HUPO

2014 MADRID

13th Human Proteome Organization World Congress

The proteome quest to understand biology and disease

Congress Program

October 5 - 8, 2014

WWW.HUPO2014.COM

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SEProt

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Contents

WELCOME MESSAGE

Dear colleagues,

It is our great pleasure to welcome you all to the 13th World Congress of the Human Proteome Organization , the 7th EuPA annual conference and the 6th Spanish Proteomics Society Congress that are celebrated conjointly in Madrid.

Despite the fast advances experienced over the last few years, Proteomics is still at its youthfulness. It is a discipline with a tremendous future that offers all kinds of opportunities to analyze biological systems with unprecedented efficacy to generate new concepts in biology, identify new diagnostic and therapeutic targets and study drug effects in cell biology.

The challenge of defining and understanding proteomes in the context of cell biology is huge and requires a multidisciplinary effort to ensure innovative technical developments, the generation of biological information as well as the integration and interpretation tools to transform the information into biological knowledge. We sincerely hope to have been able to create an ideal environment where international experts can discuss all these aspects generating new ideas and establishing productive scientific interactions.

We wish you a pleasant and productive stay in Madrid, including its art galleries offer, which will amaze you and since life is not only science, do not forget to spare some time visiting Madrid, including its art galleries offer which will amaze you. Be careful with the small and charming bars of the old town, they are pretty addictive...

We are waiting for you in Madrid

Fernando J. Corrales **Juan Pablo Albar** **Juan Calvete** **Concha Gil**

Chairs of 13th HUPO World Congress

COMMITEES

CONGRESS CO-CHAIRS

Concha Gil
Juan Pablo Albar
Juanjo Calvete
Fernando J. Corrales

ORGANIZING COMMITTEE

Fernando Vivanco
Ignacio Casal
Jesús Vázquez
Lucía Monteoliva
Jesús Jorrín
Juan A. Vizcaino

Manuel Sánchez del Pino
Montserrat Carrascal
Eliandre de Oliveira
Ángel García
José M. Mato

CHAIRS OF HUPO EDUCATION DAY, HUPO CLINICAL DAY, EUPA DAY, HUPO & EUPA AWARDS AND HUPO & EUPA INITIATIVES

CLINICAL DAY CHAIRS: Jennifer Van Eyk, Ignacio Casal

HUPO & EUPA AWARDS CHAIRS: Luca Bini, Mark Baker

HUPO & EUPA INITIATIVES CHAIRS: Gilbert Omenn, Garry Corthals, Bill Hancock

PRECONGRESS COURSE AND EDUCATIONAL DAY CHAIRS: Peter James, Montserrat Carrascal, Thierry Rabilloud

Human Proteome Organisation

WHAT IS HUPO?

The Human Proteome Organisation (HUPO) is an international scientific organization representing and promoting proteomics through international cooperation and collaborations by fostering the development of new technologies, techniques and training.

HUPO EXECUTIVE COMMITTEE

President	Pierre Legrain	(2013-2014)
Past President	Catherine Costello	(2013-2014)
Vice-President	William Hancock	(2013-2014)
Treasurer	Bruno Domon	(2014-2016)
Secretary General	Maxey C.M. Chung	(2013-2014)
President-Elect	Mark Baker	(2014)
Member-at-Large	Gilbert S. Omenn	(2013-2014)
Member-at-Large	Michael Snyder	(2014-2015)

HUPO COUNCIL (BOARD OF DIRECTORS)

The HUPO Council is the decision-making body. The Council is elected by the HUPO members.

European Proteomics Association (EuPA)

The European Proteomics Association (EuPA) is the federation of European national proteomics societies. It has been established to coordinate and integrate national initiatives within the proteomics field. The main objectives are to strengthen and promote fundamental research and applications, as well as education and training in all areas of proteomics throughout Europe. EuPA is a non-profit organization.

CURRENT EXECUTIVE COMMITTEE

President:	Gyorgy Marko-Varga
Vice-President:	Jean-Charles Sanchez
Conference & Communication committee:	Luca Bini
Education committee:	Peter James
Eu-HUPO committee:	Emøke Bendixen
Funding committee:	Peter Verhaert
New Developments Committee:	Garry Corthals

Current EuPA country members are:

Austria, Belgium, Czech Republic, Denmark, Finland, France, Germany, Greece, Hungary, Italy, Luxembourg, Netherlands, Norway, Poland, Portugal, Russia, Spain, Sweden, Switzerland, Turkey and United Kingdom

Spanish Proteomics Society (SEProt)

SEProt was founded in 2004 and it currently has about 200 members .The main objective of SEProt is to promote the development of Proteomics in Spain. This is to be done by encouraging scientific and technical research in the field of Proteomics, by promoting training, learning and formation in this field, and by sponsoring and facilitating the organization and/or participation of their members in national or international activities, courses, workshops and meetings and any kind of cooperation and interchange with other societies.

President: Fernando J. Corrales
CIMA-Universidad de Navarra, Pamplona

Vice-president: Fernando Vivanco
Universidad Complutense, Fundación Jiménez Diaz, Madrid

Secretary: Manuel M. Sánchez del Pino
Universidad de Valencia, Valencia

Treasurer: Eliandre de Oliveira
Plataforma de Proteómica, Parc Cientific de Barcelona

Vocals: Ignacio Casal
CIB, CSIC, Madrid

Concha Gil
Universidad Complutense de Madrid

Jesús Jorrín
Universidad de Córdoba

Jesús Vázquez
CBM SO-UAM-CSIC, Madrid

Juanjo Calvete
IBV-CSIC, Valencia

Ángel García
Universidad de Santiago de Compostela

Lucía Monteoliva
Universidad Complutense de Madrid

Montserrat Carrascal
IIBB-CSIC-IDIBAPS, Barcelona

Proteored

ProteoRed-ISCIII is a technological platform integrating 25 proteomics laboratories distributed all over Spain. The main objective of ProteoRed-ISCIII consortium is to coordinate and integrate activities of the Spanish proteomic facilities and services in a common network with a nodal structure, to support the whole development of proteomic research in our country.

List of Volunteers

Name	Last Name	Name	Last Name
Adan	Alpízar Morúa	Luis Felipe	Clemente Velarde
Ahinara	Amador García	Mª Carmen	Mena Valverde
Aida	Pitarch Velasco	Mª Luisa	Hernáez Sánchez
Alberto	Peláez García	Manuel	Lombardia Uria
Alberto	Paradela Elizalde	María del Mar	González Garcés
Ana	Martinez del Val	María Dolores	Segura Buitrago
Ana	Gil de Bona	Maria Isabel	Mora Orellano
Antonio	Ramos	Miguel	Marcilla Goldaracena
Beatriz	Escudero Paniagua	Miguel Ángel	López García
Carmen	González Tejedo	Noemi	Bujan
Catarina	Oliveira Vaz	Nuria	Ibarz Ferrer
Dolores	Gutiérrez Blázquez	Perceval	Vellosillo
Elvira	Marín	Pilar	Ximénez de Embún Cadarso
Emilie	Bigaud	Roi	Villar-Vázquez
Gema	Bravo Sanz	Rosana	Navajas Morillas
Gonzalo	Martínez Martínez	Sergio	Ciordia Higuera
Inés	Zapico Megido	Severine	Gharbi
Inmaculada	Cosano Maya	Víctor	Fanjul Hevia
J. Alberto	Medina Auñón	Virginia	Pavon Mañani
Jose Antonio	Reales Calderón	Vital	Vialas Fernandez
Lucía	Monteoliva Díaz		

PRE CONGRESS COURSES

PROTEOMICS INFORMATICS WITH THE TRANS-PROTEOMIC PIPELINE (TPP)

Date

29th September - 2nd October 2014

Course Venue

Edificio nuevo, Facultad de Farmacia UCM
Room: Aula de informática
Address: Plaza Ramón y Cajal S/N. 28040 Madrid
Metro Station: Ciudad Universitaria (Line 6).

Agenda

- Data Conversion
- TPP installation
- Database searching
- PeptideProphet
- iProphet
- PTMProphet
- ProteinProphet
- Quantitation software
- Spectral library searching
- TPP on Amazon Web Services
- PeptideAtlas
- SRMAtlas

Speakers

- Luis Mendoza
- David Shteynberg
- Eric Deutsch
- Ulrike Kusebauch

Fees

- **Students:** 150 EUR
- **Academic:** 250 EUR
- **Industry:** 500 EUR

Pre-registration

http://tools.proteomecenter.org/course/

PROTEOMICS INFORMATICS: MASCOT, MAXQUANT, PROGENESIS AND SKYLINE

Organisers

EuPA and HUPO Education Committees with Lund University - Peter James

Course dates: October 03 – 04, 2014

Two days, Friday 3rd Saturday 4th October before the HUPO congress. There are four half-day courses covering modern bioinformatics for Proteomics. In accordance with the HUPO/EuPA guidelines, we aim to:

- Provide a theoretical basis for understanding the software used
- Provide practical instruction in laboratory techniques

Course Venue

Edificio nuevo, Facultad de Farmacia UCM
Room: Aula de informática
Address: Plaza Ramón y Cajal S/N. 28040 Madrid
Metro Station: Ciudad Universitaria (Line 6).

COURSE OUTLINE

	Friday 3rd October	
	GROUP 1	**GROUP 2**
13:00 - 16:30h	Jurgen Cox **MAXQUANT**	John Cottrell **MASCOT**
16:30 - 17:00h	Coffee break	
17:00 - 20:30h	Mike MacCoss **SKYLINE SRM**	Martin Wells **PROGENESIS**
	Saturday 4th October	
9:30 - 13:00h	John Cottrell **MASCOT**	Jurgen Cox **MAXQUANT**
13:00 - 14:30h	Lunch	
14:30 - 18:00h	Martin Wells **PROGENESIS**	Mike MacCoss **SKYLINE SRM**

* Lunch and coffee will be provided.

Please follow the instructions below:

MASCOT Course. John Cottrell
Please bookmark the following page:
http://www.ms-ms.com/exercises/exercises.html

PROGENESIS Course. Martin Wells
Please download and install the Progenesis QI software from here
http://www.nonlinear.com/progenesis/qi-for-proteomics/download
And also the DDA tutorial dataset and user guide
http://www.nonlinear.com/progenesis/qi-for-proteomics/download

MAXQUANT Course. Juergen Cox
Please download and install the MaxQuant software from here
http://www.maxquant.org/downloads.htm

SKYLINE SRM Course. Mike MacCoss
Please download and install the Skyline software from here
https://skyline.gs.washington.edu/labkey/project/home/software/Skyline/begin.view

How to register

Use the registration form of the congress for attending to this course.

Please note you have the options to attend only to the **“Pre-Congress course”** or both **“Pre-Congress + Congress”**.

EDUCATIONAL DAY
PROTEOMICS: BASICS AND APPLICATIONS

Date

Sunday 5th October 2014
09:00 - 17:30 h. - Room: H

Organizing team

Montserrat Carrascal, Peter James and Thierry Rabilloud.

Agenda

09:00 - 10:00 h	**Introduction to proteomics. Basic concepts.** Thierry Rabilloud (Institut de Recherches en Technoloqies et Sciences pour le Vivant-Grenoble)
10:00 - 10:50 h	**MS/MS and shotgun proteomics** Mike MacCoss (University of Washington)
10:50 - 11:10h	**Coffee break**
11:10 - 12:00 h	**Quantitative mass spectrometry** Albert Heck (Netherlands Proteomics Centre, Utrecht)
12:00 - 12:50 h	**Postraslational Modifications** Martin Larsen (University of Southern Denmark, Denmarck)
12:50 - 13:40 h	**Antibody and protein arrays.** Matthias Uhlen (KTH Royal Institute of Technology, Sweden)
13:40 - 15:00 h	**Lunch time**
15:00 - 16:00 h	**Manual MS/MS Interpretation of CID data.** Peter James (Department of Immunotechnology, Lund University)
16:00 - 17:00 h	**Manual MS/MS Interpretation of ETD data** Donald Hunt (Department of Chemistry, University of Virginia)
17:00 - 17:30 h	**Concluding remarks**

CLINICAL DAY

Date

Sunday 5th October 2014
09:00 - 17:30 h. - Room: E

Organizing team

Jennifer Van Eyk, Gustavo Salem, Oliver Poetz, Jochen Schwenk, Charles Pineau and Ignacio Casal

From discovery to clinical impact: the road to translation and commercialization

Background: It is the right time to move proteomics beyond the research stage, and acknowledge that there are now protein biomarkers that can be or are used in clinical diagnostics. Efforts to commercialize protein biomarkers are currently at the stage of addressing the important new challenges of demonstrating clinical utility to physicians and establishing reimbursement plans with payers.

The translation from discovery to the clinic requires impactful clinician applications, but also requires research and development so that understanding of the disease and clinical framework can be established. The initial successes include diagnostic tests to improve patient outcomes in cancer, heart disease, metabolic disorders, and neurological disease.

Equally important are the technology platforms that allow for seamless quantification in CLIA and clinical chemistry laboratories, and potentially point-of-care. Important developments in the areas of mass spectrometry, multiplexing, and automation are underway and are improving the adoption of protein-based diagnostics.

09:30 - 09:40 h **Opening remarks: The winding path forward from discovery to patient impact**

Speakers: **Jennifer Van Eyk,** Advanced Clinical Biosystems Institute, Cedars Sinai Medical Center,
Gustavo Salem, President and CEO, SISCAPA Assay Technologies,
Charles Pineau, Research Director Inserm IRSET, Director Proteomics Core Facility Biogenouest, France

Session 1:
The reality of biomarkers and clinical utility: making it happen

Goal: The “clinical” in clinical chemistry: evaluating cohorts, biobanking, discovery, and protein quantification of new biomarkers to aid their acceptance by physicians. What are the medical needs that are not been serviced currently which proteomics are or can address? What are the needed technologies, approach and concepts to allow proteomics to meet its potential.

Moderator: **Charles Pineau**, Research Director Inserm IRSET, Director Proteomics Core Facility Biogenouest, France

09:40 - 10:15 h **Clinical Chemistry lab meets proteomics and new quantitative assays**

Keynote: The journey to launching the Xpresys Lung test: a novel protein biomarker panel for nodule classification
Paul Kearney
Co-Founder, President and CSO, Integrated Diagnostics, Seattle, USA

Session 2:
Due diligence: Beyond discovery and establishing intended use.

Goal: To provide the big view on the transition between discovery and a commercial product intended for patient care. Considerations from entrepreneurial verses established diagnostic company perspective. What is needed from academics to increase potential of successful hand off for commercialization and clinical utility?.

Moderator: Ina Schuppe-Koistrum, Scientific coordinator of the SAFET project and Director Biochemical Biomarkers, Astra Zeneca

10:15 - 10:30 h
Speaker 1: **Donna Edmonds**
President and CEO, Virginia Biosciences Commercialization Center

10:30 - 10:45 h
Speaker 2: **Gustavo Salem**
President and CEO, SISCAPA Assay Technologies, Inc. (Formerly VP and General Manager, Biological Systems Division – Agilent Technologies)

10:45 - 11:00 h Questions and debate: Discussion around commercialization and interaction with academics
Lead by **Ina Schuppe-Koistinen**. Scientific coordinator of the SAFET project and Director Biochemical Biomarkers, Astra Zeneca

11:00 - 11:20 h BREAK

Session 3:
Success in the clinic: a long road from discovery proteomics

Goal: To provide overview of the diverse commercial successes in proteomics and biomarker diagnostics.

Moderator: **Jochen M Schwenk**, SciLifeLab and KTH Royal Institute of Technology, Sweden (part 1 and 2)

11:20 - 11:50 h

Speaker 1: From discovery to building a FDA-Trial: Circulating brain injury biomarkers for pediatric and adult acute clinical assessment.
Allen Everett, Johns Hopkins University, Baltimore, USA

11:50 - 12:20 h

Speaker 1: The value of longitudinal testing for continuous and personalized assessment of wellness and disease: at-home DBS sampling for SISCAPA multiplexed protein assays.
Selena Larkin, SISCAPA Assay Technologies, Inc., USA)

12:20 - 12:35 h **Personal viewpoint: Translational route through biobanks - a key component towards clinical use?**

Goal: To summarize what are the major challenges related to biobanking and cohort collections that must be considered and overcome for bridging into a next era of biomarkers with enhance clinical impact and utility

Speaker: **Jochen Schwenk**, SciLifeLab and KTH Royal Institute of Technology, Sweden

12:35 - 13:35 h LUNCH

13:35 - 14:10 h **The reality of biomarkers and clinical utility: making it happen**

Moderator: **Katrin Marcus,** University Bochum, Germany

Keynote: Analytical development and validation of a novel biomarker panel for colon polyp detection",
Bruce Wilcox, Director of Instrumentation and Lab Operations, Applied Proteomics, Inc.

Session 4:
The technical hurdle: What are the next enabling technologies?

Goal: Next steps in generating proteomic data for clinical applications: pushing the edge of technology.

Moderator: **Christoph H Borchers**, University of Victoria, Victoria, Canada

14:10 - 14:35 h
Speaker 1: Mass spectrometry development is only the beginning
Jennifer Van Eyk, Director, Advanced Clinical BioSystems Research Inssitue, Cedar Sinai Medical College, Los Angeles, USA

14:35 - 15:00 h
Speaker 1: Evolution and next generation of immune/aptimer assays
Oliver Poetz, Head Protein Analytics, University of Tuebingen, Germany

15:15 - 15:15 h **Personal viewpoint: are we on the right road?**

Goal: To summarize what are the key challenges that need to be overcome in bringing next era of protein-based quantitation to enhance clinical impact

Speaker: **Christoph H Borchers**, University of Victoria, Victoria, Canada

15:15 - 15:20 h BREAK

Session 5:
Discussion panel and question period

Moderator: **Jennifer Van Eyk**

Discussants:
Gustavo Salem: President and CEO, SISCAPA Assay Technologies
Paul Kearney: Co-Founder, President and CSO, Integrated Diagnostics Inc.
Bruce Wilcox: Director of Instrumentation and Lab Operations, Applied Proteomics Inc.
Ralph Schiess: Proteomedix
Donna Edmonds: President and CEO, ImmunArray/Veracis Inc.

A. Given that many clinical assays today are still based on ELISA type of assays, how can MS or other proteomic technology platforms add / supplement / replace current systems in use? What does it take to get an MS-based protein assay into the market?

B. What are the key lessons one would you take to the NEXT development-stage protein panel?

C. What do the regulators think about these new, LDT protein tests?

D. Is there a place for integration of genomics and other ‘Omic data in a clinical assay?

E. What is missing when communicating proteomics and its opportunities with intended users?

F. What kind of new career opportunities are being created in these new companies?

15:20 - 17:30 h
Speaker 1: Personal viewpoint: Are we on the right road?
To summarize and discuss what are the key technical challenges in bringing the next era of protein-based quantitation to enhance clinical impact.

Speakers: **Jennifer Van Eyk, Charles Pineau and Gustavo Salem**

3D IMAGING MASS SPECTROMETRY WORKSHOP

Imaging Mass Spectrometry is an exciting, rapidly developing, and promising field of mass spectrometry and –omics sciences. 3D imaging mass spectrometry represents a new frontier in this field. The aim of this workshop is to highlight the newest achievements in this advanced field, bring scientists contributing to this field with methodological, computational, and biomedical developments, and discuss where the field can go in the future.

The workshop is organizes in the framework of the 3D-MASSOMICS project
(http://3d-massomics.eu)

Date & Place

Sunday 5th October 2014
HUPO'14 main place (Centro de Convenciones Norte), Madrid, Spain; room I

Registration

The workshop will be free of charge, sponsored by the EU FP7 3D-MASSOMICS project and Bruker Daltonics.

However, in order for us to estimate the number of participants, please register online, separately from the HUPO Congress by using this link:

https://docs.google.com/forms/d/1X0I-PL7wWSM_iWZnkyNYBcEfOfNMID6R5qVO919gZc0/edit

Workshop speakers

- Ron Heeren, FOM-AMOLF, NL
- Livia Eberlin, Stanford, US
- Per Andren, Uppsala University, SE
- Amanda Hummon, Notre Dame University, US
- John S. Fletcher, University of Gothenburg, SE
- Jeramie Watrous, University of California San Diego, US
- Ferdinand von Eggeling, Jena University Hospital, DE
- Pierre Chaurand, Université de Montréal, CA
- Olga Vitek, Northeastern University, US

Submissions

We do not plan to accept submissions for this workshop. However, if you would like to present exciting results on 3D imaging mass spectrometry either as a talk or as a poster, please contact Theodore Alexandrov **(theodore@uni-bremen.de)** over email.

Workshop organizers

- Fernando Vivanco Martínez, Fundación Jiménez Díaz, ES
- Charles Pineau, University of Rennes 1 / INSERM, FR
- Dennis Trede, SCiLS GmbH, DE
- Theodore Alexandrov, University of Bremen / University of California San Diego / SCiLS, DE/US

For more information, please email us at: **fvivanco@fjd.es**, **charles.pineau@inserm.fr**, **trede@scils.de**, **theodore@uni-bremen.de**

PROTEOMEANALYZER – WORKSHOP SUNDAY

09:00 - 11:30 h
Room G

09:00h Introduction

09:05h Viewpoints of End-user and HPP/BD Users'

09:30h Proteome Analyzer Survey – Results

09:45h Viewpoint of Manufacturers

10:10h Discussion ProteomeAnalyzer I

10:50h Discussion ProteomeAnalyzer II

11:30h Wrap up

Everyone is invited to complete this survey on the ProteomeAnalyzer project:
https://www.surveymonkey.com/s/ProteomeAnalyzer2014

October 5 - 8, 2014 MADRID

SCIENTIFIC PROGRAM

HUPO

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13th Human Proteome
Organization World Congress

SCIENTIFIC PROGRAM

Sunday October 5th

	Room A+B+C	Room D	Room E	Room F	Room G	Room H	Room I	Room K
08:30	Opening Secretariat - Documentation Delivery							
09:00 - 10:00			Clinical day		Proteome Analyzer	Educational day	3D Massomics	EuPA Council
10:00 - 11:30		Human Proteome Project						
11:30 - 14:00								
14:00 - 16:00				HUPO Council				
16:00 - 17:00								
17:00 - 17:15								
17:15 - 17:30								
17:30 - 18:00								
18:00 - 20:00	Opening Ceremony							
20:00 - 21:30	Opening Reception (Exhibition Hall)							

18:00 - 20:00

Opening Ceremony: In Memory of Juan Pablo Albar

Chairs
C. Gil
F. J. Corrales
J. J. Calvete

18:15 - 19:00 **MULTIPROTEIN ASSEMBLIES OF THE HUMAN PROTEOME: IMPLICATIONS FOR CELL SIGNALLING AND DRUG DISCOVERY**

Keynote Speaker
Tom L. Blundell
University of Cambridge, United Kingdom

19:00 - 19:45 **A GLOBAL AND GENOME-WIDE HUMAN PROTEIN ATLAS BASED ON INTEGRATION OF OMICS APPROACHES**

Keynote Speaker
Mathias Uhlen
KTH Royal Institute of Technology, Stockholm, Sweden

20:00 - 21:30

Exhibit Hall

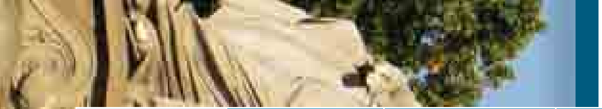
Welcome Reception

2014 MADRID

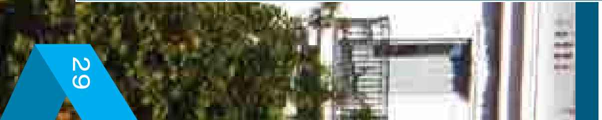
13th Human Proteome
Organization World Congress

SCIENTIFIC PROGRAM

Monday October 6th



	Room A	Room B	Room C	Room D	Room E	Room F	Room G	Room H	Room I
08:00 - 09:20	HPP Morning Sessions								
		HPPP (Plasma)	C-HPP I	Cancer I	iMOP	Liver	Extreme Conditions	Infectious Diseases	EyeOME
09:30 - 10:15	Plenary Lecture								
10:20 - 11:00	Coffee Break - Exhibition Hall								
11:00 - 12:50	Cancer Proteomics I	Regulation of cellular pathways. Role of PTMs	Proteogenomics	Microvesicle and organelle proteomics	Eupa young investigator Session				
13:00 - 14:15		Lunch Symposium *Bruker Daltonik GmbH*		Lunch Symposium *Waters Corporation*					
14:15 - 15:45	Poster Session								
16:00 - 16:45	Plenary Lecture								
16:45 - 18:35	New trends in biomarker discovery	Phosphoproteomics	Proteomics of obesity and related metabolic liver disorders. Metabolomics	Non-human and food proteomics	HUPO young investigator Session				
18:35 - 19:05		HUPO General Assembly							
19:05 - 20:00	Informal Mixer with Exhibits-Posters								



09:30 - 10:15

Room A Plenary Lecture

Chair J. Muñoz

09:30 - 10:15 **PROTEOMICS BEYOND TRYPSIN**

Keynote Speaker Albert Heck
Utrecht University, The Netherlands

10:20 - 11:00

Coffee Break - Exhibition Hall

11:00 - 12:50

Room A Cancer Proteomics I

Chair H. Rodriguez
I. Casal

11:00 - 11:25 **POWER IN COMBINING GENOMICS AND PROTEOMICS (CPTAC's COLORECTAL CANCER STUDY: NEW MOLECULAR FEATURES DISCOVERED)**

Keynote Speaker Henry Rodriguez
National Cancer Institute, Washington, USA

11:25 - 11:50 **MOLECULAR INSIGHTS IN COLON CANCER METASTASIS**

Keynote Speaker Ignacio Casal
Centro de Investigaciones Biológicas (CSIC), Madrid, Spain

11:50 - 12:05 **OP001 - A QUANTITATIVE PROTEOMIC INVESTIGATION OF PAIRED COLORECTAL CANCER AND NORMAL TISSUE SAMPLES**

Manveen Sethi
Macquarie University, Sydney, Australian

12:05 - 12:20 **OP002 - PROTEOMIC INVESTIGATION OF INTRA-TUMOR HETEROGENEITY**

Tiannan Guo
Institute of Molecular Systems Biology, ETH Zurich, Switzerland

12:20 - 12:35 **OP003 - PROTEOMIC PATTERNS UNRAVEL A NEW LUMINAL A BREAST CANCER MOLECULAR SUBGROUP**

Angelo Gámez-Pozo
Hospital Universitario La Paz-IdiPAZ. Madrid, Spain

12:35 - 12:50 **OP004 - A SYNTHETIC LETHAL INTERACTION BETWEEN APC/C AND TOPOISOMERASE POISONS UNCOVERED BY PROTEOMIC SCREENS**

Fernando Garcia
Spanish National Cancer Research Centre, Madrid, Spain

Room B

Regulation of Cellular Pathways. Role of PTMs

Chair

O. Jensen
M.M. Sánchez del Pino

11:00 - 11:25

MODIFICATION-SPECIFIC PROTEOMICS: STRATEGIES FOR THE CHARACTERIZATION OF CO-EXISTING POST-TRANSLATIONAL MODIFICATIONS IN PROTEINS

Keynote Speaker

Ole Jensen
University of Southern Denmark, Odense, Denmark

11:25 - 11:50

INNOVATIVE METHODS AND NEW MASS SPECTROMETRY INSTRUMENTATION FOR THE CHARACTERIZATION OF PROTEIN AND PEPTIDE POST-TRANSLATIONAL MODIFICATIONS

