANOMA TISSUE BIOBANK FOR PROTEOMIC STUDIES

Sugihara, Yakovleva, Welinder, Wieslander, Edula, Fehniger, Baldetorp, Marko-Varga

154

NEW INSIGHT INTO THE EFFECTS OF DECORIN ON BREAST CANCER CELLS

Di Cara, Musso, Contorno, Pucci-Minafra, Minafra

155

BRUGADA SYNDROME: AN INTEGROMICS APPROACH TO IDENTIFY NOVEL BIOMARKERS

Scumaci, Concolino, Tammè, Fiumara, Perri, Cuda

156

ALTERED RESPONSE AND PHOSPHORYLATION PROFILE IN PLATELETS FROM ALBRIGHT HEREDITARY OSTEODYSTROPHY SYNDROME PATIENTS

Swieringa, Solari, Feijge , Mattheij, Schrander-Stumpel , Rubio-Gozalbo , van der Meijden , Keularts , Zahedi, Heemskerk

157

THE ROLE OF SIL1 IN NEURODEGENERATION: FROM PROTEOMIC ALTERATIONS OF SIL1 DEPLETION IN VITRO TO NOVEL INSIGHTS OF ITS PATHOLOGICAL ROLE IN VIVO Roos, Kollipara, Buchkremer, Labisch, Brauers, Gatz, Lentz, Gerardo-Nava, Weis, Zahedi

158

BACTERIAL COMPETITION FOR FOOD SAFETY: TARGETED VALIDATION IN MILK

Alloggio, Piras, Greco, Soggiu, Cosciani, Panseri, Bonizzi, Urbani, Mortarino, Roncada

159

INVESTIGATION OF CLIC-1 INTERACTOME

Canetti, Monti, Zappa, De Matteis, Pucci

160

SYSTEMS PHARMACOLOGY OF PROSTATE CANCER: NOVEL SRM ASSAYS FOR COMBINATION THERAPY DEVELOPMENT USING THE LNCaP MODEL CELL LINE Ebbardt Poot Lin Conther Sonder Acherrold

Ebhardt, Root, Liu, Gauthier , Sander, Aebersold

161

IDENTIFYING THE FOCAL POINTS OF BIOMEDICAL RESEARCH FOR PROTEOMICS ASSAY DEVELOPMENT: A DATA SCIENCE APPROACH

Lam , Venkatraman , Cao, Wang, Dincer, Lau , Su, Yi, Ge , Van Eyk, Ping

162

PROTEOME DYNAMICS REVEALS COORDINATED PROTEIN TURNOVER NETWORKS IN DISEASE

Lau, Cao, Ng, Wang, Lam, Ping

163

PROTEOMIC STUDIES OF EGGPLANT RESPONSES TO INFECTION WITH FUSARIUM OXYSPORUM F. SP. MELONGENAE AND VERTICILLIUM DAHLIAE KLEB

Ricci, Mennella, Francese, Rinaldi, D'Alessandro, Toppino, Rotino

164

SIGNALS SECRETED BY HYPOXIC CELLS INFLUENCE THE SECRETOME OF ADJACENT CELLS Rodrigues da Cunha , Buzzo Stefanini, Mussi Polachini, Tajara

165

NOVEL SOFTWARE TOOLS FOR CROWDSOURCING MITOCHONDRIAL PROTEIN KNOWLEDGE IN GENE WIKI Polson , Wang, Garlid, Dincer, Scruggs, Lee , Su, Ping

166

STATUS OF EXTENDED-SPECTRUM &LACTAMASE (ESBL) PRODUCING ENTEROBACTERIACEAE IN CERTAIN FOODS FROM ISTANBUL-TURKEY

Özpinar ,Tekiner ,Özpinar

167

PROTEOMIC APPROACH TO STUDY A COUPLE OF MONOZYGOTIC TWINS DISCORDANT FOR THE CHRONIC FATIGUE SYNDROME: FOCUS ON MITOCHONDRIA INVOLVEMENT Ciregia, Giusti, Kollipara, Zahedi, Ronci, Bazzichi, Giacomelli, Urbani, Sickmann, Lucacchini

168

TARGETED METABOLOMICS IN THE STUDY OF GENDER DIFFERENCES IN TISSUE METABOLISM Campesi, Santorelli, Caterino, Scolamiero, Pecce, Amoresano, Pane, Fontanarosa, Franconi, Ruoppolo

169

QUANTITATIVE ANALYSIS OF DYSREGULATED PROTEOME IN METHYLMALONIC ACIDEMIA Caterino, Costanzo, Minopoli, Santorelli, Venditti, Ruoppolo

170

PROTEOMIC ANALYSIS OF GENE PRODUCTS THAT REGULATE DE- AND REMYELINATION Szilagyi, Schmidt, Nawrocki, Mark, Illes, Gallyas

171

ALDOLASE C INTERACTS WITH THE DEAD-BOX RNA HELICASE DDX1 IN MOUSE CEREBELLUM Imperlini, Spaziani, Mancini, Formiggini, Sarnataro, Orrù, Buono, Salvatore

172

THE EFFECT OF MICROGRAVITY ON HUMAN OSTEOBLAST AND MYOCYTE PRIMARY CELL LINES FROM OSTEOARTHRITIS AND OSTEOPOROTIC PATIENTS

Gioia, Longo, Marini, Romano, Dpierro, Renaldi, Scimeca, Frank, Piccirilli, Cardone, Tancredi, Marini, Coletta, Zolla, Tarantino

173 MS DATA ANALYSIS WITH A TOUCH OF SPARK Sharma, Lewis, Dahiya, Slupphaug



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ACKNOWLEDGEMENTS

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