Keynote Speaker

Donald Hunt
University of Virginia, Charlottesville,USA

11:50 - 12:05

OP005 - CONVERGENCE OF UBIQUITYLATION AND PHOSPHORYLATION SIGNALING IN RAPAMYCIN-TREATED YEAST CELLS

Vytautas Iesmantavicius
University of Copenhagen, Denmark

12:05 - 12:20

OP006 - A NOVEL DATA-INDEPENDENT APPROACH ALLOWS AN EXTREMELY DETAILED STRUCTURAL MAP OF PROTEIN COMPONENTS OF MITOCHONDRIAL COMPLEXES AND SUPERCOMPLEXES

Enrique Calvo
National Cardiovascular Research Centre ;Madrid, Spain

12:20 - 12:35

OP007 - CHAFRADIC - A NOVEL MULTIFUNCTIONAL TOOL FOR PTM-SPECIFIC PROTEOMICS

Rene P. Zahedi
Leibniz–Institut Für Analytische Wissenschaften - ISAS, Dortmund, Germany

12:35 - 12:50

OP008 - PROTEOMIC ANALYSIS OF CELLULAR CHOLESTEROL REGULATION USING TARGETED MASS-SPECTROMETRY

Peter Blattmann
Institute of Molecular Systems Biology (IMSB), Zurich, Switzerland

Room C

Proteogenomics

Chairs

V. Bafna
J Armengaud

11:00 - 11:25

PROTEOGENOMICS FOR CANCER

Keynote Speaker

Vineet Bafna
University of California, San Diego, USA

11:25 - 11:50 **PROTEOGENOMICS, THE SENSU STRICTO AND SENSU LATO PANORAMA!**

Keynote Speaker
Jean Armengaud
French Institute of Environmental Biology and Biotechnology, Saint-Paul-les-Durance, France

11:50 - 12:05 **OP009 - A NOVEL UNPRECEDENTEDLY COMPREHENSIVE PROTEIN IDENTIFICATION STRATEGY, MASS SPECTROMETRY AND RIBOSOME PROFILING: THE PERFECT MATCH.**

Gerben Menschaert
Ghent University, Belgium

12:05 - 12:20 **OP010 - PERSONALISED PROTEOMICS BY MEANS OF INDIVIDUALISED PROTEIN MICROARRAYS**

Jörg Hoheisel
German Cancer Research Center (DKFZ), Heidelberg, Germany

12:20 - 12:35 **OP011 - A FAST DECOY-FREE APPROACH FOR RELIABLE IDENTIFICATON OF PSMS**

Giulia Gonnelli
Ghent University, Belgium

12:35 - 12:50 **OP012 - AN INTEGRATED PROTEOGENOMIC STRATEGY FOR GENOME ANNOTATION AND GLOBAL POST-TRANSLATIONAL MODIFICATIONS DISCOVERY IN THE MODEL CYANOBACTERIUM SYNECHOCOCCUS SP. STRAIN PCC 7002**

Feng Ge
Chinese Academy of Sciences, Wuhan, China

Room D

Microvesicle and Organelle Proteomics

Chairs
R.J Simpson
F. Elortza

11:00 - 11:25 **SIMULTANEOUS AND DYNAMIC PROTEIN SUB-CELLULAR LOCALIZATION BY MASS SPECTROMETRY**

Keynote Speaker
Kathryn S Lilley
The Cambridge Centre for Proteomics, United Kingdom

11:25 - 11:50 **PROTEIN AND RNA TYPING OF THREE EXTRACELLULAR VESICLE (EV) SUBTYPES RELEASED FROM THE HUMAN LIM1863 COLORECTAL CANCER (CRC) CELL LINE: AN OMICS ROADMAP TO DISCOVERY**

Keynote Speaker
Richard J.Simpson
La Trobe University, Melbourne, Australia

11:50 - 12:05 **OP013 - HEPATIC EXOSOMES IN METABOLISM AND DISEASE**

Juan M Falcon-Perez
CIC bioGUNE, Derio, Spain

12:05 - 12:20 **OP014 - PROTEOME-WIDE PROFILING OF SERUM EXOSOMES FOR IDENTIFICATION OF SCIRRHOUS GASTRIC CANCER BIOMARKERS**

Koji Ueda
The University of Tokyo, Japan

12:20 - 12:35 **OP015 - GLYCOPROTEINS ON THE SURFACE OF MDSC EXOSOMES**

Catherine Fenselau
University of Maryland, USA

12:35 - 12:50 **OP016 - CLINICAL AND TECHNICAL POTENTIALS AND PROSPECTS OF THE EV ARRAY**

Malene Jørgensen
Aalborg University Hospital, Denmark

Room E EuPA young investigator Session

Chairs P. James
D. Penque

11:00 - 11:22 **OP017 - THREE DIMENSIONAL ANALYSES OF PTM PATTERNS IN LARGE SCALE PROTEOMIC DATA**

Alistair Edwards
University of Southern Denmark, Odense, Denmark

11:22 - 11:44 **OP018 - DISCOVERING THE GLUTEN FINGERPRINT: A SMALL STEP TOWARDS THE QUANTIFICATION OF GLUTEN IN PROCESSED FOODS**

Maria Jose Martinez Esteso
Institute For Reference Materials And Measurements, Geel, Belgium

11:44 - 12:06 **OP019 - CELL-CELL COMMUNICATION AND SIGNALING IN COLON CANCER**

Maria Magdalena Koczorowska
University of Freiburg, Germany

12:06 - 12:28 **OP020 - PROGNOSTIC EVALUATION OF 15 AUTOANTIBODY-TYPE SPECIFIC COLORECTAL CANCER BIOMARKERS IDENTIFIED THROUGH PROTEIN MICROARRAYS**

Roi Villar-Vázquez
Centro De Investigaciones Biológicas (CSIC), Madrid, Spain

12:28 - 12:50 **OP021 - TOP-DOWN VENOMICS - HIGH RESOLUTION MASS SPECTROMETRY AS A FAST AND ACCURATE TOOL FOR THE PROFILING OF SNAKE VENOMS**

Daniel Petras
Institut Für Chemie, Berlin, Germany

13:00 - 14:15

Lunch Seminars / Lunch Break

14:15 - 15:45

Poster Session

Odd-numbered poster boards present

16:00 - 16:45

Plenary Lecture

Chair J.M Mato

16:00 - 16:45 **PRACTICE & PERSPECTIVE OF HUMAN PROTEOME PROJECT - A TRIP FROM WASHINGTON TO MADRID (2002-2014)**

Keynote Speaker Fuchu He
Beijing Proteome Research Center. China

16:45 - 18:35

Room A

New Trends in Biomarker Discovery

Chair S. Hanash
F. Canals

16:45 - 17:10 **THE VALUE OF BIOBANK PATIENT SAMPLES IN PROTEIN EXPRESION STUDIES**

Keynote Speaker Gyorgy Marko-Varga
Lund university, Sweden

17:10 - 17:35 **MINING THE CANCER PHENOME AS A SOURCE OF BIOMARKERS**

Keynote Speaker Sam Hanash
MD Anderson Cancer Center, Houston, USA

17:35 - 17:50 **OP022 - EXCLUSION OF CEREBRAL LESIONS IN MILD TRAUMATIC BRAIN INJURY USING PLASMA NUCLEOSIDE DIPHOSPHATE KINASE A (NDKA)**

Linnea Lagerstedt
University of Geneve, Geneve, Switzerland

17:50 - 18:05 **OP023 - BLOOD BASED PROTEOMIC AND GENOMIC BIOMARKERS FOR CARDIAC TRANSPLANTATION: FROM DISCOVERY TO CLINICAL IMPLEMENTATION**

Robert McMaster
University of British Columbia, Vancouver, Canada

18:05 - 18:20 **OP024 - GERM CELL-SPECIFIC PROTEINS MEASURED IN SEMINAL PLASMA EMERGE AS MARKERS OF SPERMATOGENESIS AND MALE INFERTILITY**

Andrei Drabovich
University of Toronto, Canada

18:20 - 18:35 **OP025 - DIAGNOSIS AND PREDICTION OF PROGRESSION OF CHRONIC KIDNEY DISEASE BY ASSESSMENT OF URINARY PEPTIDES**

Adela Ramírez-Torres
Mosaiques Diagnostics GmbH, Hannover, Germany

Room B

Phosphoproteomics

Chairs
P. Thibault
J. Abian

16:45 - 17:20 **THE DEVELOPMENT OF PHOSPHOPROTEOMICS – FROM TECHNOLOGIES TO APPLICATIONS**

Keynote Speaker
Martin Larsen
University of Southern Denmark, Odense, Denmark

17:20 - 17:35 **OP026 - PHOSPHOPROTEOMICS OF ADENOVIRUS TYPE 2 PROTEINS**

Sara Bergström Lind
Uppsala University, Sweden

17:35 - 17:50 **OP027 - PHOSPHOPROTEOMIC PROFILING OF POST-NATAL HEART DEVELOPMENT UNRAVELS A NOVEL MITOCHONDRIAL PROTEIN TO BE ASSOCIATED WITH THE MINOS COMPLEX**

Sriram Aravamudhan
Max Planck Institute For Heart And Lung Research, Bad Nauheim, Germany

17:50 - 17:05 **OP028 - QUANTITATIVE PHOSPHOPROTEOMICS ON A µG-SCALE - A STRAIGHTFORWARD AND HIGHLY SENSITIVE ERLIC-SCX/RP-LC-MS STRATEGY**

Stefan Loroch
Leibniz-Institut Für Analytische Wissenschaften – ISAS, Dortmund, Germany

17:05 - 18:20 **OP029 - THE DNA DAMAGE-INDUCED PHOSPHOPROTEOME IS MODULATED BY INHIBITION OF THE RECEPTOR TYROSINE KINASE MET**

Ariel Bensimon
ETH Zürich, Switzerland

17:05 - 18:20 **OP030 - DYNAMIC PHOSPHOPROTEOMICS ANALYSES OF COLON CANCER CELLS REVEAL DIFFERENTIAL REGULATION OF SIGNALING PATHWAYS UPON RAF INHIBITION**

Pierre Thibault
Universite De Montreal/IRIC, Canada

Room C

Proteomics of Obesity and Related Metabolic Liver Disorders. Metabolomics

Chairs
T. Nilsson
F.J Corrales

16:45 - 17:10 **NEW CELL BIOLOGY THROUGH THE STUDY OF HUMAN FATTY LIVER DISEASE**

Keynote Speaker
Tommy Nilsson
McGill University and Genome Quebec Innovation Centre, Canada

17:10 - 17:35 **METABOLOMICS ILLUMINATES THE PATHS TO NONALCOHOLIC FATTY LIVER DISEASE**

Keynote Speaker
Jose María Mato
CIC BIOGUNE- CIBEREHD, Derio-Bizkaia, Spain

17:35 - 17:50 **OP031 - OMICS IN NUTRITION AND ITS PERSPECTIVES FOR PEDIATRICS RESEARCH AND HEALTHCARE**

Martin Kussmann
Nestlé Institute of Health Sciences, Lausanne, Switzerland

17:50 - 18:05 **OP032 - CHARACTERIZATION OF BLOOD PLASMA METABOLOME OF HEALTHY MEN BY MASS SPECTROMETRY APPROACH**

Oxana Trifonova
Institute of Biomedical Chemistry RAMS, Russia

18:05 - 18:20 **OP033 - TOWARDS SPATIAL METABOLOMICS: DATABASE DRIVEN METABOLIC ANNOTATION FOR IMAGING MASS SPECTROMETRY**

Theodore Alexandrov
University of Bremen, Germany

18:20 - 18:35 **OP034 - PLASMA PROFILING REVEALS NOVEL BIOMARKERS FOR DRUG-INDUCED LIVER INJURY IN HUMANS**

Maria Mikus
KTH-Royal Institute of Technology, Stockholm, Sweden

Room D

Non-Human and Food Proteomics

Chairs
W. Weckwerth
J. Jorrín Novo

16:45 - 17:15 **GREEN SYSTEMS BIOLOGY - LINKING GENOME-SCALE METABOLIC MODELLING AND OMICS DATA IN ECOLOGY, EVOLUTION AND DEVELOPMENT**

Keynote Speaker
Wolfram Weckwerth
University of Vienna, Austria

17:15 - 17:30 **OP035 - PLANT PROTEOMICS: ITS APPLICATION TO CLARIFICATION OF FLOODING TOLERANCE MECHANISM IN SOYBEAN**

Setsuko Komatsu
National Institute of Crop Science, Tsukuba, Japan

17:30 - 17:45 **OP036 - MARINE PROTEOMICS: FINDING MECHANISMS OF ADAPTATION IN LARVAE OF RED SEA BARNACLE BALANUS AMPHITRITE**

Kondethimmanahalli Chandramouli
University of Science And Technology, Thuwal, Kingdom of Saudi Arabia

17:45 - 18:00 **OP037 - SHOTGUN PROTEOMICS OF DOG CEREBROSPINAL FLUID**

Mårten Sundberg
Uppsala University, Sweden

18:00 - 18:10 **OP038 - DEVELOPMENT OF AN ABSOLUTE AND MULTIPLEX MS-BASED QUANTIFICATION METHOD FOR E. COLI CARBON CENTRAL METABOLISM PROTEINS: A TOOL TO FEED DYNAMIC PREDICTIVE MODELS**

Myriam Ferro
CEA/Grenoble, France

18:10 - 18:20 **OP039 - ONE HEALTH PROTEOMICS: MECHANISM OF BACTERIAL COMPETITION IN FOOD SAFETY OF DAIRY PRODUCTS**

Paola Roncada
Istituto Sperimentale Italiano L. Spallanzani, Milano, Italy

18:20 - 18:30 **OP040 - PROTEOMICS WORKFLOWS AND PROTOCOLS FOR THE STUDY OF ORPHAN SPECIES**

Christof Lenz
Max Planck Institute For Biophysical Chemistry, Göttingen, Germany

18:30 - 18:35 **CONCLUSIONS: HOW CAN NON-HUMAN PROTEOMICS CONTRIBUTE TO HUPO INITIATIVE?**

Wolfram Weckwerth
University of Vienna, Austria
Jesus V. Jorrín Novo
University of Cordoba, Spain

Room E HUPO young investigator Session

Chairs
T. Rabilloud
S. Srivastava

16:45 - 17:07 **OP041 - PROTEOMIC ANALYSIS OF INFLAMMATORY BOWEL DISEASE BIOPSIES IDENTIFIES PROTEINS THAT SEGREGATE CROHN'S DISEASE FROM ULCERATIVE COLITIS IN PEDIATRIC PATIENTS**

Amanda Starr
University of Ottawa, Canada

17:07 - 17:38 **OP042 - CALPAIN-DEPENDENT CLEAVAGE IN HIGHLY ACTIVATED PLATELETS REVEALED BY QUANTITATIVE N-TERMINAL CHAFRADIC: ALTERATIONS IN SCOTT SYNDROME**

Fiorella A. Solari
Leibniz-Institut Für Analytische Wissenschaften-ISAS-E.V., Dortmund, Germany

17:38 - 18:00 **OP043 - CHEMICAL PROBES FOR STUDYING CELL-TO-CELL COMMUNICATION IN PATHOGENIC BACTERIA**

Ysobel Baker
University of Cambridge, United Kingdom

18:00 - 18:22 **OP044 - PROTEOGENOMIC ANALYSIS OF AN ASIAN MALARIA VECTOR – ANOPHELES STEPHENSI**

T. S. Keshava Prasad
Institute of Bioinformatics, Bangalore, India

18:22 - 18:35 **OP045 - UNRAVELING TRKA SIGNALING IN NEUROBLASTOMA USING A QUANTITATIVE MS-BASED APPROACH**

Kristina B. Emdal
The Novo Nordisk Foundation Center For Protein Research, Copenhagen, Denmark

18:35 - 19:05

Room B

HUPO General Assembly

Chairs P. Legrain
HUPO President

19:05 - 20:00

Informal Mixer with Exhibits-Posters

2014 MADRID

13th Human Proteome
Organization World Congress

SCIENTIFIC PROGRAM

Tuesday October 7th

	Room A	Room B	Room C	Room D	Room E	Room F	Room G	Room H	Room I
08:00 - 09:20	HPP Morning Sessions								
		Diabetes	PSI/ ProteomeXchange	Antibody Proteomics	Cancer II	Glycoproteomics	Brain Project	Stem Cells	Biobanking & Pre-Analytical Sample Assesment
09:30 - 10:15	Plenary Lecture								
10:20 - 11:00	Coffee Break - Exhibition Hall								
11:00 - 12:50	Integrative proteomics and systems biology	Cancer Proteomics II	Immunobiology and cell signalling	REDOX proteomics and mitochondrial biology	EuPA initiatives				
13:00 - 14:15		Lunch Symposium *ABSciex*	Lunch Symposium *Thermo Fisher*						
14:15 - 15:45	Poster Session								
16:00 - 16:45	Plenary Lecture								
16:45 - 18:35	Glycoproteomics in biology and diseases	Inflammatory and rheumatic diseases	Proteomics of human microbiome and infectious diseases	Standardisation in proteomics:tribute to Juan Pablo Albar	EuPA Company Club				
18:45 - 20:00	Informal Mixer with Exhibits-Posters			Meeting of the Minds *Agilent Technologies*					

09:30 - 10:15

Room A — ## Plenary Lecture

Chair J. Labaer

09:30 - 10:15 **ADVANCES IN EXPRESSION AND INTERACTION PROTEOMICS**

Keynote Speaker
Matthias Mann
Max-Planck Institute of Biochemistry, Munich, Germany

10:20 - 11:00

Coffee Break - Exhibition Hall

11:00 - 12:50

Room A — ## Integrative Proteomics and Systems Biology

Chairs
L. Serrano
M. Ueffing

11:00 - 11:25 **PROTEIN INTERACTION COMPETITION IN CELL SIGNALLING**

Keynote Speaker
Luis Serrano
Centre for Genomic Regulation, Barcelona, Spain

11:25 - 11:50 **FUNCTIONAL RELATIONSHIPS IN PROTEIN NETWORKS**

Keynote Speaker
Marius Ueffing
Helmholtz Zentrum Munich, Germany

11:50 - 12:05 **OP046 - DEEP PROTEOMICS, TRANSCRIPTOMICS AND SYSTEMS BIOLOGY ANALYSIS OF VASCULAR SMOOTH MUSCLE CELLS REVEALS NOVEL ANGIOTENSIN II –REGULATED PATHWAYS UNDERLYING VASCULAR WALL THICKENING**

Fernando Garcia-Marques
National Cardiovascular Research Centre, Madrid, Spain

12:05 - 12:20 **OP047 - OSTEOGENESIS IMPERFECTA: AFFECTED PATHWAYS IN SKIN, BONE, AND LUNG FROM THE BRTLIV MURINE MODEL**

Laura Bianchi
University of Siena, Italy

12:20 - 12:35 **OP048 - PROTEOMIC CHARACTERISATION OF TIO2 NANOPARTICLE-PROTEIN CORONA FORMATION IN VITRO**

Ana Paula Farinha
Linköping University, Sweden

12:35 - 12:50	**OP049 - PROTEOMICS MOVES FROM EXPRESSION TO TURNOVER: UNDERSTANDING THE DYNAMIC PROTEOME**
	Mary Doherty *University of The Highlands And Island, Inverness, United Kingdom*

Room B Cancer Proteomics II

Chairs	D. Fenyo C. Jiménez
11:00 - 11:25	**BREAST CANCER: MOLECULAR PROFILING OF A MOVING TARGET**
Keynote Speaker	Peter James *Lund University, Sweden*
11:25 - 11:50	**FROM CANCER PROTEOMICS TO PROTEIN BIOMARKERS, DRUG TARGETS AND CLINICAL APPLICATIONS**
Keynote Speaker	Conny Jimenez *VU University Medical Center, Amsterdam, The Netherlands*
11:50 - 12:05	**OP050 - PUTTING THE PROTEOME TO WORK: NEW ADVANCES FOR CANCER RESEARCH**
	Carol Nilsson *University of Texas Medical Branch, Galveston, USA*
12:05 - 12:20	**OP051 - HIGHLY MULTIPLEXED IMAGING OF TUMOR TISSUES WITH SUBCELLULAR RESOLUTION BY MASS CYTOMETRY**
	Bernd Bodenmiller *University of Zurich , Switzerland*
12:20 - 12:35	**OP052 - SUITABILITY OF A CANCER PROTEOMICS SAMPLE**
	Christopher Kinsinger *National Cancer Institute, Bethesda, USA*
12:35 - 12:50	**OP053 - AN INTER-CANCER STUDY OF HUMAN PLASMA PROTEINS BY GLYCOSWATH MASS SPECTROMETRY**
	Tatjana Sajic *ETH Zurich, Switzerland*

Room C Immunobiology and Cell Signaling

Chairs	A. Admon O. Acuto

11:00 - 11:25	**THE HLA PEPTIDOME PRODUCTION PIPELINE**
Keynote Speaker	Arie Admon *Israel Institute of Technology, Haifa, Israel*
11:25 - 11:50	**PROTEOMICS SURVEY OF T CELL ACTIVATION AND DIFFERENTIATION**
Keynote Speaker	Oreste Acuto *University of Oxford, United Kingdom*
11:50 - 12:05	**OP054 - QUANTITATIVE PROTEOMICS TO STUDY PROTEIN SECRETION FROM IMMUNE CELLS**
	Felix Meissner *MPI of Biochemistry, Munich, Germany*
12:05 - 12:20	**OP055 - A SYSTEMATIC PROTEOMICS-BASED APPROACH TO GENERATING IMMUNOTHERAPEUTICS BASED ON HIGH AFFINITY SOLUBLE T CELL RECEPTORS**
	Alex Powlesland *Immunocore Ltd, Abingdon, United Kingdom*
12:20 - 12:35	**OP056 - IN-DEPTH ANALYSIS OF HLA-I PEPTIDOMES REVEALS THAT PROTEIN ABUNDANCE AND TURNOVER STRONGLY AFFECTS PRESENTATION – IMPLICATIONS FOR IMMUNOTHERAPY OF MELANOMA**
	Michal Bassani-Sternberg *Max Planck Institute For Biochemistry, Martinsried, Germany*
12:35 - 12:50	**OP057 - OMICS ANALYSES PROVIDE EVIDENCE FOR PERITONEAL IMMUNE-MODULATION BY AN ALANYL-GLUTAMINE CONTAINING PERITONEAL DIALYSIS SOLUTION**
	Klaus Kratochwill *Medical University of Vienna, Austrian*

Room D REDOX Proteomics and Mitochondrial Biology

Chairs	J. Vázquez E. Murphy A. Martinez
11:00 - 11:25	**NOVEL APPROACHES FOR THE STUDY OF THE DYNAMIC BEHAVIOR OF THE MITOCHONDRIAL REDOXOME AND SUPERCOMPLEXOME**
Keynote Speaker	Jesús Vázquez *National Cardiovascular Research Centre , Madrid, Spain*
11:25 - 11:50	**SIGNALING BY S-NITROSYLATION IN THE HEART**
Keynote Speaker	Elizabeth Murphy *National Heart, Lung, and Blood Institute, Bethesda, USA*

11:50 - 12:05 **OP058 - GLOBAL PROTEIN OXIDATION PROFILING OF PODOSPORA ANSERINA MITOCHONDRIA SUGGESTS EFFICIENT REMOVAL OF DAMAGED PROTEINS EVEN AT HIGH AGE**

Ansgar Poetsch
Ruhr University Bochum, Germany

12:05 - 12:20 **OP059 - A DECADE OF MITOCHONDRIAL PROTEOMICS**

Julia Maria Burkhart
Leibniz-Institut Für Analytische Wissenschaften - ISAS - E.V., Dortmund, Germany

12:20 - 12:35 **OP060 - PROTEOMIC CHARACTERIZATION OF CYSTEINE OXIDATION IN INS-1E CELLS IN RESPONSE TO CYTOKINES STIMULATION**

Honggang Huang
University of Southern DenmarK, Odense M.,Denmark

12:35 - 12:50 **OP061 - CONCURRENT ANALYSIS OF REVERSIBLE CYSTEINE OXIDATIONS: S-NITROSYLATION AND S-SULFONYLATION**

Adelina Rogowska-Wrzesinska
University of Southern DenmarK, Odense M.,Denmark

Room E

EuPA Initiatives

Chairs G. Corthals
A. Urbani

11:00 - 11:22 **STANDARDISATION**

F. Canals
Vall D'Hebron Institute Of Oncology (VHIO) , Barcelona, Spain

11:22 - 11:44 **BIOBANKS AND PROTEOMICS**

A Wheelock
Karolinska Institutet, Stockholm, Sweden

11:44 - 12:06 **MS IMAGING**

L. McDonnell
Leiden University Medical Center, The Netherlands

12:06 - 12:28 **MODEL ORGANISMS**

E. Bendixen
Aarhus University, Denmark

12:28 - 12:50 **FUTURE PERSPECTIVES**

G. Corthals
Turku Centre for Biotechnology, finland

13:00 - 14:15

Lunch Seminars / Lunch Break

14:15 - 15:45

Poster Session

Even-numbered poster boards present

16:00 - 16:45

Plenary Lecture

Chair M. C.M. Chung

16:00 - 16:45 **SIGNALING INTERACTOME DYNAMICS IN HEALTH AND DISEASE**

Keynote Speaker Anne-Claude Gingras
Lunenfeld-Tanenbaum Research Institute, Toronto, Canada

16:45 - 18:35

Room A

Glycoproteomics in Biology and Diseases

Chairs N. Taniguchi
A. García

16:45 - 17:10 **FUT8-/- MICE WHICH LACK THE CORE FUCOSE STRUCTURE SHOW THE UPREGULATED GNT-III GENE AND ITS PRODUCT, A BISECTING GLCNAC: A POSSIBLE ADAPTIVE AND COMPENSATORY MECHANISM FOR GLYCAN FUNCTION**

Keynote Speaker Naoyuki Taniguchi
RIKEN Advanced Science Institute, Osaka, Japan

17:10 - 17:35 **COMBINATION OF GLYCOPROTEOMICS TECHNOLOGIES UTILIZED IN SUCCESSFUL DEVELOPMENT OF DIAGNOSTIC SYSTEMS**

Keynote Speaker Hisashi Narimatsu
National Institute of Advanced Industrial Science and Technology (AIST), Tsukuba, Japan

17:35 - 17:50 **OP062 - GLYCOPROTEOMIC IDENTIFICATION OF CELL SURFACE ATTACHMENT MOLECULES FOR ENTEROVIRUS 71**

Chuan-Fa Chang
National Cheng Kung University, Tainan, Taiwan

17:50 - 18:05 **OP063 - PRONOUNCED DIFFERENCES IN GLYCOSYLATION PROFILES OF HUMAN PANCREATIC ADENOCARCINOMA CELL LINES AFFECT THEIR RECOGNITION BY LECTIN RECEPTORS**

Stephanie Holst§
LUMC, Center For Proteomics And Metabolomics, Leiden, The Netherlands

18:05 - 18:20 **OP064 - CHARACTERIZATION OF THE COMPETITION BETWEEN ASPIRIN-ACETYLATION AND GLYCATION ON HUMAN PLASMA PROTEINS**

Francesco Finamore
University of Geneva, Switzerland

18:20 - 18:35 **OP065 - COMPREHENSIVE N-GLYCOME PROFILING OF CULTURED HUMAN EPITHELIAL BREAST CELLS IDENTIFIES UNIQUE SECRETOME N-GLYCOSYLATION SIGNATURES ENABLING TUMORIGENIC SUB-TYPE CLASSIFICATION**

Ling Lee
Macquarie University , Sidney, Australina

Room B

Inflammatory and Rheumatic Diseases

Chairs F.Blanco
K. Marcus

16:45 - 17:20 **SPANISH HPP-16 CONSORTIUM: THE B/D APPROACH OF THE RHEUMATIC DISEASES**

Keynote Speaker Francisco Blanco
Instituto de Investigación Biomédica de A Coruña (INIBIC), Spain

17:20 - 17:35 **OP066 - AUTOANTIBODIES IN THE SERA OF PATIENTS WITH AMYOTROPHIC LATERAL SCLEROSIS**

Caroline May
Ruhr-University Bochum, Germany

17:35 - 17:50 **OP067 - 2D-DIGE/MS ANALYSIS ALLOWS THE IDENTIFICATION OF A DISTINCT SERUM PROTEIN PROFILE IN CD38-DEFICIENT MICE ASSOCIATED WITH EITHER COLLAGEN-INDUCED ARTHRITIS OR INFLAMMATION**

Jaime Sancho
Instituto de Parasitología y Biomedicina López-Neyra (IPBLN) Armilla, Spain

17:50 - 18:05 **OP068 - PROTEOMIC STUDIES OF HMGB1 INVOLVEMENT IN LUNG INFLAMMATION**

Alexander Kurosky
University of Texas Medical Branch , USA

18:05 - 18:20 **OP069 - MOLECULAR PROFILING OF AUTOIMMUNE DISEASE FOR IMPROVED DIAGNOSIS, PROGNOSIS, AND CLASSIFICATION**

Christer Wingrem
Lund University, Sweden

18:20 - 18:35 **OP070 - DETECTION OF BACTERIAL AND HOST PROTEINS IN PEDIATRIC ULCERATIVE COLITIS FROM A SINGLE COLONIC BIOPSY SAMPLE BY SWATH-MS**

Petri Kouvonen
University of Turku, Turku, Finland

Room C

Proteomics of Human Microbiome and Infectious Diseases

Chairs
I. Cristea
L. Monteoliva

16:45 - 17:10 **UNDERSTANDING CELLULAR HOST DEFENSE AGAINST VIRAL INFECTION: LESSONS FROM PROTEOMICS**

Keynote Speaker
Ileana Cristea
Princeton University, USA

17:10 - 17:35 **PROTEOMICS-BASED OPERATIONAL PIPELINES FOR ADVANCED GUT MICROBIOTA ANALYSES**

Keynote Speaker
Lorenza Putignani
Bambino Gesù Children's Hospital, IRCCS, Rome, Italy

17:35 - 17:50 **OP071 - AN OPTIMIZED METAPROTEOGENOMIC PIPELINE FOR IN-DEPTH CHARACTERIZATION OF THE MOUSE GUT MICROBIOME**

Alessandro Tanca
Porto Conte Ricerche, Alghero, Italy

17:50 - 18:05 **OP072 - HIGH-RESOLUTION LC-MS ANALYSIS OF TARGET CELLS TREATED WITH CLOSTRIDIUM DIFFICILE TOXINS**

Andreas Pich
Hannover Medical School, Germany

18:05 - 18:20 **OP073 - HIGH-THROUGHPUT TARGETED SWATH-MS PROTEOMICS OF A HUMAN PATHOGEN IMPLICATES NOVEL PROTEIN QUANTITATIVE TRAIT LOCI (PQTL) IN THE REGULATION OF KEY VIRULENCE FACTORS**

Röst Hannes
ETH Zurich, Switzerland

18:20 - 18:35 **OP074 - PROTEOMICS UNRAVELS EXTRACELLULAR VESICLES AS CARRIERS OF MOONLIGHTING PROTEINS IN CANDIDA ALBICANS**

Ana Gil de Bona
Universidad Complutense de Madrid, Madrid, Spain

Room D

Standardisation in Proteomics: Tribute to Juan Pablo Albar

Chairs
C.H. Borchers
A. Paradela

16:45 - 17:10 **INTER-LABORATORY EVALUATION OF STANDARDIZATION KITS FOR QUANTITATIVE PLASMA PROTEOMICS**

Keynote Speaker
Christoph H Borchers
University of Victoria, Canada

17:10 - 17:35	**QUANTIFICATION OF ONCOGENIC SIGNALLING BY PHOSPHOPROTEOMICS**
Keynote Speaker	Pedro Cutillas *Queen Mary University of London, United Kingdom*
17:35 - 17:50	**OP075 - SCRIPT-MAP, A DATABASE OF "BEST-RESPONDERS", PUSHES ACCURACY IN MS QUANTIFICATION** Chen Ding *Beijing Institute of Radiation Medicine, China*
17:50 - 18:05	**OP076 - THE MZTAB DATA STANDARD FORMAT FOR REPORTING MS-BASED PEPTIDE, PROTEIN AND SMALL MOLECULE IDENTIFICATION AND QUANTIFICATION RESULTS** Johannes Griss *Medical University Of Vienna, Austria*
18:05 - 18:20	**OP077 - EXPEDIENTS IN PROTEOMIC RESEARCH - STANDARDISATION AND OPTIMIZED PROTOCOLS** Albert Sickmann *ISAS, Dortmund, Germany*
18:20 - 18:35	**OP078 - AN AUTOMATED QUALITY CONTROL PLATFORM FOR NANOLC-MS BASED PROTEOMICS** Daniel Lopez-Ferrer *Thermo Fisher Scientific, San Jose, USA*

Room E

EuPA Company News Corner EuPA/HUPO MADRID

About the EuPA Company Club

The EuPA Company Club Concept was first presented in September 2011. Companies involved in Proteomics Technologies are invited to join the Club as a platform for direct interaction with the Proteomics Community at the European level and to support correspondingly EuPA's Educational mission.

Participation in EuPA's high level Educational activities provides prospective visibility for the next generation of researchers in the Proteomics field. EuPA is the organisation optimally positioned to achieve this. Both together, the Company Club members and EuPA, will eventually create a platform for a fruitful cooperation in building a system of EuPA endorsed courses at different levels giving companies high visibility as important players in the field.

About the of EuPA Company News Corner

The EuPA Company Club News Corner is established at Annual EuPA Conferences as a dedicated platform for member companies where they can present latest developments. New solutions arriving from continuous engineering efforts to improve equipment and reagents for research in Proteomics will be orally presented by leading technology providing companies in the "News Corner" session.

16:45 - 17:00 **EUPA COMPANY CLUB - INTRODUCTION AND OUTLOOK**

Peter Verhaert
Delft University of Technology, The Netherland

17:00 - 17:15 **NEW TRIPLETOF® 6600 AND SWATHTM 2.0 FOR NEXT GENERATION PROTEOMICS AND QUANTITATIVE BIOLOGY**

Joerg Dojahn
AB Sciex

17:15 - 17:30 **DEVELOPMENT, IMPLEMENTATION AND APPLICATION OF PERFORMANCE / ASSESSMENT KITS FOR QUANTITATIVE PROTEOMIC STUDIES**

Andrew Percy
Agilent Technologies

17:30 - 17:45 **PROTEOMICS BEYOND BOUNDARIES WITH A NEW UHR-QTOF SYSTEM**

Carsten Baessmann
Bruker

17:45 - 18:00 **MEASURING PROTEIN´S ACTIVITY, QUANTITY AND FUNCTION BY MULTIPLEXED BEAD-ARRAYS - APPLICATIONS IN BIOMEDICAL RESEARCH**

Oliver Poetz
Luminex

18:00 - 18:15 **COMPARATIVE TWO DIMENSIONAL FLUORESCENT ELECTROPHORESIS (COFGE)**

Simone König
SERVA

18:15 - 18:30 **APPLICATION OF PROTEOMICS TECHNOLOGIES TO DRUG DEVELOPMENT – CURRENT STATUS AND CHALLENGES**

Fabian Milz
PROTAGEN

18:45 - 20:00

Informal Mixer with Exhibits-Posters

COMPANY CLUB MEMBER
EuPA
EUROPEAN PROTEOMICS ASSOCIATION

EuPA Company Club News corner

EuPA Company Club Members share their most recent Developments with the Proteomics Community

at the

8th Annual EuPA Conference &
13th Annual HUPO Conference
Madrid, España

Tuesday, October 07, 2014; from 16:45 to 18:30

Room E

Program

16:45	Peter Verhaert	*The EuPA Company Club. Status, Report, Developments and Perspectives*	**EuPA**
17:00	Jörg Dojahn	*New TripleTOF® 6600 and SWATHTM 2.0 for next generation proteomics and quantitative biology*	**ABSciex**
17:15	Andrew Percy	*Development, implementation and application of performance/assessment kits for quantitative Proteomic studies*	**Agilent**
17:30	Carsten Baessmann	*Proteomics beyond boundaries with a new UHR-QTOF system*	**Bruker**
17:45	Oliver Poetz	*Measuring proteins' activity, quantity and function by multiplexed Bead-Arrays - Applications in biomedical research*	**Luminex**
18:00	Simone König	*Comparative two dimensional fluorescent electrophoresis (CoFGE)*	**Serva**
18:15	Fabian Milz	*Application of proteomics technologies to drug development – Current status and challenges*	**Protagen**

HUPO 2014 MADRID

13th Human Proteome Organization World Congress

SCIENTIFIC PROGRAM

Wednesday October 8th

	Room A	Room B	Room C	Room D	Room E	Room F	Room G	Room H	Room I
08:00 - 09:20	HPP Morning Sessions								
		Respiratory diseases	C-HPP III	Cardiovascular	Computational Mass Spectrometry		Mitochondria	Protein Aggregation	PediOME
09:30 - 10:15	Plenary Lecture								
10:20 - 11:00	Coffee Break - Exhibition Hall								
11:00 - 12:50	Cardiovascular and haematological proteomics: tribute to Mike Dunn	Neurological disorders	Technological horizons. MS imaging, targeted proteomics, others	From Siena to Madrid, 20 years of proteomics: tribute to Friederich Lottspeich	Mapping the Human Proteome				
13:00 - 14:15	Lunch Break								
14:15 - 15:00	Poster Session								
15:00 - 16:50	Human Proteome Project	Interactomics and beyond. Protein networks and pathways	Computational proteomics. Data analysis and biostatistics	Proteomics of neglected tropical diseases					
16:50 - 18:15	Awards Session (HUPO & EuPA)								
18:15 - 19:30	Closing Ceremony								

09:30 - 10:15

Room A

Plenary Lecture

Chair A. Bairoch

09:30 - 10:15 **DEMOCRATIZATION OF ADVANCES IN MS-BASED PROTEOMICS TOOLS AND RESOURCES**

Keynote Speaker
Rob Moritz
Institute for Systems Biology, Seattle, USA

10:20 - 11:00

Coffee Break - Exhibition Hall

11:00 - 12:50

Room A

Cardiovascular and Haematological Proteomics: Tribute to Mike Dunn

Chairs
M. Mayr
F. Vivanco

11:00 - 11:25 **TRIBUTE TO MIKE DUNN: Paying forward**

Jennifer Van Eyk
Cedar Sinai Medical Center, Los Angeles, USA

Michael J. Dunn
UCD Conway Institute. Dublin Ireland

Hans-Joachim Kraus
Wiley-VCH Verlag. Weinheim, Germany

11:25 - 11:50 **INTEGRATION OF PROTEOMICS AND LIPIDOMICS - OPPORTUNITIES AND CHALLENGES IN CARDIOVASCULAR SYSTEMS BIOLOGY**

Keynote Speaker
Manuel Mayr
King’s College London, United kingdom

11:50 - 12:15 **A MULTIOMIC APPROACH TO UNDERSTANDING ATHEROSCLEROSIS**

Fernando Vivanco
IIS-Fundacion Jimenez Diaz, Madrid, Spain

12:15 - 12:30 **OP079 - QUANTITATIVE MEMBRANE PROTEOME PROFILING TO DISCOVER THERAPEUTIC TARGETS FOR HTLV-I ASSOCIATED DISEASES**

Makoto Ishihara
The University of Tokyo, Japan

12:30 - 12:45 **OP080 - A PROTEOMIC INSIGHT TO A NOVEL THERAPEUTIC TARGET FOR MYOCARDIAL INFARCTION**

Agnese Petrera
University of Freiburg, Germany

12:45 - 12:50 **OP081 - PROTEOMIC ANALYSES OF ARCHIVAL FORMALIN-FIXED PARAFFIN-EMBEDDED HUMAN AORTAS STORED FOR 25 YEARS**

Zongming Fu
Johns Hopkins University School of Medicine, Maryland, USA

Room B

Neurological Disorders

Chairs
H. Meyer
M. Fuentes

11:00 - 11:35 **WHAT TRIGGERS THE ONSET AND PROGRESSION OF ALZHEIMER'S DISEASE?**

Keynote Speaker
Helmut Meyer
Ruhr-University Bochum, Germany

11:35 - 11:50 **OP082 - BROAD-SCALE ANTIGEN ARRAY PROFILING PROVIDES NOVEL INSIGHTS INTO AUTOIMMUNE TARGETS IN MULTIPLE SCLEROSIS**

Burcu Ayoglu
KTH Royal Institute of Technology, Stockholm, Sweden

11:50 - 12:05 **OP083 - TARGETING SYNAPTIC PATHOLOGY IN ALZHEIMER'S DISEASE – AFFINITY MASS SPECTROMETRY AS A TOOL IN BIOMARKER DISCOVERY AND CLINICAL DIAGNOSIS**

Ann Brinkmalm
The University of Gothenburg, Sweden

12:05 - 12:20 **OP084 - A NEW CEREBROSPINAL FLUID 16PLEX ASSAY FOR NEURODEGENERATION**

Christopher Lößner
Proteome Sciences plc, London, United Kingdom

12:20 - 12:35 **OP085 - ISOLATION OF MULTIPROTEIN COMPLEXES AND SYNAPSE PROTEOMES FROM HUMAN POST-MORTEM BRAIN**

Àlex Bayés
Biomedical Research Institue Sant Pau, Barcelona, Spain

12:35 - 12:50 **OP086 - A SINGLE DOSE OF THE GAMMA-SECRETASE INHIBITOR SEMAGACESTAT ALTERS THE CEREBROSPINAL FLUID PEPTIDOME IN HUMANS**

Johan Gobom
University of Gothenburg, Sweden

Room C

Technological horizons

Chairs
B. Domon
E. Oliveira

11:00 - 11:25 **ADVANCES IN HIGH-RESOLUTION QUANTITATIVE PROTEOMICS**

Keynote Speaker Bruno Domon
Centre de Recherche Public de la Santé (CRP-Santé), Luxembourg

11:25 - 11:40 **OP087 - APPLICATION OF A NOVEL INTEGRATED MICROFUIDICS DEVICE FOR HIGH-THROUGHPUT LC-MS MRM DISEASE PROTEIN MARKER VERIFICATION**

Lee Gethings
Waters Corporation, Wilmslow, United Kingdom

11:40 - 11:55 **OP088 - A NOVEL SWATH-MS PLATFORM FOR COMPREHENSIVE CHARACTERIZATION OF THE EPIGENETIC HISTONE MODIFICATIONS**

Sahana Mollah
AB SCIEX, Redwood City, USA

11:55 - 12:10 **OP089 - TOWARDS QUANTIFICATION BASED MS IMAGING: FILLING THE GAP BETWEEN MALDI MS IMAGING AND TISSUE MICROPROTEOMICS**

Isabelle Fournier
Université Lille 1, France

12:10 - 12:25 **OP090 - TARGETED PROTEOMICS VIA AUTOMATED, HIGH PRECISION TRYPTIC DIGESTION AND SISCAPA-MS QUANTIFICATION OF HUMAN PLASMA PROTEINS USING THE AGILENT BRAVO PLATFORM**

Selena Larkin
SISCAPA Assay Technologie, Dublin USA

12:25 - 12:40 **OP091 - JUST ANOTHER FISHING EXERCISE? STABLE ISOTOPE LABELLING STRATEGIES TO INVESTIGATE THE DYNAMIC PROTEOME**

Mary Doherty
University of The Highlands And Islands, United Kingdom

12:40 - 12:50 **PROTEOME ANALYZER. CURRENT STATE**

Bruno Domon
Luxembourg Clinical Proteomics Center (LCP), Luxembourg

Room D

From Siena to Madrid, 20 years of proteomics: Tribute to Fiedrich Lottspeich

Chairs J. C. Sanchez
L. Bini

11:00 - 11:10 **INTRODUCTION**

Luca Bini
University of Siena, Italy

11:10 - 11:30 **AFTER 20 YEARS OF PROTEOMICS – IS THE VISION STILL ALIVE?**

Friederich Lottspeich
Max-Planck-Institute of Biochemistry, Munich, Germany

11:30 - 11:50 **FROM SINGLE PROTEIN IDENTIFICATION TO PROTEOMIC SYSTEMS BIOLOGY IN 20 YEARS**

Mathias Mann
Max-Planck Institute of Biochemistry, Munich, Germany

11:50 - 12:10 **20 YEARS OF PROTEOMICS: WHAT DOES HISTORY TELL US ABOUT THE FUTURE?"**

Ruedi Aebersold
Institute of Molecular Systems Biology, Zurich, Switzerland

12:10 - 12:30 **TISSUE-BASED MAP OF THE HUMAN PROTEOME**

Mathias Uhlen
KTH Royal Institute of Technology, Stockholm, Sweden

12:30 - 12:50 **SHOULD WE REALLY TRUST AUTOMATED HT PEPTIDE IDENTIFICATION?**

Peter James
Lund University, Sweden

Room E

Mapping the Human Proteome

Chairs
L. Martens
E. Deustch

11:00 - 11:25 **MASS SPECTROMETRY BASED DRAFT OF THE HUMAN PROTEOME**

Keynote Speaker
Bernhard Kuster
Technische Universität München, Freising, Germany

11:25 - 11:50 **PROBING DEEPER INTO THE HUMAN PROTEOME**

Keynote Speaker
Akhilesh Pandey
Johns Hopkins Bloomberg School of Public Health, Baltimore, USA

11:50 - 12:05 **OP092 - PROTANNOTATOR: A SEMIAUTOMATED PIPELINE FOR CHROMOSOME-WISE FUNCTIONAL ANNOTATION OF THE "MISSING" HUMAN PROTEOME**

Shoba Ranganathan
Macquarie University, Sydney, Australia

12:05 - 12:20 **OP093 - PROTEOMICS STUDIES SUGGEST THAT THERE ARE JUST 19,000 PROTEIN CODING GENES IN THE HUMAN GENOME**

Michael Tress
Spanish National Cancer Research Centre (CNIO), Madrid, Spain

12:20 - 12:35 **OP094 - BIOINFORMATICS PIPELINE AND MASS SPECTROMETRY-BASED METHODOLOGIES FOR THE DISCOVERY OF MISSING PROTEINS: THE CASE OF HUMAN CHROMOSOME 2 AND 14**

Yves Vandenbrouck
CEA, Life Science Division, Grenoble, France

12:35 - 12:50 **OP095 - PROTEOGENOMICS DASHBOARD FOR THE HUMAN PROTEOME PROJECT**

Alberto Pascual-Montano
National Center For Biotechnology-CSIC, Madrid, Spain

13:00 - 14:15

Lunch Seminars / Lunch Break

14:15 - 15:45

Poster Session

All poster boards are free to present

15:00 - 16:50

Room A

Human Proteome Project

Chairs G. Omenn
Y. K. Paik

15:00 - 15:25 **COMPARATIVE PROTEOMICS AND THE ROLE OF MULTI-ORGANISM PROTEOMES IN THE HPP**

Keynote Speaker Emøke Bendixen
Aarhus University, Denmark

15:25 - 15:50 **MULTILAYERED GENETIC AND OMICS DISSECTION OF MITOCHONDRIAL ACTIVITY**

Keynote Speaker Johan Auwerx
École Polytechnique Fédérale, Lausanne, Switzerland

15:50 - 16:05 **OVERVIEW OF PROGRESS, STRATEGIES, AND METRICS OF THE HUMAN PROTEOME PROJECT**

Gilbert Omen
University of Michigan Medical Center, USA

16:05 - 16:20 **LEVERAGING THE GENOME-WIDE PROTEOME PARTS TO STUDY DISEASE BIOMARKERS THROUGH FUNCTIONAL VALIDATION OF MISSING PROTEINS**

Young-ki Paik
Yonsei University, Seoul, Korea,

16:20 - 16:35 **MULTIPLEXED AND SENSITIVE PROTEIN QUANTITATION OF FRACTIONATED HUMAN PLASMA BY MRM/MS WITH ISOTOPICALLY LABELED STANDARD**
Andrew Percy
UVic-Genome BC Proteomics Centre, Victoria, BC, Canada

16:35 - 16:50 **PANEL AND GENERAL AUDIENCE DISCUSSION**

Ruedi Aebersold, Catherine Costello, Bill Hancock, Pierre Legram, Michael Snyder, Mathias Uhlen, Jennifer Van Eyk

Room B

Interactomics and Beyond. Protein Networks and Pathways

Chairs
M.Gstaiger
P. Roepstorff

15:00 - 15:50 **INTERACTION PROTEOMICS: CURRENT CHALLENGES AND EMERGING IMPLICATIONS**

Keynote Speaker
Matthias Gstaiger
Swiss Federal Institute of Technology Zurich (ETH), Switzerland

15:50 - 16:05 **OP096 - LARGE SCALE IDENTIFICATION OF PHOSPHO-DEPENDENT PROTEIN-PROTEIN INTERACTIONS**

Ulrich Stelzl
Max Planck Institute For Molecular Genetics (MPI), Berlin, Germany

16:05 - 16:20 **OP097 - HIGHLY ACCURATE PROTEIN COMPLEX RETRIEVAL BY AFFINITY ENRICHMENT MS RATHER THAN AFFINITY PURIFICATION MS**

Eva C. Keilhauer
Max Planck Institute of Biochemistry, Martinsried, Germany

16:20 - 16:35 **OP098 - AP-MS AND BIOID ANALYSIS OF THE HBX VIRAL-HOST INTERACTOME**

Emanuela Milani
Institute of Molecular Systems Biology ETH, Zurich, Switzerland

16:35 - 16:50 **OP099 - UNTANGLING THE COLORECTAL CANCER EGFR/ERBB NETWORK USING A TRIPLE SILAC AP/MS APPROACH**

Cinzia Raso
University College of Dublin, Ireland

Room C

Computational Proteomics. Data Analysis and Biostatistics

Chairs
H. Hermjakob
A. Pascual

15:00 - 15:25 **EXPANDING THE SCOPE, SCALE, AND REPRODUCIBILITY OF TARGETED PROTEOMICS**

Keynote Speaker
M. MacCoss
University of Washington, USA

15:25 - 15:50 **PROTEOMEXCHANGE - AN INTERNATIONAL INFRASTRUCTURE FOR OPEN PROTEOMICS DATA**

Keynote Speaker
Henning Hermjakob
European Bioinformatics Institute (EMBL-EBI)

15:50 - 16:05 **OP100 - SEQUENCE VARIANT ANALYSIS WITH INCREASED SPECIFICITY AND MEANINGFUL CONFIDENCES**

Sean L Seymour
AB SCIEX, Redwood City, USA

16:05 - 16:20 **OP101 - RE-ANALYSIS OF PUBLIC DATA: DOES THE FUTURE OF PROTEOMICS LIE IN THE PAST?**

Lennart Martens
UGent / VIB, Ghent, Belgium

16:20 - 16:35 **OP102 - PINT: A NEW PLATFORM FOR THE COMPREHENSIVE INTEGRATION OF COMPLEX LARGE-SCALE PROTEOMICS DATA AND RESULTS**

Salvador Martínez-Bartolomé
The Scripps Research Institute, San Diego, USA

16:35 - 16:50 **OP103 - SCALING UP SPECTRAL CLUSTERING IN THE PRIDE DATABASE**

Juan Antonio Vizcaino
EMBL-European Bioinformatics Institute, Cambrigde, United Kingdom

Room D

Proteomics of Neglected Tropical Diseases

Chairs
J.C. Sanchez
J.J. Calvete

15:00 - 15:35 **SLEEPING-SICKNESS: FROM OMICS DISCOVERY TO A FIELD POINT OF CARE TEST**

Keynote Speaker
Jean-Charles Sanchez
Medical University Centre, Geneva, Switzerland

15:35 - 15:50 **OP104 - COMPARATIVE PROTEOMICS OF REPLETE FEMALE TICKS HIGHLIGHTS MOLECULAR MECHANISMS ASSOCIATED WITH BM86 AND SUBOLESIN VACCINE PROTECTION**

Margarita Villar
Instituto de Investigación en Recursos Cinegéticos, Ciudad Real, Spain

15:50 - 16:05 **OP105 - ROLE OF STAGE SPECIFIC LEISHMANIA A600 PROTEINS IN CELLULAR DIFFERENTIATION AND METABOLISM**

Robert McMaster
University of British Columbia, Vancouver, Canada

16:05 - 16:20 **OP106 - DISCOVERING UNIQUE PEPTIDES WITHOUT A SEQUENCE DATABASE**

Sule Yılmaz
University Of Gent, VIB, Belgium

16:20 - 16:35 **OP107 - QUANTITATIVE PROTEOMIC ANALYSIS OF HUH 7 CELLS INFECTED WITH DENGUE VIRUS BY LABEL-FREE LC-MS**

Victoria Pando-Robles
Instituto Nacional De Salud Pública, Morelos, Mexico

16:50 - 18:15

Awards Session (HUPO & EuPA)

Chairs
M. Baker
L. Bini

HUPO Awards

Distinguished Achievement in Proteomic Sciences
Sponsored by *Journal of Proteome Research/ ACS Publications*
Pier Giorgio Righetti

Translational Proteomics
Sponsored by *Translational Proteomics/ Elsevier*
Daniel W. Chan

Discovery in Proteomic Sciences
Neil L. Kelleher

Science and Technology Award
Sponsored by *HUPO Industrial Advisory Board*
Subhasish “Babu” Purkayastha, John Rogers, Rosa Viner, Andrew Thompson

This team of four is nominated for their contributions in the commercialization of isobaric labeling compounds for use in quantitative proteomics. Both programs, ITRAQ (AB SCIEX) and TMT (Thermo Fisher Scientific and Proteome Sciences) are recognized.

EUPA Award

Proteomic Pioneer Award in Proteomics Sciences
Albert Heck

EuPA Young Investigator Award

HUPO-Madrid 2014 Young Investigator Award

Poster Awards

18:15 - 19:30

Closing Ceremony

Chairs
P. Legrain
G Marko-varga
C. Gil
F.J Corrales
J. Calvete

18:15 - 18:40 **GENETIC VARIABILITY AND THE QUANTITATIVE PROTEOME**

Keynote Speaker
Ruedi Aebersold
Institute of Molecular Systems Biology, Zurich, Switzerland

CLOSING REMARKS AND ANNOUNCEMENTS

HPP Morning Sessions

HPP Investigators Meeting - Sunday, October 5, 10:00 - 17:00

Location: Room D

10:00 - 10:10	**Overview of Progress, Metrics, and Publications from the HPP** Gil Omenn, Chair, HPP, Univ. of Michigan, Ann Arbor, MI, US
10:20 - 10:40	**B/D-HPP Highlights, Priority Protein Lists by Disease, Clinician - Scientist Initiative, Workshops Plan + Discussion** • Ruedi Aebersold, ETH Zurich, Switzerland • Jennifer Van Eyk, Cedars-Sinai Health System, Los Angeles, CA, US
10:40 - 11:00	**C-HPP Highlights, Busan and Bangkok Workshops, Congress Workshops + Discussion** • Young-Ki Paik, Chair, C-HPP Initiative, Yonsei Univ., Seoul, Korea • William S. Hancock, Co-Chair, Northeastern Univ., Boston, MA, US
11:00 - 11:55	**Update of HPP Metrics:** neXtProt (9/14), PeptideAtlas (8/1/14) & GPMdb - Moderator: Gil Omenn **Bioinformatics Discussions and Standardized Re-Analyses of Major Datasets of Four Major Publications in 2014:** Kim et al (Pandey lab, PXD000561); Wilhelm et al (Kuster lab, PXD000865); Guo et al (Mirzaei lab with various proteolytic enzymes); and TCGA datasets Comments: • Amos Bairoch & Lydie Lane, SIB, Geneva, Switzerland • Eric Deutsch, Inst. Systems Biology, Seattle, WA, US • Akhilesh Pandey, Johns Hopkins & Bangalore; Bernhard Kuster, TUM, Munich; Henry Rodriguez, Bethesda
12:00 - 12:50	**Working Lunch Discussion** (lunch provided by RSVP only) **Inter-Relationships across HPP Components and Bioinformatics Approaches** - Bill Hancock **From China: Latest Database Search for Evidence of Missing Proteins** - Pengyuan Yang
13:00 - 13:30	**Antibody and MS Resource Pillars** Cross-Validation with Ab and MS Approaches Including MRM Based Quantitation for HPP • Emma Lundberg, SciLifeLab, Stockholm, Sweden ProteomeAnalyzer Project • Bruno Domon, Centre Sante' Clinical Proteomics Center, Luxembourg
13:30 - 14:00	**SSAB Panel, Overview, Strategic Comments from SSAB Members** Moderator: Mike Snyder, Stanford Univ., Stanford, CA, US • Cathy Costello, Boston Univ, Boston, MA, US; Matthias Mann, Max Planck, Munich, Germany; Kate Rosenbloom, *Univ of California Santa Cruz/ENCODE, US*

14:00 - 16:00 **Town Hall Meeting Open Forum – on B/D- and C-HPP Collaboration**
Co-Chairs: Ruedi Aebersold and Young-Ki Paik

Part 1. Integrated Data Management
“Priority Proteins”/”Popular Proteins”, Including PTMs, Splice Isoforms, SNPs/SAAPs, for Specific Diseases; Use of SRM Peptides, Spectral Libraries, and SRMAtlas
- Jennifer Van Eyk, Ruedi Aebersold, Eric Deutsch and B/D Teams

ProteomeExchange Experience: PDX Identifiers and Release of Data on Acceptance, Uploading Large Data Sets
- Juan Vizcaino, EBI, Hinxton, UK

Proteogenomics/RNA Seq, Integrated ‘Omics analyses
- Gyorgy Marko-Varga, Jennifer Harlow, Kate Rosenbloom, Michael Snyder (ENCODE)

Part 2. Biological Impact of Missing Proteins on C-HPP and B/D-HPP Research
Updates from neXtProt on the missing and orphan proteins
- Lydie Lane and Amos Bairoch, SIB, Switzerland

A Strategy for Bioinformaticians to Take a Deep Dive on Chr-Specific Missing Protein Lists (as discussed in Bangkok C-HPP workshop)
- William S. Hancock and Gyorgy Marko-Varga, Co-Chairs, C-HPP Consortium

Timing of JPR Special Issue and Standardization of Data Bases for Publication Metrics: What is the Best Theme and Date (middle of 2015) for this Special Issue?
- Bill Hancock and Young-Ki Paik, C-HPP Consortium

Part 3. Opportunities to Explore Collaborations Within and Between B/D-HPP and C- HPP
- Young-Ki Paik and Ruedi Aebersold, entire C-HPP & B/D-HPP Groups

16:00 - 17:00 **Meeting of SSAB with HPP-EC for Feedback:** Mike Snyder and SSAB Group

HPP Early Morning Sessions

The Human Proteome Project (HPP) has grown to become a strong focus of HUPO activities. Most existing HUPO initiatives have found a focus within the HPP and a wide range of new initiatives and projects have also been started by the HPP. All congress attendees are invited to participate in the early morning HPP sessions. These lively, smaller sessions are an invaluable opportunity to connect with colleagues and contribute to the HPP.

Refer to the following pages for detailed description of the initiative sessions Monday, Tuesday and Wednesday mornings 8:00 - 9:20 am. For details on the Wednesday, October 8 HPP Parallel, please refer to the main congress program.

Overview of HPP Early Morning Sessions

Open to ALL Congress Attendees

MONDAY, OCTOBER 6 08:00 - 09:20	TUESDAY, OCTOBER 7 08:00 - 09:20	WEDNESDAY, OCTOBER 8 08:00 - 09:20
HPPP (Plasma) *Room B*	Diabetes *Room B*	Respiratory Diseases *Room B*
C-HPP, Part I: New Technology *Room C*	C-HPP, Part II: Poster Session *Inside Poster Hall*	C-HPP, Part III: PIC *Room C*
Cancers I *Room D*	PSI / ProteomeXchange *Room C*	Cardiovascular *Room D*
iMOP *Room E*	Antibody Proteomics *Room D*	Computational Mass Spec. *Room E*
Liver *Room F*	Cancers II *Room E*	Mitochondria *Room G*
Extreme Conditions *Room G*	Glycoproteomics *Room F*	Protein Aggregation Diseases *Room H*
Infectious Diseases *Room H*	Brain Project *Room G*	PediOme *Room I*
EyeOme *Room I*	Stem Cells *Room H*	
	Biobanking & Pre-Analytical Sample Assessment *Room I*	

Please see the following pages for details on each workshop.

HPP Early Morning Sessions - Monday, October 6, 2014

Human Plasma Proteome Project (HPPP) Plasma Proteomics Underpins a Translational HPP

Organizers: Mark Baker, Martin Kussman, Eric Deutsch, and Simon Fredericksson

Room B

8:00 - 8:12 am	Loïc Dayon: A Comprehensive and Scalable Automated Workflow for Human Plasma Proteomics and Its Application to the DiOGenes Clinical Study
8:15 - 8:27 am	Simon Fredriksson: Multiplexed and Sensitive Immunoassays by the Highly Specific Proximity Extension Assay
8:30 - 8:42 am	Eric Deutsch: The PeptideAtlas Plasma Proteome Build
8:45 - 8:50 am	Jochen Schwenk: Affinity Proteomics in Plasma from Cancer Biobanks
8:50 - 8:55 am	Sadia Mahboob: Targeted Proseek Multiplexed Immunoassays of Candidate Plasma Biomarkers for Dukes' Stage A-D CRC
8:55 - 9:00 am	Tatjana Sajic: An Inter-Cancer Study of Human Plasma Proteins by gly coSWATH Mass Spectrometry
9:00 - 9:20 am	Panel: Baker, Aebersold, Omenn, Kussmann, Deutsch, Fredriksson

C-HPP, Part I: New Technology

Organizer: Bill Hancock

Room C

The following topics will be discussed in the New Technology C-HPP session.

- SRM measurement of missing proteins
- RNA analysis, including predicting when transcript forms protein
- Integration of RNA-Seq and proteomics
- Approaches to ASV and SNV characterization such as down top MS, adoption of protein chemistry methods
- Identification of protein families and sharing of specific data across chromosome families

HPP Early Morning Sessions - Monday, October 6, 2014

Cancer I

Organizers: Hui Zhang, Christopher Kinsinger and Edouard Nice

Room D

8:00 - 8:10 am	Hui Zhang: Overview of the Ca-B/D HPP
8:10 - 8:25 am	Ruedi Aebersold: Quantifying Cancer Related Proteins via Targeting MS Assay
8:25 - 8:40 am	Christopher Kinsinger: The CPTAC Initiative
8:40 - 8:55 am	Robert Moritz: MRM
8:55 - 9:10 am	Edouard Nice: Towards the Human Proteome Analysis of Alternate Clinical Samples
9:10 - 9:20 am	Open Discussion

iMOP

Organizers: Emøke Bendixen, Sabine Schrimpf

Room E

8:00 - 8:05 am	Emøke Bendixen: Introduction
8:05 - 8:25 am	Erik Bongcam-Rudloff: The ALLBIO Project, Beyond Human Centric Bioinformatics Resources
8:25 - 8:45 am	Fabrize Bertil: Deciphering New Anti-Obesity Mechanisms Using Non-Sequenced Species
8:45 - 9:10 am	Dorothea Rutishauser: Levels of Chemosensory and Odorant-Binding Proteins from Caterpillar Saliva are Affected by Host Plant and Immune Challenge
9:10 - 9:20 am	Open discussion

HPP Early Morning Sessions - Monday, October 6, 2014

Human Liver B/D Initiative

Organizers: Pumin Zhang and Fernando J. Corrales

Room F

The Human Liver Proteome Project (HLPP) was launched in 2002, aiming to establish a biological atlas of the human liver, uncover the proteomic basis of liver development, physiology and pathology, and develop diagnostics and therapeutics for liver diseases. It is a large-scale international collaborative initiative of the Human Proteome Project (HPP). In the past decade, under the efforts of HLPP international consortium, HUPO has set up standard operating procedures, optimized the strategies for proteomic analysis and investigated the proteomes of liver tissues, healthy and diseased. More specifically, in 2010, Human Liver 1.0 was published, in which 6788 gene products have been identified, whilst in 2013, proteome of liver cellular organelles was profiled and totally 12,168 gene products in human liver were identified. The next goals will be, first, to profile the four major cell types in the liver to produce Liver Proteome 3.0 that will include around 13,000 proteins in total; second, to investigate post-translational modifications of liver proteins, and finally, focusing on the Biology/Disease (B/D)-driven Liver Proteome Project and looking for biomarkers for liver disease.

This session will feature talks from the following speakers:

- Opening Remarks: Pumin Zhang (Baylor College of Medicine, USA)
- Reference Material-Based Liver Proteome Quantitation: J Eugene Lee (Korea Research Institute of Standards and Science, Korea)
- Proteomic Analysis of Human Urine Exosomes and Hepatoblastoma Tissue Samples by Label-Free nLC MS/MS: Felix Elortza (CIC bioGUNE)
- Deciphering Essential Genes by Comparative Analysis Transcriptoproteome of Liver Tissue and HepG2 Cell Line: Andrey Lisitsa (Institute of Biomedical Chemistry, Russia)
- From Protein Lists to the Pathogenesis of Chronic Liver Disorders. Role of One Carbon Metabolism: Fernando J Corrales (CIMA, University of Navarra, Spain)
- Proteomics on Post-Translation Modifications of Proteins: Ping Xu (Beijing Proteome Research Center, China)
- Laura Beretta (MD Anderson Cancer Center, USA)
- New Cell Biology through the study of Human Fatty Liver Disease: Tommy Nilsson (McGill University, Canada)
- Characterization of Altered Membrane Lipid Profiling in Hepatocellular Carcinoma
- Progression: Pengyuan Yang (Fudan University, China)

HPP Early Morning Sessions - Monday, October 6, 2014

Extreme Conditions

Organizer: Evgeny Nikolaev and Irina Larina

Room G

8:00 - 8:05 am Evgeny Nikolaev: Introduction

8:05 - 8:20 am Irina Larina: Adaptation of Human Organism to Long Space Flight (Institute of Biomedical Problems, Moscow, Russia)

8:20 - 8:30 am Saik Olga: System for Automated Literature Mining and Protein Interactome Networks Reconstruction (Institute of Cytology and Genetics, Novosibirsk)

8:30 - 8:40 am Igor Popov: Technical Aspects of Proteomic Assays of People Under Extreme Conditions (Talroze Institute for Energy problems of Chemical Physics, Moscow Institute of Physics and Technology, Dolgoprudnyj, Russia)

8:40 - 8:50 am Alexey Kononikhin: Proteomics of Exhaled Breath Condensate of People in Extreme Conditions (Talroze Institute for Energy problems of Chemical Physics, Moscow Institute of Physics and Technology, Dolgoprudnyj, Russia)

8:50 - 9:00 am Ludmila Pastushkova: Cardiovascular Proteins in the Urine of Healthy Volunteers During the “Dry” Immersion; (Institute of Biomedical Problems, Moscow, Russia)

9:00 - 9:10 am Andrew Chambers: Plasma and Urine MRM Assay Development for the Cosmonaut Samples (UVic-Genome BC Proteomics Centre, Victoria, Canada)

9:10 - 9:20 am Bruno Domon, Nina Khristenko, Irina Larina, Eugene Nikolaev: Systematic Analysis of Proteins in Urine Samples; Application to the Mars-500 Program; (Luxembourg Clinical Proteomics, (Institute of Biomedical Problems, Moscow, Russia, Institute for Energy problems of Chemical Physics, Moscow, Russia)

HPP Early Morning Sessions - Monday, October 6, 2014

Infectious Diseases (HID)

Organizers: Ileana Cristea and Concha Gil

Room H

Infectious diseases are disorders caused by (micro) organisms (viruses, bacteria, fungi and parasites). These have the potential to rapidly become global epidemics and pandemics, and are a leading cause of human disease and death worldwide, in particular in low income countries. Lower respiratory infections, HIV/AIDS and diarrheal diseases are ranked in the top ten causes of death globally, whereas malaria and tuberculosis are two of the major ten causes of death in low income countries. In developed countries infectious diseases are also important in immunosuppressed patients and transplant recipients. New diagnostic tests and therapeutic agents are required to reduce the mortality of these infectious diseases.

8:00 - 8:05 am HID-HPP Initiative Introduction

8:05 - 8:40 am Round Table Discussion
Panelists: Ileana Cristea, Concha Gil, Manuel Fuentes, Sanjeeva Srivastava, Rafa Cantón, Jesús Fortún, Catherine Costello, Christopher Overall, Frank Schmidt, Joshua LaBaer, Peter Nilsson

Key discussion points:

A. How to organize a community of scientists working in Infectious disease proteomics?

B. Potential scientific goals for this initiative

1. Selection of human proteins related to infectious diseases and immune system response based on published data using literature searches and bioinformatic analysis
2. Definition of human infectious disease-specific protein profiles (viruses, bacteria, fungi and parasites)
3. Selection of microbial proteins useful as diagnostic biomarkers.
4. Development of SRM methods for detection and quantification of human and microbial proteins
5. Generation of PeptideAtlas and SRMAtlas of selected microorganisms
6. Detection and quantification of these proteins by targeted proteomics in clinical samples
7. Detection and quantification of these proteins by affinity or antibodies based technolgies
8. Identification of novel host factors for antiviral therapeutic intervention
9. Characterization of host-pathogen protein-protein interactions
10. Building of a web page to freely-access data
11. Collaboration with other HPP Initiatives (e. g. HAI - Antibodies, HPPP – Plasma Proteins, DBI- Disease Biomarkers Initiatives, iMOP- Initiative on Model Organism Proteomes

HPP Early Morning Sessions - Monday, October 6, 2014

C. Contribution to J. Proteomics HUPO 2014 special issue
D. HID-HPP initiative Organization and future actions

8:40 - 8:50 am Discovery and Validation of Biomarkers to Guide Clinical Management of Pneumonia; Climent Casals-Pascual, University of Oxford, UK

8:50 - 9:00 am Label-Free Proteomic Analysis of Environmental Acidification-Influenced Streptococcus Secretome Reveals a Novel Acid-Induced Protein Histidine Triad Protein A (HtpA) Involved in Necrotizing fasciitis Pyogenes; Pao-Chi Liao, National Cheng Kung University, Taiwan

9:00 - 9:10 am Phosphoproteomic Characterization of Influenza A Virus Infected Human Primary Macrophages; Tuula Nyman, Institute of Biotechnology, Finland

9:10 - 9:20 am Open Discussion

EyeOme
The EyeOME: A View on the Proteomics Side of Vision

Organizer: Richard Semba, Marius Ueffing, and Hyewon Chung

Room I

In this session, eight speakers will present the current state-of-the-art of proteomic investigations of the eye. Tear, aqueous, vitreous, and serum sampling offers great potential for identifying biological pathways leading to eye disease. A comprehensive catalogue of eye proteins should provide a solid basis for proteomic studies of the eye. Animal models help increase the understanding of uveitis and diabetic macular edema. Proteomics provides new insight into major causes of blindness and visual disability such as glaucoma, retinal vascular disease, diabetic retinopathy, and age-related macular degeneration.

8:00 - 8:10 am Proteomics and Immunoproteomics Biomarker in Glaucoma; Franz Grus, *Experimental Ophthalmology, Department of Ophthalmology, University Medical Center, Mainz, Germany*

8:10 - 8:20 am Diagnostic Aspects of Proteomics and Metabolomics in Ophthalmology; Sascha Dammeier[1]; Dario Bosch[1]; Focke Ziemssen[2]; Marius Ueffing[1], *[1]Medical Proteome Center, Institute for Ophthalmic Research, Eberhard-Karl-University Tuebingen, Tuebingen, Germany; [2]Centre for Ophthalmology, University Eye-Hospital, Tuebingen, Germany*

8:20 - 8:30 am The Human Eye Proteome Project - Update 2014; Richard D. Semba[1]; Pingbo Zhang[1]; Randi Turner[1]; Sara Ferri[1]; Jennifer E. Van Eyk[2]; Craig Dufresne[3], *[1]Wilmer Eye Institute, Johns Hopkins School of Medicine, Baltimore, MD, USA; [2]Cedars-Sinai Medical Center, Los Angeles, CA, USA; [3]Thermo Fisher Scientific, West Palm Beach, FL, USA*

HPP Early Morning Sessions - Monday, October 6, 2014

8:30 - 8:40 am A Peculiar Translational Animal Model for Recurrent Uveitis; Cornelia A Deeg, *Department of Veterinary Sciences, LMU Munich, Munich, Germany*

8:40 - 8:50 am The Vitreous is an Accessible Source for Retinal and Choroidal Disease Biomarkers; Vinit B. Mahajan[1, 2], Stephen H. Tsang[3], Jessica M. Skeie[1,2], *[1]Omics Laboratory, [2]Department of Ophthalmology and Visual Sciences, University of Iowa, Iowa City, IA, USA; [3]Departments of Ophthalmology, Pathology & Cell Biology, College of Physicians & Surgeons, Columbia University, New York, NY, USA*

8:50 - 9:00 am Clinical Vitreous Biopsy Reveals Molecular Signature of the Retina; Jeffrey M. Sundstrom[1], Alexey Nesvizhskii[2], *[1]Department of Ophthalmology, Penn State Hershey Medical Center, Hershey, PA, USA1; [2]Department of Computational Medicine & Bioinformatics, University of Michigan, Ann Arbor, MI, USA*

9:00 - 9:10 am Identification of Protein Biomarkers for Retinal Thickening in Diabetic Macular Edema; Edward P. Feener[1,3]; Nivetha Murugesan[1,3]; Allen Clermont[1,2,3]; Ward Fickweiler[1]; Takeshi Kita[1]; Lloyd P. Aiello[1,2,4]; *[1]Joslin Diabetes Center, [2]Beetham Eye Institute, Departments of [3]Medicine and [4]Ophthalmology, Harvard Medical School, Boston, MA, USA*

9:10 - 9:20 am Exosomal Proteins in the Aqueous Humor as Novel Biomarkers in Patients with Neovascular Age-related Macular Degeneration; Hyewon Chung[1]; Ae Jin Choi[1]; Jeehyun Yoon[1]; Joo Young Bang[2]; Je-Hyun Baek[2]; Hyung Soon Park[2]; *[1]Department of Ophthalmology, Konkuk University School of Medicine, Seoul, Republic of Korea; [2]Diatech Korea Co., Ltd., Seoul, Republic of Korea*

HPP Early Morning Sessions - Tuesday, October 7, 2014

Human Diabetes Proteome Project (HDPP)

Organizer: Martin Kussmann

Room B

Diabetes prevalence has increased dramatically during recent years with rising numbers of both individuals suffering from relative (type 2 diabetes mellitus, T2DM) and absolute (type 1 diabetes mellitus, T1DM) insulin deficiency.

To slow down, eventually stop, and ideally prevent this epidemic, deeper knowledge of the pathophysiological mechanisms responsible for impaired function of the multiple organs and cell-types affected is required.

We have leveraged a worldwide constellation of expertise into the Human Diabetes Proteome Project (HDPP) initiative to generate systems-level insights into diabetes-associated cellular changes by gathering multivariate data sets over time from specialized cells and organs of healthy and diabetes-affected individuals.

The HDPP has begun not only to deliver comprehensive information on disease mechanisms but also to identify proteins and isoforms associated with diabetic pathogenesis and crucial for the development of better diagnostics, therapies and preventions.

8:00 - 8:10 am	Welcome and Presentation / Introduction of the HDPP Group & Partners; Martin Kussmann, Chair, Nestle Inst. Health Science (NIHS), Lausanne, Switzerland
8:10 - 8:20 am	Update on the HDPP Project and HDPP Protein List Domitille Schvartz and Jean-Charles Sanchez, Univ. Geneva, Switzerland
8:20 - 8:35 am	HDPP Partner Presentation
8:35 - 8:50 am	Peter Bergsten, Uppsala Univ. Sweden: Beta Cell Function HDPP Partner Presentation
8:50 - 9:05 am	Loïc Dayon, NIHS: Mitochondrial Function HDPP Partner Presentation
9:05 - 9:20 am	Y.A. Goo Univ. Maryland, USA / Univ. Turku, Finland: The DIPP Study Diabetes Protein Panel Project: SRM/MRM Assays (Open Discussion for all presenters and attendees)

HPP Early Morning Sessions - Tuesday, October 7, 2014

C-HPP, Part II: Poster Session

Organizer: Gyorgy Marko-Varga

Inside Poster Hall

Poster Awards (Cash Prize and Award Certificate) will be given to Total 10 Best Outstanding Poster Presenters

Each team needs to load the poster no later than 5 pm, Monday. In addition to the C-HPP, any papers related to common technology or resources can be presented.

Presentation Times: 8:00 - 8:40 am: Group A: Chromosome 1-12 and 8:40 - 9:20 am: Group B: Chr 13-22, X, Y and Related Technologies (bioinformatics, MS, Ab, reagents etc.)

HUPO Proteomics Standards Initiative (PSI) and ProteomeXchange

Organizers: Eric Deutsch and Henning Hermjakob

Room C

The HUPO Proteomics Standards Initiative defines community standards for data representation in proteomics to facilitate data comparison, exchange and verification. We contribute to data management and integration in all other HUPO initiatives, and have published a modular set of standards for proteomics data representation.
For details of the HUPO PSI please see http://www.psidev.info

For a publication list see http://scholar.google.com/citations?user=oNoChlcAAAAJ

Based on the HUPO PSI standards, we have developed ProteomeXchange, an international consortium for efficient collection and dissemination of open proteomics data (http://www.proteomexchange.org). We will provide an overview of current PSI activities, and discuss practical aspects of data deposition in ProteomeXchange through a short tutorial and Q&A session.

8:00 - 8:15 am	The Proteomics Standards Initiative – Introduction and Status Report Eric Deutsch, ISB Seattle
8:15 - 25 am	Fine-grained modelling of molecular interactions in PSI MI XML 3.0 Henning Hermjakob, European Bioinformatics Institute, Cambridge, UK
8:25 - 8:35 am	Mass Spectrometry Informatics Gerhard Mayer, MPC, Bochum, Germany
8:35 - 8:55 am	Submitting Your Data to ProteomeXchange – A Mini-Tutorial Juan Antonio Vizcaino, European Bioinformatics Institute, Cambridge, UK
8:55 - 9:05 am	Representing Imaging MS Data Juan Antonio Vizcaino, European Bioinformatics Institute, Cambridge, UK
9:05 - 9:20 am	Open Q&A session

Antibody Proteomics

Organizers: Tadashi Yamamoto and Mathias Uhlen

Room D

- **“ Validation of antibodies in the Human Protein Atlas project “** presented from Antibody Atlas project by Emma Lundberg, Sophia Hober, Caroline Kampf, Peter Nilsson, Jenny Ottosson Takanen, Kalle von Feilitzen and Mathias Uhlén.
  Science for Life Laboratory, KTH—Royal Institute of Technology, Stockholm, Sweden

- **“ Antibodypedia – guiding antibody users to find the right antibody for the right application “** presented from Antibodypedia project by Tove Alm, Kalle von Feilitzen, and Mathias Uhlén.
  Science for Life Laboratory, KTH—Royal Institute of Technology, Stockholm, Sweden

- **“AntibodyRanker”** from Antibody Ranker project by Naohiko Kinoshita and Tadashi Yamamoto
  Biofluid Biomarker Center and Institute of Nephrology, Graduate School of Medical and Dental Sciences, Niigata University, Niigata, Japan

- **“Antibodyregistry.org and the Resource Identification Initiative: identifying research resources in biomedical literature, one antibody at a time”** presented from Antibodyregistry project by Anita Bandrowski.
  UCSD, La Jolla, CA 92093-0608, USA

- **“Monoclonal antibody-based strategies for missing proteins”** presented from Antibody Initiative by Ed Nice.
  Monash Antibody Technologies Facility, Monash University, Melbourne, Australia

- **“Development and validation of a high specificity, high affinity antibodies”** presented from a Antibody producing company by Simon Braschi, Gary Dillon, Weimin Zhu, Mark Bushfield, Alejandra Solache.
  Abcam plc, 330 Cambridge Science Park, Cambridge, CB4 0FL, UK

HPP Early Morning Sessions - Tuesday, October 7, 2014

Cancer II
Roundtable Discussion Chaired by Joseph Kagen

Organizers: Hui Zhang, Christopher Kinsinger and Edouard Nice

Room E

Chair/Moderator: Jacob Kagan

Discussion Panel: Bill Hancock, Bryan Krastins, Christopher Kinsinger, Connie Jimenez, Daniel Chan, Edouard Nice, Henry Rodriguez, Hui Zhang, Jacob Kagan, Joshua LaBaer, Josip Blender, Mark Baker, Peter James, Robert Moritz, Ruedi Aebersold, Shoba Ranganathan, Sam Hanash, Zhen Zhang

Key Discussion Points

- Mining the existing datasets and databases
- Dissemination of data and resources: generation and/or linking of appropriate websites
- Generation of a directory of key players, skills, cancer targets, and available assays
- Key persons to take responsibilities
- Prioritization of targets in the top 5 cancers
- Use of animal models
- Understand the normal/personalized medicine

Glycoproteomics / HGPI

Organizer: Hisashi Narimatsu

Room F

Through the past three pilot studies, the Human Disease Glycomics/Proteome Initiative (HGPI) had tried an evaluation and standardization of glycomic technologies for discovery and application of disease-related glycome. To establish the glycomic technologies, there are many technical problems even now. However, disease/biology-driven glycomic studies should make solid progress into the analyses of glyco-conjugates such as glycoproteins or glycopeptides rather than released glycans. This research direction was proposed and agreed by many committee members at the last two HGPI sessions in the HUPO annual meetings at Boston and Yokohama.

In this session, we would like to discuss on the researches generating the large-scale knowledge on glycomes, glycosylation site maps, and recent hot technologies on site-specific glycomics, as well as the construction of database for the resultant huge resources.

HPP Early Morning Sessions - Tuesday, October 7, 2014

Tentative Speakers:

- Novel Protocol for Preparation and nLC-MS/MS Characterization of Proteoglycan Linkage Region Glycopeptides of Human Plasma, Urine and Cerebrospinal Fluid Samples; **Goran Larson**; *Institute of Biomedicine, University of Gothenburg;*
- Mass Spectrometry-Based Novel Techniques and Methods for N-Glycomics; **Haojie Lu**, Ying Zhang, Yan Cai, Jing Jiao and Pengyuan Yang; *Dept of Chemistry, Institutes of Biomedical Sciences, Fudan University*
- Construction of the Standard Method for Mouse Tissue Glycome Mapping in HUPO BD-GPP Initiative; **Atsushi Kuno**[1], Jun Iwaki[1], Maki Yoshida[1], Atsushi Matsuda[1], Takashi Sato[1], Yoko Itakura[2], Masashi Toyoda[2], Binbin Tan[3], Sheng-Ce Tao[3], Yan Zhang[3], Hiroyuki Kaji[1], Hisashi Narimatsu[1]; *[1]Glycomedicine Technology Research Center, National Institute of Advanced Industrial Science and Technology; [2]Department of Vascular Medicine, Tokyo Metropolitan Institute of Gerontology; [3]Ministry of Education, Key Laboratory of Systems Biomedicine, Shanghai Center for Systems Biomedicine, Shanghai Jiao Tong University*
- Development and Application of a Method for the Glycopeptide-Based Site-Specific Glycomic Analysis; Hiroyuki Kaji, Azusa Tomioka, Erika Noro, Maki Sogabe, Takashi Sato, Toshihide Shikanai, Hisashi Narimatsu; *Glycomedicine Technology Research Center, National Institute of Advanced Industrial Science and Technology*

Human Brain Project

Organizers: Lea T. Grinberg, Young-Mok Park, Fouzi El Magraoui, Helmut E. Meyer
Room G

8:00 - 8:02 am Welcome Address; Helmut E. Meyer

8:02 - 8:14 am Bridging Old and New Anatomo-Proteomic Characterization of Human Brain Subcortical Nuclei; Enrique Santamaría Martínez

8:14 - 8:26 am Proteomic Characterization of Neuromelanin Granules; Katrin Marcus

8:26 - 8:38 am Autoantibodies as Disease Markers in ALS and Other Neurodegenerative Diseases; Caroline May

8:38 - 8:50 am Molecular Predictive Diagnosis of Preclinical Alzheimer’s Disease: On the Way Towards the Development of Future Preventive Treatment Options; Jens Wiltfang

8:50 - 9:02 am Discovery of Regulated Brain Proteins in Mouse Multiple Sclerosis Models and the Presence of Their Homologues in Human CSF; Frode Berven

9:02 - 9:20 am Open Discussion

HPP Early Morning Sessions - Tuesday, October 7, 2014

Proteome Biology of Stem Cells

Organizers: Javier Muñoz, Jeroen Krijgsveld, Albert Heck

Room H

8:00 - 8:20 am Reprogramming in vivo Produces Teratomas and iPS Cells with Totipotency Features; Maria Abad (CNIO, Madrid, Spain)

8:20 - 8:40 am Proteome profiling of human healthy and tumor colon organoids; Alba Cristobal, Marc van de Wetering, Henk van den Toorn, Hans Clevers, Albert Heck, Shabaz Mohammed (Biomolecular Mass Spectrometry and Proteomics Group, Utrecht, The Netherlands)

8:40 - 9:00 am Characterisation of a novel spontaneous model of epithelial to mesenchymal transition using a primary prostate cancer cell line using quantitative label-free proteomics (SWATH™); David Boocock, Clare Coveney, Naomi Dunning-Foreman, Jayakumar Vadakekolathu, Matthew Nicklin, Graham Hickman, Graham Pockley, Sibylle Heidelberger, Thomas Knapman, Robert Rees (John van Geest Cancer Research Centre, Nottingham, UK)

9:00 - 9:20 am Dynamics of locus-specific chromatin composition in stem cells; Mahmoud-Reza Rafiee and Jeroen Krijgsveld (European Molecular Biology Laborator, Heidelberg, Germany)

Biobanking and Pre-Anlytical Sample Assessment

Organizer: Andrea Urbani

Room I

8:00 - 8:15 am Opening and General Concepts; Andrea Urbani

8:15 - 8:35 am Biobanking Workflow for Proteomics Investigation; Gyorgy Marko Varga

8:35 - 8:55 am Intergating and Developing Quality Controls in System Biology; Garry Corthals

8:55 - 9:00 am Direct Analytical Sample Quality Assessment (DASQ) for Biomarker Investigation: Qualifying CSF Samples; Viviana Greco

9:00 - 9:15 am Round Table Discussion for the Preparation of Seeding Initiative on Standardization and Biobanking

9:15 - 9:20 am Closing; Andrea Urbani

HPP Early Morning Sessions - Wednesday, October 8, 2014

Respiratory Diseases

Organizer: Rainier Bischoff
Room B

This workshop has the goal to establish Respiratory Disease as a new area in the B/D-HPP program of HUPO.

8:00 - 8:10 am The Need to Establish a Respiratory Disease Area as Part of the B/D-HPP Program
Rainer Bischoff,
University of Groningen, Netherlands

8:10 - 8:20 am What We Can Learn from Proteogenomics Approaches
Peter Horvatovich,
University of Groningen, Netherlands

8:20 - 8:30 am Biobanking
Gyorgy Marko-Varga,
Tom Fehniger,
Lund University, Sweden

8:30 - 8:40 am The Role of Glycans in COPD
Naoyuki Taniguchi,
RIKEN and RIKEN-Max Planck Joint Research Center, Japan

8:40 - 8:50 am The Clinical Need for Proteomics Research in Respiratory Disease
Xiangdong Wang
Fudan University, Shanghai, China

8:50 - 9:20 am Panel Discussion: Consortium Building, Sub-Topics (e.g. asthma, COPD), Funding Opportunities / Strategies

HPP Early Morning Sessions - Wednesday, October 8, 2014

C-HPP, Part III: Principal Investigators Council

Organizer: Young-Ki Paik

Room C

This meeting is intended for Principal Investigator Council members and guests (by invitation).

1. Approval of new Chr 16 PI
2. A New Strategy for Stimulating C-HPP Activities.
3. Election of the C-HPP EC member-at-large
4. 2015 C-HPP workshop plans
5. 2015 JPR Special Issue on thematic topics with publication timing may possibly be explored.
6. Organization Matters

Looking to the Future: The Cardiovascular Initiative

Organizers: Jennifer Van Eyk, Catherine Costello, Peipei Ping, Vidya Venkatraman, Maggie Lam

Room D

Session Chair: Peipei Ping, PhD

Popular Proteins in the Heart

8:00 - 8:10 am	Jennifer Van Eyk, PhD; Peipei Ping, PhD; Vidya Venkatraman, PhD; Maggie Lam, PhD Cedars-Sinai Medical Center; University of California Los Angeles

Perspectives and Updates on Proteomics in Cardiovascular Sciences

8:10 - 8:20 am	Moving to Populations in Biomarkers; Manuel Mayr, MD, PhD, King's College, London
8:20 - 8:30 am	Dynamic Regulations of the Cardiac Proteome; Maggie Lam, PhD, University of California, Los Angeles
8:30 - 8:40 am	PTM in Heart Disease - Which Are Your Favorite?; Melanie White, PhD, The University of Sydney, Australia
8:40 - 8:50 am	Large-Scale Pre-Clinical/Clinical Profiling; Jun Qu, PhD, University at Buffalo
8:50 - 9:00 am	The Complexity of Oxidative Modifications; Catherine Costello, PhD, Boston University School of Medicine
9:00 - 9:20 am	Panel Discussion

HPP Early Morning Sessions - Wednesday, October 8, 2014

CompMS - HUPO Computational Mass Spectrometry Initiative

Organizers: Henning Hermjakob

Room E

CompMS is a new, joint initiative of HUPO and the International Society for Computational Biology (ISCB). It promotes the efficient, high quality analysis of mass spectrometry data through dissemination and training in existing approaches and coordination of new, innovative approaches. The CompMS initiative aims to exploit synergies between different application domains, in particular proteomics and metabolomics. We aim to

- build a community of scientists working in computational mass spectrometry
- integrate experimental and theoretical research
- bridge the gaps between proteomics, metabolomics, and other MS-driven fields

For more information on CompMS please see http://compMS.org.
This will be the constitutive meeting of CompMS as a HUPO initiative, and will provide an opportunity for all attendees to engage with the initiative and its future activities.

8:00 - 8:10 am	Introduction to the Computational Mass Spectrometry Initiative, Oliver Kohlbacher (U Tuebingen)
8:10 - 8:30 am	Computational Challenges in Spatial Mass Spectrometry, Laurent Gatto (U Cambridge)
8:30 - 8:50 am	Spatial Metabolomics Using Imaging Mass Spectrometry, Theodore Alexandrov (U Bremen / EMBL Heidelberg)
8:50 - 9:20 am	Open Business Meeting of the HUPO Initiative for Computational Mass Spectrometry

HPP Early Morning Sessions - Wednesday, October 8, 2014

Mitochondria

Organizers: Andrea Urbani

Room G

8:00 - 8:05 am	Opening, Andrea Urbani
8:05 - 8:17 am	Characterization, Design, and Function of the Mitochondrial Proteome: From Organs to Organisms, Peipei Ping
8:17 - 8:29 am	Decoding the Mitochondrial Interaction Landscape in Neurodegenerative Diseases, Mohan Babu
8:29 - 8:41 am	The Mitochondrial Proteome from the Human Protein Atlas Perspective, Emma Lundberg
8:41 - 8:53 am	Mitochondrial Proteomics of Cellular Models of Parkinson's Disease Pathogenesis, Mauro Fasano
8:53 - 9:05 am	Bacterial Resistance and Host Mitochondria Rearrangements, Alessio Soggiu
9:05 - 9:17 am	Investigating Mitochondria Proteome in Fatigue Syndrome, Federica Ciregia
9:17 - 9:20 am	Wrap up

Protein Aggregation Diseases B/D HPP Working Group

Organizers: Paola Picotti

Room H

8:00 - 8:10 am	Introduction
8:10 - 8:20 am	Amyloidoses: fatal diseases caused by Misfolded Proteins; Bouke Hazenberg (University of Groningen, Netherlands)
8:20 - 8:30 am	Targeted MS Assays for the Clinical Diagnosis and Subtyping of Systemic Amyloidoses in Subcutaneous Fat Aspirates; Paul Boersema (ETH Zurich, Switzerland)
8:30 - 8:40 am	Proteomics in the Understanding and Management of Systemic Amyloidoses: The Pavia Experience; Giampaolo Merlini (University of Pavia, Italy)
8:40 - 8:50 am	Disease developments in Parkinson and Malignant Melanoma; Melinda Rezeli (Lund University)
8:50 - 9:00 am	Towards MS-Based Conformational (Bio)Markers?; Paola Picotti (ETH Zurich, Switzerland)
9:00 - 9:20 am	Wrap-up

HPP Early Morning Sessions - Wednesday, October 8, 2014

PediOme
Pediatric Proteomics Initiative (PediOme): Exploring Child Health with Proteomics

Organizers: Allen Everett and Vera Ignjatovic

Room I

Overview of the project will be followed by these talks:

- Differences in Platelet Proteome and Secretome between Children and Adults: The Role in Protection from Thrombosis and Cardiovascular Disease. - Vera Ignjatovic
- The Regenerative Abilities of Resident Cardiac Stem Cell Depends on Secreted Paracrine Factors - Sunjay Kushal
- Monitoring the Status of Infants Being on Nursing in Incubators by Urine Proteome Analysis. - Alexey Kononikhin
- Urine Proteomics for the Discovery of Non-Invasive Diagnostic Biomarkers for Pediatric Diseases. - Hanno Steen
- Omics in Nutrition and Its Perspectives for Pediatrics Research and Healthcare - Martin Kussmann

INDUSTRY WORKSHOP PROGRAMS

Industry Workshop Programs

DAY	TIME	COMPANY	ROOM	SESSION
MONDAY 6 OCTOBER 2014	13:00 - 14:15	BRUKER	ROOM B	LUNCH SYMPOSIUM
	13:00 - 14:15	WATERS	ROOM D	LUNCH SYMPOSIUM
TUESDAY 7 OCTOBER 2014	13:00 - 14:15	ABSciex	ROOM B	LUNCH SYMPOSIUM
	13:00 - 14:15	THERMO FISHER	ROOM C	LUNCH SYMPOSIUM
	18:45 - 20:00	AGILENT	ROOM D	MEETING OF THE MINDS

Industry Workshop Programs

13:00 - 14:15 **MONDAY 6 OCTOBER 2014**

Room B

Bruker Daltonic GmbH Lunch Symposium

We are pleased to invite you to the Bruker sponsored lunch seminar on Monday, October 6th, Room B, 1.00-2.15 p.m.

"Qualitative and quantitative proteomics on the Impact Q-TOF platform"

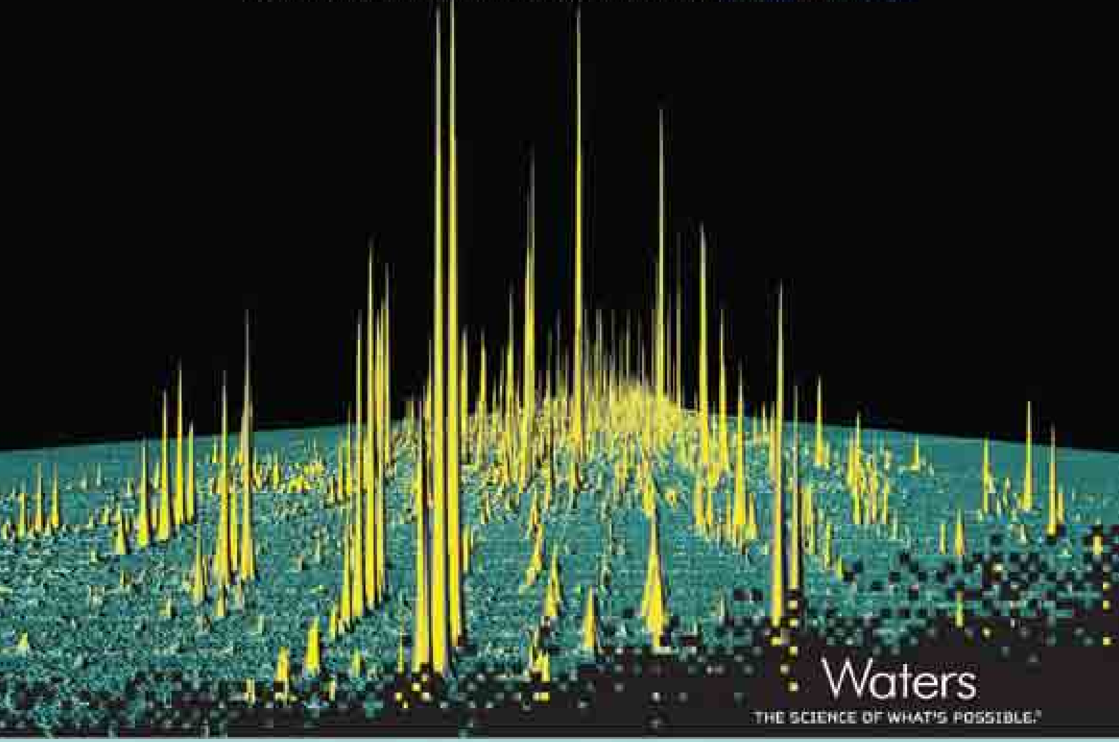
Dr. Stephanie Kaspar
Application Development Scientist, Bruker Daltonics, Germany

"Evaluation of quantitative proteomics performance and robustness on a benchtop UHR-QTOF platform"

Professor Dr. Alain Van Dorsselaer
LSMBO, Strasbourg

"Modern time of flight instrumentation fullfilling the needs of shotgun proteomics"

Scarlet Beck
Research Department Proteomics and Signal Transduction, MPI Munich



Industry Workshop Programs

13:00 - 14:15 MONDAY 6 OCTOBER 2014

Room D

Waters Corporation Lunch Symposium

Developments in Progenesis QI for proteomics

Dr. Robert Tonge
Waters Corporation, Wilmslow, UK

Proteomic analyses pose a massive analytical challenge in which thousands of structurally similar analytes are distributed over a wide dynamic range. Our unique approach and analytical strategy combines three orthogonal techniques to separate, characterise and quantify the components of very complex biological samples. We integrate Ultra Performance Liquid Chromatography (UPLC) or Ultra Performance Convergence Chromatography (UPC2), Travelling Wave Ion Mobility Separation (TW-IMS) and high resolution Time-Of-Flight (TOF) mass spectrometry to enable High Definition Transomics Analysis. The combination of complimentary orthogonal methods allows the total Peak Capacity of the analytical system to be increased by an order of magnitude compared to the conventional methodologies. Endogenous metabolite/lipid and protein profiling are performed with highly specific analytical systems where analytes are fully separated before identification and quantification, minimising the potential misleading effects of contaminant data.

Alongside instrumentation, software is increasingly important to realize the value in feature-rich experimental data. Progenesis QI for proteomics software, co-developed with Nonlinear Dynamics, delivers highly intuitive, flexible, common workflows for bottom-up protein profiling with comprehensive data visualizations to facilitate robust transomics studies on all scales. We will present the latest development and applications of Progenesis for proteomic studies.

Using Skyline to extend targeted proteomics to IMS-TOF

Dr. Michael MacCoss
University of Washington, Seattle, USA

Skyline is a freely-available Windows client application for building Selected Reaction Monitoring (SRM) / Multiple Reaction Monitoring (MRM), Parallel Reaction Monitoring (PRM - Targeted MS/MS), Data Independent Acquisition and targeted DDA with MS1 quantitative methods and analyzing the resulting mass spectrometer data. It aims to employ cutting-edge technologies for creating and iteratively refining targeted methods for large-scale proteomics studies. This presentation will focus upon the development of Skyline for targeted proteomics experiments using the unique ion mobility functionality contained within the Waters Synapt systems.

Industry Workshop Programs

13:00 - 14:15 TUESDAY 7 OCTOBER 2014

Room B

AB SCIEX Lunch Symposium

SOLUTIONS FOR NEXT GENERATION PROTEOMICS AND QUANTITATIVE BIOLOGY

Extending the Power of SWATH™ Acquisition – Advances in Data Acquisition and Processing

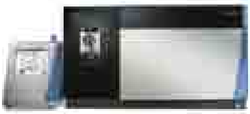
Christie Hunter
AB SCIEX

Bioinformatics Solutions for the Next Generation of Quantitative Omics

Anne-Claude Gingras
Samuel Lunenfeld Research Institute, Mount Sinai Hospital

**Lunch included*


GLYCOSYLATION
PROTEOFORMS
PROTEINS
PEPTIDES
PROTEIN-PROTEIN INTERACTIONS
ACETYLATION
SUMOYLATION
UBIQUITINATION
PHOSPHOPEPTIDES
PROTEIN COMPLEXES
PHOSPHORYLATION
PROTEIN NETWORKS



Industry Workshop Programs

13:00 - 14:15 TUESDAY 7 OCTOBER 2014

Room B

Thermo Fisher Scientific Lunch Symposium

Multiplexed quantitation: The need for moredata to drive understanding of functional biology and disease".

Introduction: Julian Saba

DIA analyses – Confirmed title: "Novel DIA methods for pathways analysis".

Michael Blank,
Thermo Fisher Scientific

NTAILS workflow – Confirmed title: "TMT10 plex analysis of the N-terminome by TAILS in NFkbeta stimulation"

Chris Overall,
Canada Research Chair, The University of British Columbia, Canada

Industry Workshop Programs

18:15 - 20:00 **TUESDAY 7 OCTOBER 2014**

Room D

Agilent Technologies - Meeting of the Minds

Continuing what has become a tradition at HUPO meetings, Agilent Technologies is pleased to host the “Meeting of the Minds” on 7th October. This event allows young scientists to meet with established leaders in Proteomics in a social environment.

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Journal of proteome research
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POSTERS

Odd numbers: Monday 6, 2014

Even numbers: Tuesday 6, 2014

Odd and Even numbers: Wednesday 7, 2014

01 - CANCER PROTEOMICS

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OVEREXPRESSION OF AVß6 INTEGRIN ALTERS THE COLORECTAL CANCER CELL PROTEOME IN FAVOR OF ELEVATED PROLIFERATION AND A SWITCHING IN CELLULAR ADHESION THAT INCREASES INVASION

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2 University of New South Wales
3 Australian Proteome Analysis Facility

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CIRCULATING PROTEOLYTIC PRODUCTS OF TUMOR-RESIDENT ENZYME AS POTENTIAL BIOMARKERS FOR EARLY DETECTION OF BREAST CANCER

Tony Hu
Houston Methodist Research Institute, Weill Cornell Medical College of Cornell University

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CHARACTERISATION OF THE UPAR•AVß6 INTERACTION IN COLORECTAL CANCER CELL LINES

Seone Ahn[1], Samyuktha Anand[2], Abidali Mohamedali[1], Harish Cheruku[1], Sowmya Gopichandran[2], David Cantor[1], Shoba Ranganathan[2], Ronald Frank[3], Edouard Nice[4], Mark Baker1
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MEMBRANE PROTEOME ANALYSIS OF TGFB STIMULATED COLORECTAL CANCER CELL LINES

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MAPPING THE FUNCTIONAL PROTEIN COMMUNICATION BETWEEN DIFFERENT CELL TYPES IN THE TUMOR MICROENVIRONMENT OF PANCREATIC CANCER

Mohamed Saiel Saeed Alhamdani, Jörg D Hoheisel
DKFZ/Functional Genome Analysis

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IMPROVING THE CHROMATOGRAPHIC SEPARATION OF DMB-LABELED SIALIC ACIDS FOR THE COMPARISON OF BIOSIMILARS TO REFERENCE MATERIALS

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Sigma-Aldrich

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Yichu Shan[1], Lingfan Chen[1,2], Lihua Zhang[1], Yukui Zhang[1]
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Lei Chang[1,2], Valerie Wasinger[3], Peter Graham[1,2], Jingli Hao[1,2], Jie Ni[1,2], Julia Beretov[1,2], Joseph Bucci[1,2], Paul Cozzi[2,4] John Kearsley[1,2] Yong Li[1,2]
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Kiyoshi Yanagisawa, Takashi Takahashi
Division of Molecular Carcinogenesis, Nagoya University Graduate School of Medicine

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Indiana University

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Daisuke Kubota[1], Akihiko Yoshida[2], Akira Kawai[1], Tadashi Kondo[3]
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3 Division of Pharmacoproteomics, National Cancer Center Research Institute

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3 University Medical Center Groningen

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3University of Geneva (CMU, UNIGE)

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The Walter And Eliza Hall Institute

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3 Royal Prince Alfred Hospital, Camperdown, NSW, Australia
4 Brain and Mind Research Institute, Camperdown, NSW, Australia

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Samsung Medical Center

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Yoon Pin Lim[1], Lee Yee Choong[1], Sandy Lee[1], Naing Naing Mon[1], Ssu Yi Lu[1], Brian Druker[2], Jean Paul Thiery[1], Patrick Tan[3] Chwee Teck Lim[4] Christian Harteneck[5]
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2 Oregon Health and Science University
3 Duke-NUS Medical Graduate School
4 Mechanoniology Institute
5Eberhard-Karls-Universitát

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Haruhiko Kamada[1], Shintaro Taki[1], Masaki Inoue[1], Kazuya Nagano[1], Yohei Mukai[1], Yasuo Yoshioka[3], Kazuma Higashisaka[3], Yasuo Tsutsumi[3] Shin-ichi Tsunoda[1]
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2 MEI Center, Osaka University
3 Lab Toxicol Safety Sci, Osaka University

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Ruben A Bartolome[1], Irene Garcia-Palmero[1], Sofia Torres[1], Maria Lopez-Lucendo[1], Irina V Balyasnikova[2], J Ignacio Casal[1]
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Lewis M. Brown[1], Rohitha SriRamaratnam[1], Wan Seok Yang[1], Matthew E. Welsch[1], Kenichi Shimada[1], Clary B. Clish[2], Albert W. W. Girotti[3], Virginia W. Cornish[1] Stuart L. Schreiber[2] Brent R. Stockwell[1]
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3 Medical College of Wisconsin, Milwaukee, WI

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Amity Institute of Biotechnology, Amity University, Noida

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Pooria Ghadiri[1], Alireza Nikseresht[2], Maryam Sharifian[3], Nazila hassanabadi[4], amirhossein sharifian[5], Abbas mohammadi[4], Alireza Setarehaseman[4]
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Alireza Setarehaseman[1], Alireza Nikseresht[2], Sadegh Izadi[2], Pooria Ghadiri[3], amirhossein sharifian[4], Abbas Mohammadi[4], Maryam Sharifian[5], Nazila Hassanabadi[1]
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UNDERSTANDING LAPATINIB ACTION BY CHEMICAL – AND PHOSPHOPROTEOMICS

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UNCOVERING AQUIRED RESISTANCE MECHANISMS TO EGFR-SPECIFIC KINASE INHIBITORS USING CHEMICAL PROTEOMICS

Heiner Koch[1,2,3], Estela Del Castillo Busto[1], Karl Kramer[1], Guillaume Medard[1], Bernhard Kuster[1,2,3,4]
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AFFINITY PROTEOMICS IN PLASMA FROM CANCER BIOBANKS

Jochen Schwenk, Kimi Drobin, Sanna Byström, Burcu Ayoglu, Ulrika Qundos, Mun-Gwan Hong, Frauke Henjes, Claudia Fredolini, Peter Nilsson, Mathias Uhlen
SciLifeLab, KTH - Royal Institute of Technology

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A UNIQUE CELLULAR MODEL OF THE COLORECTAL ADENOMA-TP-CARCINOMA SEQUENCE REVEALS CONSISTENT SERIES OF PROGRESSION MARKERS IN TWO INDEPENDENT DIFFERENTIAL LABEL-BASED (ITRAQ-MALDI) AND LABEL-FREE (TRIPLE-TOF) MASS SPECTROMETRIC SETTINGS

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PROTEIN BIOMARKERS FOR PROSTATE CANCER IN URINARY EXOSOME-LIKE VESICLES

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Irene Garcia-Palmero[1], Sofia Torres[1], Alberto Peláez-García[1], María Lopez-Lucendo[4], María Jesús Larriba[3], Mercedes Herrera[2], Alberto Muñoz[3], Felix Bonilla[2] J. Ignacio Casal[1]
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MOUSE MONOCLONAL ANTIBODIES AGAINST HUMAN URINARY PROTEIN SM-UP2IP OF SCHISTOSOMA MANSONI

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COMPREHENSIVE PROTEOMIC PROFILING OF BEVACIZUMAB-RESISTANT GLIOBLASTOMA MULTIFORME

Kimberley Kaufman[1], Linda Ly[1], Matthew McKay[2], Duthika Mallawaaratchy[1], Swetlana Mactier[1], Ben Crossett[1], Mark Molloy[2], Michael Buckland[1,3] Kerrie McDonald[4] Richard Christopherson[1]
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MELANOMA; THE UNFOLDED PROTEIN RESPONSE AND MEMBRANE-ASSOCIATED PROGESTERONE RECEPTOR COMPONENT 1

Erin Sykes, Swetlana Mctier, Kimberley L. Kaufman, Munther Alomari, Duthika M. Mallawaaratchy, Richard I. Christopherson
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PROTEOMIC DYNAMICS IN UTERINE CERVICAL CANCER TUMORS FROM THE CANCER CELL LINES HELA AND SIHA.

Sergio Encarnación-Guevara, Luis-Fernando Delgadillo-Silva, Alberto Checa-Rojas
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TARGETED PROTEOMIC IMMUNOASSAYS OF CANDIDATE PLASMA BIOMARKERS FOR STAGE A-D CRC

Sadia Mahboob[1], Sock-Hwee Tan[3], Seong B Ahn[1], Harish Cheruku[1], David Cantor[1], Alamgir Khan[2], Emma Rennel[4], Shoba Ranganathan[3] Ed Nice[5] Mark S Baker[1]
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PROTEOMIC ANALYSIS OF NXS2 NEUROBLASTOMA CELL LINE TREATED WITH FASTING IN COMBINATION WITH DOXORUBICIN

Danilo Marimpietri[1], Andrea Petretto[1], Giovanna Bianchi[1], Roberto Martella[1], Elvira Inglese[1], Chiara Lavarello[1], Valter Longo[2], Vito Pistoia[1] Lizzia Raffaghello[1]
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QUANTITATIVE MS-BASED ANALYSIS OF HISTONE MODIFICATION PATTERNS AS MARKERS FOR RESPONSE TO HDAC INHIBITORS IN BREAST CANCER

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FFPE TISSUE PROTEOMICS: WAKING SLEEPING BEAUTY

Maria Filippa Addis, Alessandro Tanca, Daniela Pagnozzi, Sergio Uzzau
Porto Conte Ricerche

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DIFFERENTIAL PROTEIN EXPRESSION ANALYSIS IN HEPATOBLASTOMA BY 2D-DIGE AND LABEL FREE LC-MS

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PHOSPHOPEPTIDE ENRICHMENT ON A MONOLITHIC COLUMN CONTAINING SUPERFICIALLY IMMOBILIZED NANO TIO2

Andreas Fichtenbaum[1], Pungor András[2], Nagy Zoltán[2], Cernigoj Urh[3], Vidic Jana[3], Barut Miloš[3], Mitulovic Goran[4]
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THE IDENTIFICATION OF BIOMARKERS FOR LUNG CANCER USING PLASMA COLLECTED PROXIMAL AND DISTAL TO THE SITE OF THE TUMOUR.

Michael Walker[1], Phillip Crosbie[1], Maria Pernemalm[2], Cong Zhou[1], Caroline Dive[1], Anthony Whetton[1]
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PROTEOMICS ARGUES TOWARDS MTOR/PI3K DOMINANCE IN PEDIATRIC MEDULLOBLASTOMA TUMORS WITH 17P DELETION

Athanasios Anagnostopoulos, George Tsangaris
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METHOD DEVELOPMENT FOR THE QUANTITATION OF A HUMAN URINE BIOMARKER FOR ACUTE KIDNEY INJURY USING A QTRAP® MASS SPECTROMETER

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COMPARISON OF EARLY STAGES OF COLORECTAL CANCER FFPE SAMPLES BY LABEL FREE PROTEOMICS

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DECIPHERING THE RESISTANCE MECHANISMS TO EGFR TYROSINE KINASE INHIBITORS IN NON-SMALL CELL LUNG CANCER: A QUANTITATIVE PROTEOMIC APPROACH

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PROTEOMIC ANALYSIS OF SECRETOME AND TOTAL CELL EXTRACT FROM NORMAL AND MALIGNANT CERVICAL CELL LINES

Georgia Kontostathi[1, 2], Vasiliki Lygirou[1, 2], Jerome Zoidakis[1], Antonia Vlahou [1],
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MULTIPLEXED MRM FOR THE VERIFICATION OF PLASMA PROTEINS BIOMARKER: APPLICATIONS TO HEPATOCELLULAR CARCINOMA DEVELOPMENT AND METASTASIS

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MASS SPECTROMETRY-GUIDED DEVELOPMENT OF A LUMINEX-BASED DIAGNOSTIC TEST FOR THE REDUCTION OF UNNECESSARY PROSTATE BIOPSIES

Kathrin Endt[1], Jens Goepfert[2], Kerstin I Pohl[2], Aurelius Omlin[3], Daniel Engeler[3],
Silke Gillessen[3], Thomas O Joos[2], Ralph Schiess[1]
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MS-BASED IMMUNOASSAYS FOR TRANSPORTER QUANTIFICATION IN XENOGRAFT-BASED TUMOR MODELS

Helen Hammer, Bart van den Berg, Frederik Weiss, Hannes Planatscher, Thomas O. Joos,
Oliver Poetz
Nmi

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CAN PROFILING FOR PLASMA PHOSPHORYLATION BE A USEFUL TOOL IN AIDING THE DIAGNOSIS OF ALZHEIMER'S DISEASE?

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MALDI TOF/TOF DETERMINATION OF SERUM PLASMINOGEN SIALYLATION PROFILE FROM PATIENTS WITH GASTRIC PRECANCEROUS LESIONS

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DECIPHERING ALTERED CELL SIGNALING PATHWAYS IN B- LYMPHOCYTIC CHRONIC LEUKEMIA (B-CLL) BY FUNCTIONAL PROTEOMICS APPROACHES

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KNOCKDOWN OF C-FOS SUPPRESSES THE ACTIVATION AND ECM PROTEINS PRODUCTION OF PANCREATIC STELLATE CELL

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SHOTGUN PROTEOMIC ANALYSIS OF PANCREATIC CANCER STEM CELLS

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PROTEOMIC INVESTIGATION OF BIOMARKERS USING HUMAN PLASMA AND SERUM SAMPLES FOR EARLY BREAST CANCER DIAGNOSIS.

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ITRAQ TECHNOLOGY COMBINED 2DLC-MS/MS DIFFERENTIALLY EXPRESSED PROTEINS IN RENAL CELL CARCINOMA SCREENING

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METABOLIC ADAPTATION IN NON-SMALL CELL LUNG CANCER

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GLOBAL PROTEOME CHANGES INDUCED BY C-MYB SILENCING IN K562 HUMAN CHRONIC MYELOID LEUKEMIA CELLS

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PROFILING URINARY PROTEOME FOR STRESS INDUCED FEMALE URINARY INCONTINENCE

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DISCOVERY AND LONGITUDINAL MEASUREMENT OF CANDIDATE BIOMARKERS OF BIOCHEMICAL RECURRENCE IN PROSTATE CANCER PATIENTS TREATED WITH CHRT

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DAILY RHYTHMS IN THE CYANOBACTERIUM SYNECHOCOCCUS ELONGATUS PROTEOME AND PROTEIN COMPLEXES

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THE ANTITUMOR NATURAL COMPOUND CURCUMIN PROMOTES PROSTATE CANCER CELL DEATH BY INDUCING ENDOPLASMIC RETICULUM STRESS.

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PROTEOMIC PROFILING OF THYROID NEOPLASMS IDENTIFIES CANDIDATE MARKERS OF TUMOUR MALIGNANCY

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QUANTITATIVE ANALYSIS OF N-LINKED GLYCOPROTEIN IN THE BRAIN OF APP/PS-1 ALZHEIMER'S DISEASE MODEL

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CALIBRATION FREE CONCENTRATION ANALYSIS (CFCA) OF PROTEINS IN COMPLEX SERUM SAMPLES USING SURFACE PLASMON RESONANCE

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STUDY OF GRADE-SPECIFIC PROTEOMIC ALTERATIONS IN GLIOMAS

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QUANTITATIVE SERUM PROTEOMIC ANALYSIS OF MENINGIOMAS FOR THE IDENTIFICATION OF SURROGATE PROTEIN MARKERS

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IMPROVING SELECTIVITY AND SENSITIVITY IN CLINICAL ASSAYS USING PARALLEL REACTION MONITORING

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MULTIPRONGED QUANTITATIVE TISSUE PROTEOMIC ANALYSES INDICATE MODULATION OF VARIOUS SIGNAL TRANSDUCTION PATHWAYS IN MENINGIOMAS

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IDENTIFICATION OF AN EXOSOMAL PROTEIN INVOLVED IN INVASION OF BREAST CANCER CELL AND STUDY ON CLEARANCE OF THE EXOSOMES FROM THE CIRCULATION

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THE CANCER-DERIVED SECRETORY/RELEASING PROTEOME: A VALUABLE RESOURCE FOR DISCOVERING TUMOR MARKERS

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BREAST CANCER TUMOUR TRANSFORMATION FROM PRIMARY TUMOUR TO SECONDARY SITE

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ALPHA-ACTININ 4 IS ASSOCIATED WITH CANCER CELL MOTILITY AND IS A POTENTIAL DIAGNOSTIC BIOMARKER IN NON-SMALL-CELL LUNG CANCER

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IMMOBILIZATION OF ANTIBODIES ON FE3O¬4@POLYDOPAMINE CORE¨CSHELL MICROSPHERES FOR SELECTIVE ENRICHMENT OF LYSINE-ACETYLATED PROTEINS AND PEPTIDES

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THE EFFECT OF MUTATIONS IN BETA-AMYLOID ON ZINC ION COORDINATION

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IMPROVED METHOD FOR SEQUENCING OF IMMUNOGLOBULIN MOLECULES; COMBINING NEXT GENERATION SEQUENCING AND MS/MS.

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OPTIMIZATION OF A WORKFLOW FOR FAST AND DEEP PROTEOME SEQUENCING

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MS- AND AB-BASED PROTEOMICS TO UNDERSTAND BIOLOGY AND DISEASE OF KIDNEY

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A QUANTITATIVE PROTEOMICS TOWARDS THE TISSUE INTERSTITIAL FLUID FROM AOM-DSS MOUSE MODEL OF COLORECTAL CANCER

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THE VITREOUS PROTEOME IN YOUNG AND MATURE NEW ZEALAND WHITE (NZW) RABBITS

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CHARACTERISTIC PATTERNS OF PROTEIN AND GENE EXPRESSION AS MARKERS FOR DIAGNOSIS AND PROGNOSIS OF MALIGNANT MELANOMA

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COMPREHENSIVE ANALYSIS OF RADIOTHERAPY EFFECTS AFTER IRRADIATION WITH CARBON AND PHOTON USING GENOME-WIDE TRANSCRIPTOMICS AND QUANTITATIVE PROTEOMICS

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CHEMOKINE RECEPTOR CXCR7 PROMOTES HEPATOCELLULAR CARCINOMA CELL GROWTH AND METASTASIS IN VITRO AND IN VIVO VIA ACTIVATING MAPK PATHWAY

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A NOVEL PANEL OF PROTEINS CORRELATING WITH LYMPH NODE METASTASIS OF LOW-GRADE BREAST CANCER AS IDENTIFIED BY COMBINED PROTEOMICS AND TRANSCRIPTOMICS APPROACH

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COMPREHENSIVE CHARACTERIZATION OF CELL SECRETOME VIA LC MS/MS ANALYSIS OF CONDITIONED MEDIUM AND SECRETORY PATHWAY ORGANELLES.

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ANTIBODY-BASED PLASMA PROFILING FOR THE IDENTIFICATION OF PROTEIN SIGNATURES IN LYMPHOMA

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CHARTING THE TEMPORAL SIGNALING NETWORK OF EGFR UPON EGF STIMULATION

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COMBINING BOTTOM-UP AND MIDDLE-DOWN APPROACHES TO MAP HYPER-MODIFIED HISTONE PEPTIDES USING UHPLC SEPARATION AND QEXACTIVE INSTRUMENT.

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NEW POTENTIAL BIOMARKERS FOR PROSTATE CANCER DIAGNOSIS AND PROGNOSIS USING 2D-DIGE

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RELATIVE QUANTITATION OF N-LINKED GLYCANS USING CARBONYL-REACTIVE TANDEM MASS TAG™ (TMT™) REAGENTS

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GC-MS-BASED SEMI-QUANTITATIVE ANALYSIS OF TARGETED METABOLITES IN HUMAN PLASMA

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LC-MS/MS-BASED SERUM PROTEOMICS FOR IDENTIFICATION OF BIOMARKERS FOR HEPATOCELLULAR CARCINOMA

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BIOMARKERS BREAST CANCER IDENTIFICATION THROUGH ITRAQ LABELING AND TANDEM MASS SPECTROMETRY

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SERUM PROTEOMIC ANALYSIS OF PATIENTS WITH THE CERVICAL HIGH-GRADE SQUAMOUS INTRAEPITHELIAL LESION

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PROTEOMIC MAPPING OF GLIOMA ENDOTHELIAL CELL SURFACE PROTEINS

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EMILIN-1 AND TALIN-2 ARE MATRIX METALLOPROTEINASE-9 DEPENDENT MECHANISMS OF STIFFNESS IN THE AGING HEART

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STEAROYL-COA DESATURASE AS A POTENTIAL NOVEL THERAPEUTIC TARGET IN HEAD AND NECK SQUAMOUS CELL CARCINOMA

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MACROPHAGE MIGRATION INHIBITORY FACTOR - A THERAPEUTIC TARGET IN GALLBLADDER CANCER

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INVESTIGATION OF DIFFERENTIALLY EXPRESSED PLASMA MEMBRANE GLYCOPROTEINS IN ORAL SQUAMOUS CELL CARCINOMAS

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MEASURING WNT-PATHWAY ACTIVITY IN CANCER MODELS

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Robert Swift, Deb Ayers, Ying Chang, Eduardo Tabacman, Darryl Perry, Sheri Wilcox, Nicholas Saccomano
SomaLogic, Inc.

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PROTEOMIC STUDY OF CHROMATOME DYNAMICS REVEALS REGULATORY SWITCHES OF EPIGNOME IN HYPOXIA-INDUCED ONCOGENESIS

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N-LINKED GLYCOPROTEIN PROFILING FOR BIOMARKER DISCOVERY IN COLORECTAL CANCER

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TEAR PROTEIN BIOMARKERS IDENTIFY LACRIMAL GLAND TUMORS

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SYSTEM-WIDE CHARACTERIZATION OF DYNAMICS OF CYTOSOLIC MACROMOLECULAR PROTEIN COMPLEXES IN ONCOGENE-INDUCED CELL TRANSFORMATION

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PROTEIN CARBONYLATION IN HEPATOCELLULAR CARCINOMA DERIVED FORM VIRUS C AND METABOLIC SYNDROME. TWO DIMENSIONAL FLUORESCENCE DIFFERENCE IN GEL DETECTION.

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PROTEOMIC ANALYSIS OF THE HETEROGENEITY OF IN BREAST CANCER

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VALIDATION OF POTENTIAL BIOMARKERS FOR AJCC STAGE III MELANOMA

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MOLECULAR MECHANISMS RELATED TO IRON HOMEOSTASIS AND DISTURBED IN BREAST CANCER

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A DISTRIBUTED SYSTEM FOR THE ANALYSIS OF HIGH THROUGHPUT PROTEOMICS DATA

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IMAGING MASS SPECTROMETRY (IMS) TO DISCRIMINATE BREAST FROM PANCREATIC CANCER METASTASIS IN FFPE TISSUES

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PROFILING OF TRANSMEMBRANE PROTEINS IN HUMAN LYMPHOMA CELLS BASED ON MEMBRANE-EMBEDDED PEPTIDES

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IDENTIFICATION AND SPATIAL LOCALIZATION OF PROTEINS FROM MOUSE BRAIN TUMOR USING A COMBINATION OF MALDI IMAGING AND LC-MALDI

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A SILAC MOUSE-BASED QUANTITATIVE PHOSPHOPROTEOMIC APPROACH TO ANALYZE SRC ONCOGENIC SIGNALING IN XENOGRAFT TUMORS

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EXPLORING THE DETECTION LIMITS OF ERG ONCOPROTEIN IN PROSTATE CANCER USING DIFFERENT SAMPLE TYPES SIMULATING CLINICAL SPECIMENS

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PROTEOGENOMIC ANALYSIS OF GLIOMA STEM CELLS: A POTENTIAL TOOL FOR THE DISCOVERY OF GBM BIOMARKERS

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TRANSFORMING GROWTH FACTOR BETA REGULATES NOVEL PROTEINS IN A HUMAN TROPHOBLASTIC CELL MODEL.

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FUNCTIONAL PROTEOME ANALYSIS OF TRANSLATIONALLY CONTROLLED TUMOR PROTEIN (TCTP), A NOVEL NEUROFIBROMATOSIS TYPE 1 (NF1)-RELATED PROTEIN

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STATHMIN-1 SILENCING INHIBITS METASTATIC PROCESSES IN COLORECTAL CANCER

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PROFILING EGFR KINASE INHIBITOR RESISTANCE PATHWAYS IN NON-SMALL LUNG CANCER CELL LINES

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RELATIVE QUANTITATION OF N-LINKED GLYCANS USING CARBONYL-REACTIVE TANDEM MASS TAG REAGENTS

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PROTEIN DEEP SEQUENCING IN MALIGNANT MELANOMA PATIENT SAMPLES

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PROTEOMIC ANALYSIS OF NOVEL NGF-REGULATED TRKA-DEPENDENT TARGETS ASSOCIATED WITH PI3K SIGNALING AND JNK SIGNALING IN SK-N-MC NEUROBLASTOMA CELLS

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COMPREHENSIVE IDENTIFICATION OF GENETIC VARIATIONS AT PROTEIN LEVEL WITH LARGE SCALE MS DATASETS

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PROTEOME PROFILING OF HUMAN CANCER CELL LINES USING DATA-INDEPENDENT ACQUISITION LABEL-FREE LC-MS

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DECIPHERING PROTEOME CONTENT OF EXOSOMES SECRETED BY LIVER CANCER CELL LINES

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IMMUNOPROFILING OF CANCER – HARVESTING THE IMMUNE SYSTEM AS A SENSOR FOR CANCER

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DIAGNOSIS OF THE PRESENCE OF NON-SMALL-CELL-LUNG CARCINOMA (NSCLC) USING AUTOANTIBODIES

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IMMUNOCAPTURE LC-MS; A TOOL FOR ISOZYME DIFFERENTIATED MEASUREMENT AND CP-DETERMINATION OF CANCER MARKERS

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PARALLEL REACTION MONITORING ANALYSIS OF NIPPLE ASPIRATE FLUID FROM BRAZILIAN BREAST CANCER PATIENTS: LOOKING FOR MOLECULAR SIGNATURES

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TARGETED PROTEOMIC ANALYSIS OF POTENTIAL NEW THERAPEUTIC TARGETS FOR PSORIASIS

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MOLECULAR EVIDENCE FOR TUMOUR HETEROGENEITY IDENTIFIED BY MALDI TOF IMAGING AND INTACT CELL MASS SPECTROMETRY

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THE QUEST FOR ENDOMETRIAL CANCER PROTEIN BIOMARKERS IN UTERINE ASPIRATES

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ECM PROTEOMICS AND CYTOKINE PROFILING IN 3D-CELL CULTURE MODELS

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LPS- INDUCED COLORECTAL TUMOR PROTEINS

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PROTEOMIC AND DEGRADOMIC PROFILING OF GLIOBLASTOMA MULTIFORME

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SECRETOME AND DEGRADOME PROFILING SHOWS THAT KALLIKREIN-RELATED PEPTIDASES 4, 5, 6, AND 7 INDUCE TGFB–1 SIGNALING IN OVARIAN CANCER CELLS

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PROTEOMICS PROFILING OF THE THE INTERSTITIAL FLUID OF MURINE BREAST CANCER.

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BORNA DISEASE VIRUS INFECTION IMPACTS HOST PROTEOME AND HISTONE LYSINE ACETYLATION IN HUMAN OLIGODENDROGLIA CELLS

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PATHOPHYSIOGICAL TENSILE STRETCH CHANGES THE HUMAN CEREBRAL ENDOTHELIAL CELL PROTEOME

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MRM-BASED QUANTIFICATION OF ACETYLATION METABOLISM ENZYMES

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THE INFLUENCE OF SIALIC ACID MODIFICATION OF SURFACE PROTEINS ON INTRACELLULAR SIGNALLING

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QUANTITATIVE PROTEOMICS FOR STUDYING HUMAN STEM CELLS DIFFERENTIATION

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IDENTIFICATION OF N-TERMINALLY ACETYLATED KINETOCHORE PROTEINS USING HIGH RESOLUTION MASS SPECTROMETRY

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GLYCOPROTEOMIC STUDY IN RAT SERUM USING ALBUVOID-A SERUM REDUCTION TOOL

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IMMOBILIZATION OF ANTIBODIES ON FE3O4@POLYDOPAMINE CORE¨CSHELL MICROSPHERES FOR SELECTIVE ENRICHMENT OF LYSINE-ACETYLATED PROTEINS AND PEPTIDES

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IMMOBILIZATION OF ANTIBODIES ON FE3O¬4@POLYDOPAMINE CORE¨CSHELL MICROSPHERES FOR SELECTIVE ENRICHMENT OF LYSINE-ACETYLATED PROTEINS AND PEPTIDES

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UNCOVERING SMALL UBIQUITIN-LIKE MODIFIER SIGNALING NETWORKS

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DEFINING THE INTERACTOME OF THE TUMOR SUPPRESSOR CYLD AND ITS ROLE IN EGF SIGNALING

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BOTTON-UP AND MIDDLE-DOWN APPROACHES FOR COMPREHENSIVE ANALYSIS OF CHROMATIN-BINDING PROTEINS AFTER TREATMENT WITH SODIUM BUTYRATE.

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IDENTIFICATION OF THE MYOFIBRILLAR Z-DISC AS A NODAL POINT IN SKELETAL MYOCYTE SIGNALING BY LARGE-SCALE PHOSPHOPROTEOMICS

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INTEGRATIVE BIOINFORMATICS FOR PROTEIN PTM NETWORK DISCOVERY: ANALYSIS OF A CANCER DRIVER GENE

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THE ROLES OF HAUSP/USP7 DEUBIQUITINATING ENZYME REGULATING DNA DAMAGE RESPONSE

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SIRT5 DESUCCINYLATES MITOCHONDRIAL ISOCITRATE DEHYDROGENASE 2 AND REGULATES TUMORGENESIS

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TARGETED LC-MS EXPERIMENTS FOR THE ACCURATE MAPPING OF ADP-RIBOSYLATION SITES

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ELUCIDATING THE ROLES OF LYSINE METHYLTRANSFERASES BASED ON THEIR NON-HISTONE PROTEIN TARGETS USING A NOVEL TECHNIQUE

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ACETYLATION,¡AINSTEAD OF UBIQUITINATION, MEDIATES PROTEASOMAL DEGRADATION OF CORE HISTONES DURING SPERMATOGENESIS AND DNA REPAIR

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A SECRETED PROTEIN FROM M. TUBERCULOSIS SUPPRESSES NF-¦ÊB SIGNALING PATHWAY AND PROMOTES INTRACELLULAR SURVIVAL OF MYCOBACTERIA

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QUANTITATIVE PHOSPHORYLATION ANALYSIS OF HOST RESPONSES TO DENGUE VIRUS INFECTION

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PROTEOME ANALYSIS OF ENRICHED CARDIAC PROGENITOR AND DOPAMINERGIC NEURONS DERIVED FROM HUMAN EMBRYONIC STEM CELLS REVEALS NOVEL PATHWAYS AND MARKERS

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A PROTEOMIC ANALYSIS OF P27(KIP1)-BINDING PROTEINS REVEALS A ROLE OF THIS PROTEIN ON THE REGULATION OF TRANSCRIPTION THROUGH ITS INTERACTION WITH RNA POLYMERASE II

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A POST-TRANSLATIONAL MODIFICATION PROTEOMICS STUDY OF INS CELL MITOCHONDRIA

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NUCLEAR PROTEOMICS REVEALS THE LINK BETWEEN MINICHROMOSOME MAINTENANCE COMPLEX AND GLUCOSE-INDUCED PROLIFERATION OF RAT PANCREATIC INS-1E B-CELLS

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LABEL-FREE QUANTITATIVE MASS SPECTROMETRIC ANALYSIS OF COMPLEX PROTEOME ALTERATIONS IN THE AGING MUNICH WISTAR FRÖMTER RAT BRUSH BORDER MEMBRANE

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ISOLATION AND PROTEOMIC ANALYSIS OF EXTRACELLULAR MEMBRANE VESICLES OF STREPTOCOCCUS PNEUMONIAE

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PROTEOMIC ANALYSIS OF IMMUNOAFFINITY-ISOLATED URINARY EXOSOMES

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MILK FAT GLOBULE PROTEOMICS FOR UNDERSTANDING THE CONTRIBUTION OF EPITHELIAL CELLS IN INNATE IMMUNITY OF THE MAMMARY GLAND

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PROTEOMIC ANALYSES OF EXTRACELLULAR VESICLES FROM THE PARASITIC TREMATODES FASCIOLA HEPATICA AND DICROCOELIUM DENDRITICUM

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QUANTITATIVE PROTEOMIC ANALYSIS OF MICROPARTICLES IN HYPERTENSIVE PATIENTS WITH ELEVATED CARDIP-RENAL RISK

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PROTEOMIC STUDY OF BLOOD-DERIVED MICROPARTICLES IN MULTIPLE SCLEROSIS

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A TRANSFER LEARNING FRAMEWORK FOR ORGANELLE PROTEOMICS DATA

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FRACTIONATION PROFILING: A FAST AND VERSATILE APPROACH FOR MAPPING VESICLE PROTEOMES AND PROTEIN-PROTEIN INTERACTIONS.

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SUBCELLULAR PROTEOMICS OF HUMAN EMBRYONIC STEM CELLS

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URINARY EXOSOMES REFLECT PROTEOMIC CHANGES AT TISSUE LEVEL. A NOVEL TOOL FOR NON-INVASIVE DETECTION OF KIDNEY INJURY IN DIABETIC NEPHROPATHY.

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PROTEOMIC PROFILING OF EXOSOMES FROM CEREBROSPINAL FLUID

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PROTEOMIC IDENTIFICATION OF MICROVESICLE BIOMARKERS IN ST-ELEVATION MYOCARDIAL INFARCTION

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PHENOTYPIC CHARACTERIZATION OF EXOSOMES PRESENT IN BLOOD BY EXTRACELLULAR VESICLE (EV) ARRAY – IS THE EXOSOME PROFILE A REFLECTION OF THE DISTRIBUTION OF THE LEUKOCYTE SUBPOPULATIONS IN BLOOD?

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COMPARISON OF SUPER-SILAC AND SWATH-MS TECHNIQUES: APPLICATION FOR QUANTIFYING THE MOUSE SYNAPTIC MITOCHONDRIAL PROTEOME.

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THE AGING MOUSE BRAIN SYNAPTIC MITOCHONDRIAL PROTEOME: PRESERVATION OF FUNCTION THROUGH HORMESIS.

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PROTEOMIC STUDY OF EXTRACELLULAR VESICLES OF HUMAN MACROPHAGES IN RESPONSE TO CANDIDA ALBICANS INFECTION

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PROTEOMIC CHARACTERIZATION OF DETERGENT-RESISTANT PLASMA MEMBRANE MICRODOMAINS: SIMILARITIES AND DISSIMILARITIES BETWEEN PLANT AND OOMYCETE

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PROTEOMIC ANALYSIS OF CEREBROSPINAL FLUID EXTRACELLULAR VESICLES: A COMPREHENSIVE DATASET

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QUANTITATIVE AND QUALITATIVE PROTEOME CHARACTERISTICS EXTRACTED FROM IN-DEPTH INTEGRATED GENOMICS AND PROTEOMICS ANALYSIS

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NEXTSEARCH: DISCOVERY OF NOVEL TRANSCRIPTS USING NUCLEOTIDE-BASED SPLICE GRAPHS

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CAPER 3.0: A SCALABLE CLOUD-BASED PIPELINE FOR THE DATA-INTENSIVE ANALYSIS OF PROTEOMIC DATASETS

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REVISITING THE IDENTIFICATION OF CANONICAL SPLICE ISOFORMS THROUGH INTEGRATION OF FUNCTIONAL GENOMICS AND PROTEOMICS EVIDENCE

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PROTEOMIC ANALYSIS IN PTERYGIUM

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THE FUNCTIONAL ROLE OF INFLAMMATORY BIOMARKER IN RECURRENT PREGNANCY LOSS

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SPLICE ISOFORMS IN TRIPLE-NEGATIVE BREAST CANCERS

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A COMPREHENSIVE AND SCALABLE AUTOMATED WORKFLOW FOR HUMAN PLASMA PROTEOMICS AND ITS APPLICATION TO THE DIOGENES CLINICAL STUDY

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MATURE ADIPOCYTE PROTEOME REVEALS ALTERED METABOLIC AND REGULATORY ACTIVITY BETWEEN LEAN, OVERWEIGHT AND OBESE: USING PROTEOMIC APPROACH AND NETWORK ANALYSIS.

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HEPATIC SILAC PROTEOMIC ANALYSIS OF THE PANDER TRANSGENIC MOUSE REVEALS NOVEL LIPOGENIC PATHWAYS

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INVESTIGATION OF ADIPOCYTE PROTEOME DURING THE DIFFERENTIATION OF BROWN PREADIPOCYTES

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A STUDY OF TWO SEQUENTIAL MEDIA FOR IVF

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DIAGNOSING IMPAIRED GLUCOSE TOLERANCE USING DIRECT MASS SPECTROMETRY OF BLOOD PLASMA METABOLITES

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A PROTEOMIC APPROACH TO IDENTIFY BIOMARKERS OF FOOD CRAVING AND RESPONSE TO BARIATRIC SURGERY IN MORBID OBESITY

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QUANTITATIVE STUDY OF HUMAN ADIPOSE TISSUE SECRETION BY CILAIR SHOWS LOCATION-SPECIFIC DIFFERENCES BETWEEN VISCERAL AND SUBCUTANEOUS FAT DEPOTS

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EVALUATION OF INTRACELLULAR TRACE ELEMENTS, MRNA EXPRESSION AND PROTEIN ABUNDANCES IN HUMAN LIVER

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COMPREHENSIVE PROTEOMIC ANALYSIS OF 3D HUMAN LIVER SPHEROIDS FOR DRUG TOXICITY INVESTIGATION

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SERUM PROTEOMIC PROFILE OF MEXICAN PATIENTS WITH “DIABESITY”

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DISSECTION OF METABOLIC PATHWAYS IN THE DBDB MOUSE MODEL BY INTEGRATIVE PROTEOME AND ACETYLOME ANALYSIS

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PROTEOMIC ANALYSIS OF SERUM INDICATE FIBRINOGEN AS POTENTIAL BIOMARKER IN EARLY DIAGNOSIS OF HEPATOLENTICULAR DEGENERATION IN PEDIATRIC AND ADULT SUBJECTS

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SUBTRACTIVE PROTEOMIC ANALYSIS ALLOWS DEFINITION OF LIPID DROPLET ASSOCIATED PROTEIN (LDP) AND UNRAVELS DIFFERENTIAL LIVER LDP PROFILING IN FATTY LIVER DISEASE

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HIGH FAT DIET INDUCED ISOFORM CHANGES OF THE PARKINSON'S DISEASE PROTEIN DJ-1

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GAINING INSIGHT INTO OBESITY AND RELATED PATHOLOGIES BY HIGH-THROUGHPUT PROTEOMIC ANALYSIS OF HUMAN ADIPOSE TISSUE

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A LABEL-FREE PROTEOME WIDE BINDING STUDY TO REVEAL FUNCTIONALLY RELEVANT SNP VARIANT DNA BINDERS

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ADVANCED GLYCATION END-PRODUCTS AS PROSPECTIVE DIABETIC PEPTIDE-BIOMARKERS

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MS BASED APPROACHES FOR STUDYING THE PHARMACOKINETICS OF AN INNOVATIVE LIVER TARGETED COPPER CHELATOR IN ATP7B -/ MICE USED AS A MODEL FOR STUDIES OF WILSON'S DISEASE

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ONE-WEEK PALMITATE TREATMENT MODIFIES HUMAN ISLET INSULIN SORTING AND PROCESSING

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MYOCARDIAL PROTEOME DURING METABOLIC SYNDROME AND TYPE 2 DIABETES IN ZUCKER DIABETIC FATTY RATS

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NUCLEAR PROTEOMIC STUDY OF C2C12 MYOTUBES WITH ALTERNATED INSULIN SENSITIVITY INDUCED BY PALMITIC ACID

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IMPLICATIONS OF METHYLTHIOADENOSINE PHOSPHORYLASE DEFICIENCY IN LIVER INJURY

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PROFILING OF CELL SURFACE PROTEOME AND METABOLOME FROM AN IN-VITRO MODEL SYSTEM, USING LC-MS TECHNOLOGIES

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COMPARISON OF AN ORBITRAP FUSION SYSTEM PERFORMANCE WITH AN ORBITRAP VELOS PRO USING SOLID PHASE AMINP-LABELLING WITH TMTS ON COMPLEX DIGESTS FOR SUBSEQUENT PHOPHOPEPTIDE ENRICHMENT

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EXPANDING THE MYCOBACTERIUM TUBERCULOSIS PHOSPHOPROTEOME CATALOGUE AND IDENTIFICATION OF TYROSINE-PHOSPHORYLATION THROUGH LABEL-FREE PHOSPHOPROTEOMIC ANALYSIS OF A CLINICAL ISOLATE

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PHOSPHOPROTEOMIC ANALYSES REVEAL THAT GALECTIN-1 AUGMENTS THE DYNAMICS OF B-CELL RECEPTOR SIGNALING

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SIMPLIFIED AND MINIMIZED FRACTIONATION USING STAGETIPS FOR IN-DEPTH PROTEOME AND PHOSPHOPROTEOME ANALYSIS

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IRON-TRIGGERED SIGNAL TRANSDUCTION IN THE PARASITIC PROTOZOAN TRICHOMONAS VAGINALIS

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A PHOSPHOPROTEOMIC VIEW OF CHICKPEA EXTRACELLULAR MATRIX ILLUSTRATE COMBINATORIAL INTERPLAY OF PREDICTED AND UNEXPECTED COMPONENTS OF CELL WALL INTEGRITY SIGNALING IN PLANT

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MASS-SPECTROMETRIC IDENTIFICATION OF AMPK PHOSPHOSITES IN RAT MITOCHONDRIAL FUMARATE HYDRATASE

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COMPLEMENTARY PROTEASES SUBSTANTIALLY EXPAND PHOSPHOPROTEOME COVERAGE

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GLIOBLASTOMA PHOSPHOTYROSINE-CONTAINING PROTEINS IDENTIFIED WITH TWP-DIMENSIONAL WESTERN BLOTTING AND TANDEM MASS SPECTROMETRY

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QUALITATIVE AND QUANTITATIVE PHOSPHOPROTEOMICS ANALYSIS OF CHICK RETINA OF TIO2-ENRICHED STRATEGY

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ADAPTATION OF CELLULAR SIGNALING BY INTRINSICALLY ACTIVE P38 MAP KINASES

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PHOSPHOPEPTIDE ENRICHMENT USING SYNTHETIC BIOMIMETIC LIGANDS

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SIGNALLING NETWORK PLASTICITY IN RESPONSE TO CHRONIC CLASS I PI3K OR MTORC1/2 INHIBITION

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MAGNETITE-DOPED POLYDIMETHYLSILOXANE (PDMS) AS A SOLID PHASE SUPPORT FOR PHOSPHOPEPTIDE ENRICHMENT.

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QUANTITATIVE PHOSPHOPROTEOMICS FOR BREAST CANCER VIA PHOSPHORYLATION BY AMPK

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IMPROVED DETECTION OF MULTIPHOSPHORYLATED PEPTIDES USING NOVEL TIO2 BASED NANOMATERIALS

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SEA URCHIN PHOSPHOPROTOEMICS REVEAL THE NEW LIGHTS ON EGG ACTIVATION

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PARTICULATE MATTER DEPHOSPHORYLATES EZRIN/RADIXIN/MOESIN (ERM) PROTEIN ON BEAS-2B CELL

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PLK2 SPECIFICITY AND SUBSTRATES IDENTIFICATION BY PROTEOME-DERIVED PEPTIDE LIBRARIES AND QUANTITATIVE PROTEOMICS

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QUANTITATIVE PROTEOMICS APPLIED TO THE STUDY OF THE MAMMALIAN CIRCADIAN PROTEOME AND PHOSPHOPROTEOME

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EVALUATION OF PHOSPHOTYROSINE IMMUNOPRECIPITATION FOR LABEL-FREE PHOSPHOPROTEOMICS USING CANCER CELL LINE MODELS

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IS LESS ENOUGH? SCALING DOWN PROTEIN INPUT FOR PHOSPHOPROTEOMICS BASED TREATMENT SELECTION IN PATIENTS WITH ADVANCED SOLID TUMORS

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PHOSPHOPROTEOMICS OF A PANEL OF AML CELL LINES

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DEVELOP A MALDI-IMAGING MASS SPECTROMETRY METHOD IN MOUSE SKIN TISSUE PEPTIDE DISTRIBUTION STUDY.

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POTENTIAL BIOMARKERS BETWEEN BURKHOLDERIA PSEUDOMALLEI WILD TYPE AND ITS RPON2 MUTANT STRAIN USING MALDI-TOF MASS SPECTROMETRY APPLICATION

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IDENTIFICATION OF POTENTIAL BIOMARKERS OF HEPATOTOXICITY BY PROTEOMIC ANALYSIS OF BLOOD PLASMA IN A LOWER VERTEBRATE EXPOSED TO ARSENIC

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LABEL-FREE QUANTITATIVE PROTEIN PROFILING OF VASTUS LATERALIS MUSCLE DURING HUMAN AGING

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A NOVEL APPROACH FOR PROCESSING LC - ION MOBILITY - MS METABONOMICS DATA SETS

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DEVELOPING A HIGH-THROUGHPUT, LABEL FREE TARGETED-MS APPROACH FOR VALIDATION OF PLASMA PROTEIN CONCENTRATIONS ASSOCIATED WITH DISEASE RISK.

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PROTEOMICS-DRIVEN SELECTIVE MITOCHONDRIAL TARGETING FOR TREATING ANXIETY DISORDERS

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NOVEL BIOMARKERS OF ANDROGEN DEFICIENCY FROM SEMINAL PLASMA PROTEOMIC PROFILING USING HIGH-RESOLUTION MASS SPECTROMETRY.

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INCREASING DEPTH OF COVERAGE IN DATA INDEPENDENT ACQUISITION

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THE DISCUSSION ABOUT RESULTS FROM IMMUNOASSAYS AND TARGETED PROTEOMICS - NEVER-ENDING STORY OF THE QUANTIFICATION OF PROTEINS

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TEAR PEPTIDOMICS: IDENTIFICATION OF TEAR NATURALLY OCCURRING PEPTIDES BY CID, HCD AND ETD

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NEOPTERIN PLASMA LEVELS PREDICT INFECTION DEVELOPMENT IN ANEURYSMAL SUBARACHNOID HEAEMORRHAGE PATIENTS

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SEARCH FOR NOVEL ALLERGEN OF HEN FS EGG ALLERGY USING WESTERN BLOT ANALYSIS

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INTEGRATION OF SWATH AND MRM FOR BIOMARKER DISCOVERY OF ESOPHAGEAL SQUAMOUS CELL CARCINOMA

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STOP ENZYMATIC ACTIVITY AND PRESERVE PROTEOME INTEGRITY OF TISSUE SAMPLES BY HEAT STABILIZATION

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INVESTIGATING BIOLOGICAL VARIATION IN HUMAN HEPATOCYTES OF PHASE I AND II DRUG METABOLISM ENZYMES

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NOVEL BIOMARKERS FOR BLADDER CANCER: EVALUATION OF ELISA ASSAY PERFORMANCE IN URINE

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DOWNSCALING TISSUES PROTEOMICS, TOWARD PRECIOUS FFPE TISSUE SAMPLES PREPARATION. APPLICATION TO EARLY EVENTS OF CERVIX CANCER DECIPHERING.

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DATA DEPENDENT VERSUS DATA INDEPENDENT ACQUISITION APPLIED TO SAMPLES OF DIFFERENT PROTEIN DYNAMIC RANGE

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PROFILING OF HUMAN PLASMA CLUSTERIN USING A GLYCOPROTEOMICS APPROACH TO DISCOVER POTENTIAL BIOMARKERS OF ALZHEIMER'S DISEASE

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TIO2 ENRICHMENT REVEALS LOW-ABUNDANCE, CANCER-ASSOCIATED PROTEINS IN HUMAN SERUM

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A NEXT GENERATION PROTEOMIC APPROACH FOR BIOMARKER DISCOVERY LINKING MULTIPLEXED SINGLE BINDER ASSAYS TO MASS SPECTROMETRY (MS) FOR DIRECT MOLECULAR VERIFICATION AND INVESTIGATION OF CANDIDATE BIOMARKERS.

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DESCRIPTION OF BAL PROTEOME IN LUNG TRANSPLANT RECIPIENTS: OPTIMIZATION OF SAMPLE ANALYSIS AND COMPARISON WITH HEALTHY VOLUNTEERS

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IDENTIFICATION OF HUMAN TEAR FLUID BIOMARKERS IN DIFFERENT DRY EYE DISEASE SUBGROUPS USING LABEL-FREE QUANTITATIVE PROTEOMICS

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IDENTIFICATION OF POTENTIAL ISCHEMIC STROKE BIOMARKERS THROUGH SECRETOME ANALYSIS OF A BRAIN ENDOTHELIAL CELL LINE USING SILAC

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IMMUNP-LASER MICRODISSECTION COUPLED TO LABEL-FREE PROTEOMICS FOR THE ANALYSIS OF HUMAN BRAIN CELLS TO IDENTIFY POTENTIAL STROKE BIOMARKERS

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MALDI IMAGING MASS SPECTROMETRY IN SUBTYPING BREAST CANCER: A PILOT STUDY

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DETECTION OF TEAR PROTEIN BIOMARKERS FOR DIABETIC RETINOPATHY SCREENING

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HIGH THROUGHPUT MRM TARGETED PROTEIN QUANTIFICATION USING MICRO LC

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QUANTIFYING DRUG INDUCED ORGAN INJURY BIOMARKERS ACROSS THE SPECIES BARRIER

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PATIENT-DERIVED MELANOMA CELL LINE PROFILING BY MULTIPHASE-CHIPLC COUPLED SWATH CORRELATES WITH SENSITIVITY TO MEK INHIBITION

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DEVELOPMENT OF DIAGNOSTIC BIOMARKERS FOR DIABETIC RETINOPATHY AT EARLY STAGES USING ABSOLUTE QUANTITATIVE PROTEOMIC METHOD

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AUTOANTIBODY PROFILING OF MENINGIOMAS TO IDENTIFY BIOMARKERS USING HUMAN PROTEOME ARRAYS

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CHARACTERIZATION OF PROTEIN ISOFORMS PREDICTIVE OF CANCER USING IMMUNP-AFFINITY CAPTURE AND FAST LC-MS.

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PROTEOMICS APPLICATION OF CLINICALLY ARCHIVED FORMALIN-FIXED PARAFFIN EMBEDDED TISSUES: QUALITY EVALUATION BY 2-D PAGE

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MEASUREMENT OF GLYCOSYLATED ALPHA-FETOPROTEIN IMPROVES DIAGNOSTIC POWER OVER NATIVE FORM ON HEPATOCELLULAR CARCINOMA

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MULTIPLEXED QUANTIFICATION OF PRETERM INFANT PLASMA PROTEINS USING HEAVY PROTEIN STANDARDS AND MS-BASED IMMUNOASSAYS

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CHANGE IN BLOOD CAN BE MORE SENSITIVELY DETECTED IN URINE

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NOVEL BIOMARKER DISCOVERY FOR ACUTE MYOCARDIAL INFARCTION: PROTEOMIC ANALYSIS OF FORMALIN-FIXED PARAFFIN-EMBEDDED TISSUE FROM AUTOPSY

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PROTEOME ANALYSIS AND COMPARATIVE STUDY OF NORMAL ENDOMETRIAL STEM CELLS, ENDOMETRIOSIS STEM CELLS AND BONE MARROW MESENCHYMAL STEM CELLS

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QUANTITATIVE PROTEOMIC ANALYSIS OF VITREOUS IN DIABETIC RETINOPATHY USING SWATH

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PROTEOSEPSIS: PROTEOMIC ANALYSIS OF PLASMA PROTEINS DURING THE COURSE OF SEPSIS.

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SUBREGIONAL PROTEOMIC ANALYSIS OF HIPPOCAMPI FROM PATIENTS WITH ALZHEIMER'S DISEASE

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PROTEOME ALTERATION INDUCED BY DIFFERENT-SIZED SILVER NANOPARTICLES (AG NPS) IN AN INTESTINAL CP-CULTURE MODEL

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IDENTIFICATION OF NEW POTENTIAL MARKERS OF PRETERM BIRTH IN AMNIOTIC FLUID

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IDENTIFICATION OF HUMAN HEMOGLOBIN-ACETAMINOPHEN ADDUCT

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ISOLATION AND IDENTIFICATION OF SERUM PEPTIDES - A USEFUL TOOL FOR IDENTIFICATION OF NOVEL DISEASE BIOMARKERS FOR ALZHEIMER'S DISEASE

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3D MALDI IMAGING OF MOUSE HEART AFTER MYOCARDIAL INFARCTION

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IN-DEPTH IDENTIFICATION OF PROTEIN IMAGES BY COMBINING HIGH MASS RESOLUTION MALDI FTICR IMAGING AND HIGH PERFORMANCE QTOF NLC-MS/MS

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PROTEOMIC PATTERNS IN THE NCI60 CANCER CELL COMPENDIUM COMPLEMENT GENOMIC FEATURES IN PREDICTIVE MODELING OF ANTICANCER DRUG SENSITIVITY

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PROTEOMIC LANDSCAPE OF THE HUMAN CHOROID-RPE

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SCREENING FOR NEW FIBROSIS BIOMARKERS IN RAT BRONCHOALVEOLAR LAVAGE FLUID

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CHARACTERIZATION OF AMNIOTIC FLUID PEPTIDOME IN PPROM PREGNANCIES WITH INFECTIOUS AND INFLAMMATORY COMPLICATIONS

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IN-DEPTH ANALYSIS OF THE HUMAN VITREOUS PROTEOME USING A RESIN DEPLETION-BASED METHOD: APPLICATION TO THE DISCOVERY OF NEW BIOMARKERS FOR PROLIFERATIVE DIABETIC RETINOPATHY.

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NEW APPROACH TO THYROID-ASSOCIATED ORBITOPATHY DISEASE IN TEARS BY QUANTITATIVE PROTEOMICS

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REDOX-STATE OF PENTRAXIN 3 AS A NOVEL BIOMARKER FOR RESOLUTION OF INFLAMMATION AND SURVIVAL IN SEPSIS

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PROTEOMICS OF RED BLOOD CELLS FROM PATIENTS WITH OBSTRUCTIVE SLEEP APNEA

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SECOND-HAND TOBACCO SMOKE EFFECTS EVALUATED BY PROTEOMICS

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DEEP PROTEOME PROFILING USING HR/AM SELECTED ION MONITORING AND DATA INDEPENDENT ACQUISITION ON THE ORBITRAP FUSION TRIBRID MS

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BRONCHOALVEOLAR LAVAGE FLUID PROTEIN PROFILE IN HEMATOPOIETIC STEM CELL TRANSPLANT RECIPIENTS

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SMFAP4 – A NOVEL BIOMARKER FOR GRADING AND MANAGEMENT OF HEPATITIS C INFECTION

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AFFIMER ARRAYS FOR BIOLOGICAL AND BIOMARKER DISCOVERY

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HIGH THROUGHPUT PROTEIN PURIFICATION: 235,000 PROTEINS A YEAR, AND COUNTING

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ROLE OF COMPLEMENT COMPONENTS IN RETINOPATHY OF PREMATURITY?

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CHARACTERIZATION OF UROKINASE VIA ELECTROPHORESIS AND MASS SPECTROMETRY ANALYSES

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STROMAL MARKERS OF BREAST CARCINOMA IDENTIFIED BY PROTEOMICS OF LASER MICRODISSECTED TISSUE

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POTENTIAL BIOMARKER DISCOVER OF THE WILSON'S DISEASE BY TOP-DOWN PROTEOMIC INVESTIGATION OF WHOLE SALIVA

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RAPID DIRECT DETECTION OF THE MAJOR FISH ALLERGEN BY HIFU-SMIM

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METABOLOMIC PROFILE IN XYLITOL INTOXICATION OF DOGS

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PROTEOMIC ANALYSIS OF ESCAMOLES (LIOMETOPUM APICULATUM MAYR, LARVAE), THE “MEXICAN CAVIAR”: A NEW MODEL FOR DISEASE RESEARCH?

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PROTEOMICS OF RICE AND COCHLIOBOLUS MIYABEANUS FUNGAL INTERACTION: INSIGHT INTO PROTEINS AT INTRACELLULAR AND EXTRACELLULAR SPACES

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COMPARATIVE METABLOMICS AND PROTEOMICS ANALYSIS REVEAL CHANGES OF ISOFLAVONE PATHWAY FLOW IN SEED COAT OF GLYCINE MAX CV. MALLIKONG AND MALLIKONG MUTANT

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INVESTIGATION OF NUTRIENT DEFICIENCY RESPONSES OF POTATO ROOTS USING PROTEOMICS AND METABOLOMICS APPROACHES

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Kanika Narula, Sudip Ghosh, Shubhendu Shekhar, Priyanka Jawa, Niranjan Chakraborty, Subhra Chakraborty
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PROTEOME ANALYSIS OF PROGRAMMED CELL DEATH FOLLOWING SPINAL CORD INJURY

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Salvatore Pisanu, Grazia Biosa, Roberto Anedda, Luca Pretti, Sergio Uzzau, Daniela Pagnozzi, Maria Filippa Addis
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IDENTIFICATION OF CHITINOLYTIC PROTEINS IN THE SECRETOME OF CELLVIBRIO JAPONICUS

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MULTIPLE REACTION MONITORING ANALYSIS REVEALS CHANGES IN S1P-S1 PRECEPTOR AXIS FOLLOWING SPINAL CORD INJURY

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DE NOVO SEQUENCING AND QUANTITATIVE PROTEOMICS IN A NON-SEQUENCED SPECIES AS A WAY TO DISCOVER NEW ANTI-OBESITY MECHANISMS

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APPLICATION OF CESI-MS ON SILAC-BASED QUANTITATIVE PROTEOMICS

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IDENTIFICATION OF WELFARE BIOMARKERS IN PIGS USING PERIPHERAL MONONUCLEAR CELLS (PBMCS) AND DIFFERENTIAL GEL ELECTROPHORESIS (DIGE)

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MINING OF PROTEINS INVOLVED IN NUTRITION AND TRANSDIFFERENTIATION IN BOVINE SKELETAL MUSCLE

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PROTEOMICS APPLIED TO OENOLOGY, CHARACTERIZATION OF AUTOCHTHONOUS WINE YEAST STRAINS

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PROTEOMIC ANALYSIS OF CARDIAC TISSUE FROM RESISTANCE TRAINED RATS REVEALS CHANGES COMPATIBLE WITH HEART FAILURE

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SEMINAL PLASMA PROTEOMES OF RABBITS, BOARS AND BULLS AND THEIR ASSOCIATIONS WITH SPERM PARAMETERS.

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LACTOBACILLUS REUTERI SUB-PROTEOME STUDY TO ELUCIDATE UPTAKE, METABOLISM AND RELEASE OF SELENIUM FOR NUTRACEUTICAL APPLICATION

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TYPE I COLLAGEN COMPOSITION IN THE BONY FISH DANIO RERIO

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DYNAMIC CHANGES OF CONA-ENRICHED URINARY PROTEINS IN A FOCAL SEGMENTAL GLOMERULOSCLEROSIS RAT MODEL

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PROTEOMIC IDENTIFICATION OF POTENTIAL LIVER BIOMARKERS IN AYU, PLECOGLOSSUS ALTIVELIS AS AN AGING ANIMAL MODEL

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UNDERSTANDING THE INTERACTION OF ORGANISMS WITH THEIR BIOLOGICAL ENVIRONMENT – INITIATIVE ON MULTI ORGANISM PROTEOMES (IMOP)

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A VALIDATED METHOD FOR COW MILK DETECTION AND QUANTIFICATION IN BAKERY PRODUCTS BY LC-MS/MS.

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PHENOTYPING CHICKEN MALE FERTILITY BY INTACT CELL MALDI-TOF MASS SPECTROMETRY

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CHANGES IN THE PROTEIN PROFILES OF PLASMA MEMBRANE PREPARATIONS FROM BETA VULGARIS ROOTS AS AFFECTED BY FE DEFICIENCY

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PROTEOMIC STUDY OF BOVINE ENDOMETRIAL CELL STIMULATED WITH LPS

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META-OMICS ANALYSIS TO INVESTIGATE MICROBIAL CONSORTIUM IN CHEESE PRODUCTION

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PROTEOMIC APPROACH TO INVESTIGATE THE ESCHERICHIA COLI MEMBRANE PROTEOME IN SEVERE ENVELOPE STRESS CONDITIONS.

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PROTEOMIC INSIGHTS INTO SULFUR METABOLISM IN THE HYDROGEN-PRODUCING HYPERTHERMOPHILIC ARCHAEON THERMOCOCCUS ONNURINEUS NA1

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A PROTEOMIC APPROACH UNRAVELS GENOTYPE DIFFERENCES IN GRAPEVINE RESISTANCE TO DOWNY MILDEW

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PROTEOMICS TO UNRAVEL MECHANISMS OF NANOPARTICLE TOXICITY

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PROTEOMICS OF THE AGING LIVER MITOCHONDRIA

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CHARACTERIZATION OF PROTEINS AND PUTATIVE FUNCTIONAL PATHWAYS IN ROTIFER ENCYSTED DORMANT EMBRYOS (RESTING EGGS)

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CHARACTERIZATION OF PLANT GLYCATED PROTEOME AND ITS CHANGES DURING AGEING AND UNDER ENVIRONMENTAL STRESS CONDITIONS

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LEVELS OF CHEMOSENSORY AND ODORANT-BINDING PROTEINS FROM CATERPILLAR SALIVA ARE AFFECTED BY HOST PLANT AND IMMUNE CHALLENGE

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FRACTIONATION OF TOTAL, SOLUBLE AND INSOLUBLE PROTEINS IN GLOEOBACTER VIOLACEUS PCC7421

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UNDERSTANDING PHYTOCHELATIN PROFILE IN NICOTIANA TABACUM UNDER CD, CU AND AS STRESS: A STEP TOWARDS PHYTOREMEDIATION-APPLICATIONS

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THE PROTEOME OF OLIVE AND THE INVISIBLE PROTEOME OF OLIVE OILS

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PROTEOMIC FINGERPRINTING OF ITALIAN APERITIFS

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PROTEOMIC CHANGES OF CERVICAL ADENOCARCINOMA CELLS (HELA) INDUCED BY THE TREATMENT WITH A SNAKE VENOM DERIVED PHOSPHOLIPASE A2 (BOTHROPS MARMORATUS)

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EXTENDED-SPECTRUM ??-LACTAMASE (ESBL) PRODUCING GRAM (-) ENTEROBACTERIACEAE STRAINS IN FOODS FROM TURKEY

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MASS SPECTROMETRY ANALYSIS OF RAT ALVEOLAR MACROPHAGES NR8383 SECRETOMES: EFFECT OF PROPROTEIN CONVERTASE 1/3 (PC1/3) DOWN-REGULATION.

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COMPARISON OF IMMEDIATE RENAL DYSFUNCTION IN SPLIT AND PARTIAL LIVER TRANSPLANTATION VERSUS FULL SIZE LIVER TRANSPLANTATION IN SHIRAZ TRANSPLANT CENTRE

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INSIGHTS INTO SIGNALLING PATHWAYS INVOLVED IN ALLERGIC IMMUNE RESPONSES THROUGH DIFFERENTIAL PROTEOME AND SECRETOME ANALYSIS OF DENDRITIC CELLS.

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A LABEL FREE APPROACH TO CHARACTERIZE THE INTERACTION OF HUMAN NATURAL KILLER CELLS WITH POLARIZED MACROPHAGES.

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IMMUNOMODULATORY MECHANISM OF A NOVEL POLYSACCHARIDE FROM LENTINULA EDODES

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THE ANALYSIS OF HUMAN SPERM PROTEOME BY MEANS OF POLYCLONAL ANTISPERM ANTIBODIES.

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IL-2 AND IL-15 SIGNALING NETWORKS: SIMILAR BUT NOT IDENTICAL

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STAIN FREE TOTAL PROTEIN QUANTITATION – A METHOD FOR GREATER RELIABILITY IN WESTERN BLOT LOADING CONTROLS

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OPTIMIZED ANTIBODY PANEL FOR MULTIPLEXED DETECTION OF AKT/MAPK PHOSPHORYLATION EVENTS BY WESTERN BLOTTING

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COOPERATION OF LIVER CELLS REVEALED BY CELL-SPECIFIC GENES

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LARGE-SCALE, LABEL-FREE QUANTITATIVE PROTEOMIC CHARACTERIZATION OF REGULATORY VERSUS CONVENTIONAL T LYMPHOCYTES ISOLATED FROM MOUSE

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PHOSPHOPROTEOMIC CHARACTERIZATION OF INFLUENZA A VIRUS INFECTED HUMAN PRIMARY MACROPHAGES

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INFLAMMATORY BOWEL DISEASES - A CLINICAL PROTEOMICS STUDY SEEKING TO IDENTIFY THE UNDERLYING BIOLOGICAL TRIGGERS.

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IMMUNE DYSREGULATION LEADS TO PATHOLOGICAL NEOVASCULARISATION IN SUBJECTS WITH RETINOPATHY OF PREMATURITY

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CHEMICAL PROTEOMICS HIGHLIGHTS PROTEIN KINASES INVOLVED IN MACROPHAGE DIFFERENTIATION AND FUNCTION

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A SILAC-PHOS STRATEGY TO DETERMINE THE PMA-PKCA DEPENDENT SIGNALING MAP

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GLOBAL-SCALE NITRATION IDENTIFICATION AND RELATIVE QUANTITATION USING STABLE ISOTOPE-CODED NITROTYROSINE INTERNAL STANDARDS

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TARGETTED MASS SPECTROMETRY METHODS FOR DETECTING OXIDATIVE POST-TRANSLATIONAL MODIFICATIONS.

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THE REDOX INTERACTOME OF PTEN: CELLULAR AND PROTEIN SPECIFIC CHANGES

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PROFILING THE CYSTEINE REDOX PROTEOME: CHEMICAL VS. METABOLIC LABELING

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MITOCHONDRIAL PROTEOME CHANGES IN ETHE1-DEFICIENT MICE:INDICATION OF METABOLIC IMBALANCE

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NEW FRONTIERS IN BACTERIAL INFECTION: THE ‘TARGET’ MITOCHONDRIA

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MITOCHONDRIA PROTEIN REPERTOIRE ADAPTATION IN ANIMAL MODELS OF AMIOTROPHIC LATERAL SCLEROSIS

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CHARACTERIZATION OF DRUG RESISTANCE BY NOVEL DATA INDEPENDENT ANALYSIS METHODS

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ANALYSIS OF THE THIOL REDOX PROTEOME OF HYPOXIC TREATED HUH7 CELLS AND POST-ISCHEMIC REPERFUSION MOUSE LIVER

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MONOCLONAL ANTIBODY AND RELATED PRODUCT CHARACTERIZATION UNDER NATIVE CONDITIONS USING A BENCHTOP EXACTIVE PLUS EMR MASS SPECTROMETER

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SIMPLIFIED MONOCLONAL ANTIBODY CHARACTERIZATION BY MIDDLE-DOWN/UP STRATEGY

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HIGH-MOLECULAR-MASS PROTEOMICS BY TWP-DIMENSIONAL GEL ELECTROPHORESIS WITH AGAROSE AND POLYACRYLAMIDE HYBRID GELS IN THE SECOND DIMENSION

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UNDERSTANDING THE STRUCTURAL DETERMINANTS FOR THE SELECTIVE INHIBITION OF SNAKE VENOM METALLOPEPTIDASES

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NEW WEAPONS AGAINST PERVASIVE FISH FRAUD: TOP DOWN PROTEOMICS AND A NEW HIGH THROUGHPUT LC-MS PLATFORM

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EVALUATION OF PROTEOLYTIC EXCISION ONLINE SAW-BIOSENSOR-MASS SPECTROMETRY TO MAP CONTACT SURFACES: APPLICATION TO VEGF-AVASTIN SYSTEM

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CLINICAL SCREENING OF HEMOGLOBINOPATHIES USING TOP DOWN MASS SPECTROMETRY

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A SYSTEMS BIOLOGY APPROACH UNRAVELS THE ROLE OF MIR-17-92 IN FINE-TUNING MYC-CENTERED REGULATORY NETWORKS TO SUSTAIN CANCER PROGRESSION

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DIGESTOMICS OF HUMAN MILK DURING LACTATION AND MASTITIS

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THE HUMAN KIDNEY SPECIFIC PROTEOME DEFINED BY TRANSCRIPTOMICS AND ANTIBODY-BASED PROFILING

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IDENTIFICATION OF ENRICHED PTM CROSSTALK MOTIFS FROM LARGE-SCALE EXPERIMENTAL DATASETS

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CONSERVED AND DIVERSE ASPECT OF PROTEOME PROFILE ACROSS MULTIPLE YEAST SPECIES

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SANXOT: A NOVEL FUNCTIONAL CLASS-SCORING ALGORITHM FOR SYSTEMS BIOLOGY AND ANALYSIS OF COORDINATED PROTEIN BEHAVIOR

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THE PROTEOMIC POINT OF VIEW ON HUMAN TEETH AND SALIVA SAMPLES

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AN EXTENSIVE PROTEOME PROFILING OF VISCERAL ADIPOSE TISSUES FOR UNDERSTANDING THE RELATION WITH EARLY PATHOGENESIS OF TYPE 2 DIABETES MELLITUS

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INVESTIGATION OF DRUG-INDUCED STEATOSIS IN HEPARG CELLS AFTER LONG-TERM TREATMENT WITH VALPROIC ACID USING LC/MS-BASED QUANTITATIVE PROTEOMICS

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DYNAMIC ASSESSMENT OF FIN REGENERATION IN ZEBRAFISH USING A PULSED SILAC APPROACH

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AN ENHANCED INDUSTRIAL-RELEVANT PRODUCTS PORTFOLIO FOR CORYNEBACTERIUM GLUTAMICUM BY MEANS OF PROTEOMIC APPROACHES.

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PROTEOMIC ANALYSIS OF THE ENZYMATIC EXTRACT OF THE FERULOYL ESTERASE PRODUCER PENICILLIUM CHRYSOGENUM B13

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PROTEOMIC ANALYSIS OF A MUTANT OF TRICHODERMA ARUNDINACEUM IMPAIRED IN TRICHOTHECENE BIOSYNTHESIS REVEALS A SYSTEMIC FUNCTION OF THESE COMPOUNDS IN FUNGAL PHYSIOLOGY

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SERUM PROTEOMICS IN MELANOMA BIOMARKER DISCOVERY

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AN INTEGRATED PROTEOMICS AND METABOLOMICS APPROACH FOR MOLECULAR CHARACTERIZATION OF ESOPHAGEAL SQUAMOUS CELL CARCINOMA

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UTILIZING A QUANTITATIVE PROTEOMIC APPROACH TO DISCOVER NOVEL SUBSTRATES OF PROPROTEIN CONVERTASE 7

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PROTEOMICS AND BIOMARKERS IN OSTEOARTHRITIS

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ITRAQ-BASED PROTEOME PROFILING OF THREE HUMAN LIVER-DERIVED CELL LINES: COMPARISON WITH PRIMARY HEPATOCTYES AS MODELS FOR DRUG SAFETY ASSESSMENT

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THE METACASPASE MCA1P HAS A DUAL ROLE IN FARNESOL-INDUCED APOPTOSIS IN CANDIDA ALBICANS

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A SENTINEL PROTEIN ASSAY FOR THE QUANTIFICATION OF CELLULAR PROCESS ACTIVITIES USING PRM AND DIA

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ABSOLUTE QUANTIFICATION OF PROTEINS AND PROTEIN MODIFICATIONS ON THE SINGLE-CELL LEVEL BY COMBINING MASS CYTOMETRY AND TARGETED PROTEOMICS

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SWATH-MS FOR QUANTITATIVE PROTEOMICS OF NUCLEIC ACID BINDING AND REGULATORY PROTEINS

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WEAK LINEAR MOTIF-MEDIATED INTERACTIONS CONTRIBUTE TO THE REARRANGEMENT OF MODULAR ARCHITECTURE IN COMPLEX PROTEIN INTERACTION NETWORKS

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INTEGRATIVE MAPPING OF THE ZEBRAFISH EMBRYO PROTEOME AND TRANSCRIPTOME

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GENE ESSENTIALITY ON MODEL ORGANISM EXPLAINS CLINICAL SEVERITY OF HUMAN GENETIC DISORDERS

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USING AN ITRAQ APPROACH TO INVESTIGATE THE EFFECT OF CIGARETTE SMOKE EXPOSURE IN A 90-DAYS INHALATION STUDY FOLLOWED BY 42-DAYS RECOVERY PERIOD ON SPRAGUE-DAWLEY RATS LUNG TISSUE.

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DYNAMICS PERSONAL OMICS PROFILES DURING PERIODS OF HEALTH, DISEASE, WEIGHT GAIN AND LOSS

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THE GLOBAL LANDSCAPE OF HEMATOPOIETIC STEM CELLS AND THEIR IMMEDIATE PROGENY

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COMMUNITY PROTEOMIC ANALYSIS OF ARCHAEAL COMMUNITY OF CELLULOSE-ENRICHED MUD AND WATER SLURRY FROM MT. MAKILING MUD SPRING, LOS BAÑOS, PHILIPPINES

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STRUCTURE-BASED PREDICTION AND BIOINFORMATICS ANALYSIS OF THE THIAMIN-DEPENDENT PROTEOME: IMPLICATIONS FOR THE THIAMIN DEFICIENCY STATES AND MODELS.

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TARGET IDENTIFICATION OF NON-TAGGED SMALL MOLECULES WITH DARTS AND LC/MS/MS

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PROTEOMIC COMPARATIVE STUDY OF SMOOTH MUSCULE CELLS ISOLATED FROM SMALL PULMONARY AND SYSTEMIC ARTERIES

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IDENTIFICATION OF SMALL OPEN READING FRAMES WITH HIGH CODING POTENTIAL IN MOSS PHYSCOMITRELLA PATENS

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ADVANCED TI4+-IMAC (PHOSPHO)PROTEOMICS TO IDENTIFY NOVEL MELANOMA COMPANION DRUG TARGETS AND UNCOVER PHOSPHORYLATION DYNAMICS AND PATHWAY DEPENDENCE IN SENESCENCE SIGNALING

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DISCOVERY OF SERUM BIOMARKERS FOR PREDICTION OF RESPONSE TO ADALIMUMAB IN RHEUMATOID ARTHRITIS TREATMENT

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DIFFERENTIALLY EXPRESSED PROTEINS IN PATIENTS WITH SYSTEMIC LUPUS ERYTHEMATOSUS

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

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POTENTIAL PROTEOMIC BIOMARKERS ASSOCIATED TO MUCOSAL HEALING IN CROHN'S DISEASE

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PROTEOMIC ANALYSIS OF CLUBFEET

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MOLECULAR PROFILING OF PERIPHERAL BLOOD MONONUCLEAR CELLS (PBMCS) FOR THE IDENTIFICATION OF CELLULAR RESPONSES TO DEXAMETHASONE

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PROTEOMIC ANALYSIS USING NUCLEID ACID PROGRAMMABLE PROTEIN ARRAYS FOR SERUM AUTOANTIBODY PROFILING IN RHEUMATIC DISEASES

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PROFILING OF CARTILAGE-CHARACTERISTIC PROTEINS TO IDENTIFY A NOVEL PANEL OF OSTEOARTHRITIS BIOMARKER CANDIDATES.

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SILAC-BASED PROTEOMIC ANALYSIS REVEALED DIFFERENTIALLY EXTRACELLULAR PROTEIN PROFILES OF OSTEOARTHRITIC AND NORMAL MESENCHYMAL STEM CELLS UNDERGOING CHONDROGENESIS.

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SERUM PEPTIDE PROFILES OF OSTEOARTHRITIS AND RHEUMATIC DISORDERS BY MALDI-TOF MASS SPECTROMETRY

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CHARACTERIZATIONS OF HEPARIN-BINDING PROTEINS IN HUMAN URINE AND IDENTIFICATION OF "L-X(2,3)-A-X(0,1)-L" AS A NOVEL HEPARIN-BINDING MOTIF.

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PROTEOMICS REVEALED AN IMPORTANT ROLE OF LAMIN A/C IN KIDNEY STONE DISEASE.

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DYNAMIC PROFILING OF CHROMATIN PROTEOME AT ENHANCERS OF INFLAMMATORY GENES

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QUANTITATIVE PROTEOMICS (ITRAQ) REVEALS PUTATIVE BIOMARKERS IN PRE-RADIOLOGICAL OSTEOARTHRITIS

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SECRETED PEPTIDOME OF HUMAN CARTILAGE: A NOVEL SOURCE FOR EARLY OA BIOMARKER DISCOVERY

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EVALUATION OF ADHERENCE TO "GLOBAL INITIATIVE FOR CHRONIC OBSTRUCTIVE LUNG DISEASE" GUIDELINES FOR MANAGEMENT OF COPD EXACERBATION IN FAGHIHI HOSPITAL, SHIRAZ, IRAN 2012-13

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CHARACTERIZATION OF THE HOST AND MICROBIOTA PROTEOME IN PEDIATRIC IBD

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ITRAQ APPROACH TO INVESTIGATE THE IMPACT OF CIGARETTE SMOKE, SMOKING CESSATION AND SWITCHING TO A PROTOTYPIC MODIFIED RISK TOBACCO PRODUCT ON THE LUNG PROTEOME OF C57BL/6 MICE

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THE EFFECT OF HMGB1 A BOX ON ACUTE LUNG INJURY

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MOLECULAR PORTRAITS OF SYSTEMIC LUPUS ERYTHEMATOSUS USING AFFINITY PROTEOMICS FOR IMPROVED DIAGNOSIS BASED ON A BLOOD TEST

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A MECHANISTIC STUDY USING 2D-PAGE PROTEOMIC APPROACH TO INVESTIGATE THE EFFECT OF CIGARETTE SMOKE-INDUCED COPD, CESSATION AND SWITCHING TO MODIFIED RISK TOBACCO PRODUCT IN THE LUNGS OF C57BL/6 MICE

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PROTEOMIC ANALYSIS OF ULCERATIVE COLITIS (UC): REDUCED MUCOSAL LEVEL OF INSOLUBLE KERATIN 8 PROTEOFORMS IN ACTIVE UC RELATIVE TO PROXIMAL UNINVOLVED COLONIC MUCOSA.

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ON THE WAY TOWARD A THERAPEUTIC DECISION-MAKING TOOL FOR A BETTER MANAGEMENT OF PATIENTS WITH RHEUMATOID ARTHRITIS

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SHARED IMMUNOLOGICAL TARGETS IN THE LUNGS AND JOINTS OF PATIENTS WITH RHEUMATOID ARTHRITIS: IDENTIFICATION AND VALIDATION.

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NOVEL PROTOCOL FOR PREPARATION AND NLC-MS/MS CHARACTERIZATION OF PROTEOGLYCAN LINKAGE REGION GLYCOPEPTIDES OF HUMAN PLASMA, URINE AND CEREBROSPINAL FLUID SAMPLES

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EVALUATION OF SERUM CARBOHYDRATE-DEFICIENT TRANSFERRIN BY HPLC AND MALDI-TOF MS

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A MULTIPLE REACTION MONITORING METHOD TO SPECIFICALLY CHARACTERIZE AND RELATIVELY QUANTIFY THE P-GLYCANS OF THE POTENTIAL BIOLOGIC LUBRICIN

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USE OF HYDRAZINONICOTINIC ACID AS DERIVATIZATION REAGENT FOR ENHANCED DETECTION OF OLIGOSACCHARIDES BY MALDI-MS

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N-GLYCOMIC AND N-GLYCOPROTEOMIC ANALYSIS OF THREE SNAKE VENOMS

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CAPILLARY ELECTROPHORESIS FOR MONITORING GLYCOPROTEIN CHANGES ASSOCIATED TO VASCULAR DISEASES AND PROSTATE CANCER

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PREPARATION OF A NOVEL SENSITIVITY LECTIN SUSPENSION MICROARRAY SYSTEM AND APPLICATIONS TO SERUM PEPTIDOME GLYCAN PROFILING

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N-LINKED GLYCOPROTEOMIC ANALYSIS OF ESOPHAGEAL CELLS STIMULATED BY PRP-INFLAMMATORY CYTOKINES

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GLYCOPATTERNS OF HUMAN SALIVARY GLYCOPROTEINS AND THEIR ROLES AGAINST INFLUENZA A VIRUS

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CARBOHYDRATES MODIFICATIONS IN GRASS POLLEN GROUP 13 ALLERGENS

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GLYCAN CHANGES OF PLASMA TRANSFERRIN IN ELASTASE-INDUCED EMPHYSEMA AND LPS-INDUCED ACUTE LUNG INJURY MICE MODELS

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GRIP-GUI: GRAPHIC USER INTERFACE FOR GLYCOPEPTIDE REVEAL & INTERPRETATION PLATFORM.

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THE SEPARATION AND IDENTIFICATION OF GLYCANS USING AN ULTRA HIGH RESOLUTION COLUMN AND AN ULTRA HIGH RESOLUTION MASS SPECTROMETER

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GLYCOFOREST - DISTILLING GLYCOMIC MS/MS DATA

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INFORMATICS SUPPORT FOR ISOMERIC SEPARATION AND THE STRUCTURAL IDENTIFICATION OF LABELED N-GLYCANS FROM PROTEINS

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IMPROVED GLYCOPEPTIDE ANALYSIS USING ACETONITRILE ENRICHED SHEATH GAS AND OXONIUM ION DEPENDENT ETD

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DEVELOPMENT AND APPLICATION OF A METHOD FOR THE GLYCOPEPTIDE-BASED SITE-SPECIFIC GLYCOMIC ANALYSIS

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HIGH-SENSITIVE DIFFERENTIAL GLYCAN PROFILING OF SERUM MUC1 TOWARD THE DEVELOPMENT OF A GLYCP-DIAGNOSTIC AGENT FOR CHOLANGIOCARCINOMA

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COMPREHENSIVE IDENTIFICATION OF GLYCOPROTEINS CARRYING LEWIS X AND SITE-SPECIFIC GLYCAN ALTERATION IN FUT9 KNOCKOUT MICE

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ASSIGNMENT OF SACCHARIDE IDENTITIES THROUGH ANALYSIS OF OXONIUM ION FRAGMENTATION PATHWAYS IN LC-MS/MS OF GLYCOPEPTIDES

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A GLOBAL BOTTOM-UP STRATEGY FOR THE ANALYSIS OF GLYCOPROTEINS

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GLYCOPROTEOMIC CHARACTERIZATION OF TRICHOMONAS VAGINALIS

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LIQUID CHROMATOGRAPHY AND MASS SPECTROMETRY FOR COMPARING CLINICAL ISOLATES OF MRSA AND MSSA

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DISCOVERY AND VALIDATION OF BIOMARKERS TO GUIDE CLINICAL MANAGEMENT OF PNEUMONIA IN AFRICAN CHILDREN

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APPLICATIONS OF PROTEOMIC METHODS IN SEVERE SEPSIS RESEARCH

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ANTIMICROBIAL ACTIVITIES OF SEVEN ESSENTIAL OILS FROM IRANIAN AROMATIC PLANTS AGAINST COMMON CAUSES OF ORAL INFECTIONS

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HYDATID CYST DISEASE OF THE SPINE: A CASE REPORT

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CEREBROSPINAL FLUID BIOMARKER CANDIDATES ASSOCIATED WITH HUMAN WNV NEUROINVASIVE DISEASE

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DEVELOPMENT OF A RAPID MICROBIAL PREPARATION SYSTEM FROM A BLOOD CULTURE BOTTLE USING CATIONIC PARTICLES FOR BACTERIAL IDENTIFICATION WITH MATRIX-ASSISTED LASER DESORPTION IONIZATION TIME-OF-FLIGHT MASS SPECTROMETRY.

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QUANTIFICATION OF BEXSERO® OMV PROTEINS BY A LABEL FREE LC MS/MS APPROACH

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IDENTIFICATION OF NATURALLY PROCESSED MHC CLASS I-RESTRICTED HIV EPITOPES PRESENTED BY HUMAN HIV-INFECTED CELLS

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WHY DATABASE MATTERS: IMPACT OF SEQUENCE DATABASES ON METAPROTEOME ANALYSIS OF A MOCK MICROBIAL MIXTURE

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WHOLE PROTEOME AND MAIN POST-TRANSLATIONAL MODIFICATIONS (PTMS) ANALYSIS OF K. PNEUMONIAE CLINICAL ISOLATES

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IDENTIFICATION OF API88 BINDING PARTNERS IN ESCHERICHIA COLI USING PHOTOAFFINITY-CROSSLINK STRATEGIES AND LABEL FREE QUANTIFICATION

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AFFINITY PROTEOMICS REVEALS ELEVATED MUSCLE PROTEINS IN PLASMA OF CHILDREN WITH CEREBRAL MALARIA

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COMPARATIVE 2D-DIGE ANALYSIS OF DEPLETED SERUM SAMPLES OF PATIENTS WITH 2009 INFLUENZA A (H1N1).

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A COMPARISON OF SEVERE AND NON-SEVERE VIVAX MALARIA PATIENTS FOR THE IDENTIFICATION OF DISEASE MONITORING MARKERS USING QUANTITATIVE PROTEOMICS

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THE STAPHYLOCOCCUS AUREUS HG001 PROTEOTYPE RESOURCE

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SURFACOME CHANGES OF METHICILLIN-RESISTANT STAPHYLOCOCCUS AUREUS IN BACTERIAL GROWTH UNDERGOING USNIC TREATMENT BY PROTEOMIC APPROACH

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QUANTITATIVE ANALYSIS OF THE SALIVARY PROTEOME IN HUMAN PAPILLOMAVIRUS (HPV) PATIENTS

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A HUMAN PROTEOME MICROARRAY IDENTIFIES THAT THE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K (HNRNP K) RECOGNIZES THE 5' TERMINAL SEQUENCE OF THE HEPATITIS C VIRUS RNA

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COMPARATIVE SALIVA PROTEOME OF HEPATITIS B AND C-INFECTED SUBJECTS

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A NOVEL STRATEGY FOR TYPING MYCOPLASMA PNEUMONIAE USING MALDI-TOF MS-CLINPROTOOLS

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LABEL-FREE PROTEOMIC ANALYSIS OF ENVIRONMENTAL ACIDIFICATION-INFLUENCED STREPTOCOCCUS PYOGENES SECRETOME REVEALS A NOVEL ACID-INDUCED PROTEIN HISTIDINE TRIAD PROTEIN A (HTPA) INVOLVED IN NECROTIZING FASCIITIS

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THIORIDAZINE INDUCES ALTERATIONS IN THE MYCOBACTERIUM TUBERCULOSIS CELL WALL PERMEABILITY BARRIER

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DIFFERENTIAL PROTEOMICS OF ANTIBIOTIC RESISTANCE PROFILING OF ESCHERICHIA COLI FROM CLINICAL SOURCE

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SEROLOGIC PROFILING TO THE CANDIDA ALBICANS INTRACELLULAR PROTEOME FOR THE DIAGNOSIS OF INVASIVE CANDIDIASIS IN NON-NEUTROPENIC PATIENTS

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COMBINING NEUCODE WITH LYSC AND LYSN DIGESTION FOR DE NOVO SEQUENCING APPLICATIONS

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FAST AND EFFICIENT CHARACTERIZATION OF BRACHYSPIRA´S PROTEOMA BY ONE-SHOT LC/MS ANALYSIS

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SEMIQUANTITATIVE PROTEOMIC ANALYSIS OF THE INTERACTION BETWEEN CANDIDA ALBICANS AND ACINETOBACTER BAUMANNII

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SOLUBLE HLA ISOTYPES AND PEPTIDOME ASSOCIATED WITH HIV PATHOGENESIS

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SUBCELLULAR FRACTIONATION AND SEVERAL GROWING CONDITIONS TO INCREASE PROTEOME COVERAGE IN CANDIDA ALBICANS PEPTIDEATLAS

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EFFECT OF THE GLOBAL REGULATOR CRC IN VESICLE AND VESICLE-FREE EXTRACELLULAR PROTEOME OF PSEUDOMONAS AERUGINOSA

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A COMPREHENSIVE PROTEOMIC STUDY OF CANDIDA ALBICANS SURFACE AFTER INTERACTION WITH HUMAN SERUM

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UNRAVELLING THE PATHOGENESIS PROCESSES OF STAPHYLOCOCCUS PSEUDINTERMEDIUS TOWARD NEW THERAPEUTIC STRATEGIES

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PROTEOMIC CHARACTERIZATION OF HUMAN PROINFLAMMATORY M1 AND ANTI-INFLAMMATORY M2 MACROPHAGES AND THEIR RESPONSE TO CANDIDA ALBICANS.

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HIGH-ACCURACY, LABEL-FREE QUANTITATION OF HUMAN PLASMA PROTEINS FOR ESTIMATION OF BLOOD-DERIVED PROTEINS INCLUDED IN CLINICAL TISSUE SPECIMENS

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COMPARISON OF METHODS FOR THE QUANTIFICATION OF STABLE ISOTOPE LABELLED PROTEIN AND PEPTIDE STANDARDS FOR QUANTITATIVE PROTEOMICS

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COMPARISON OF DESALTING METHODS FOR PROTEOMIC ANALYSIS OF WHOLE SALIVA AS AN EXAMPLE FOR HUMAN BIOFLUIDS

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PROTEOSUITE - STANDARD SUPPORTING SOFTWARE FOR QUANTITATIVE ANALYSIS

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EVALUATION OF STAIN-FREE SDS-PAGE FOR GELC-MS APPLICATIONS

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ELIMINATING WESTERN BLOT VARIABILITY WITH SALLY SUE

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INTEGRATED WORKFLOW FOR PROTEIN PURIFICATION/FRACTIONATION BY NGC SYSTEM AND VISUALIZATION BY STAIN-FREE SDS-PAGE

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SYSTEMATIC COMPARISON OF SDS-PAGE AND HIGH-PH RPLC FRACTIONATION METHODS

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A SIMPLE PROTOCOL TO ROUTINELY ASSESS THE UNIFORMITY OF PROTEOMICS ANALYSES

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NORMALIZATION OF CAPTURE PROBE CONCENTRATION USING A FLUORESCENT CALIBRANT IMPROVES ANTIBODY MICROARRAY REPRODUCIBILITY

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COMPARATIVE PROTEOMIC ANALYSIS OF AQUEOUS HUMOR FROM HUMAN EYES AFTER CATARACT SURGERY AND FROM POST-MORTEM EYES WITHOUT OPHTHALMIC DISEASES

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THE NASAL FLUID PROTEOME IN HEALTHY CHILDREN

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QUICK AND CLEAN PEPTIDE MAPPING USING ULTRAFAST LC-MS SAMPLE DELIVERY SYSTEM

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PROCESS – PROTEOMICS DATA COLLECTION, SOFTWARE AND STANDARDS TO SUPPORT OPEN ACCESS AND LONG TERM MANAGEMENT OF DATA.

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A HIGH-THROUGHPUT AND REPRODUCIBLE WORKFLOW TO PREPARE HUMAN PLASMA SAMPLES FOR PROTEOMIC ANALYSIS

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Xiaoyue Jiang, Daniel Lopez Ferrer, Andreas Hühmer
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THE VALUE OF SUBCELLULAR FRACTIONATION IN PROTEOMIC STUDIES

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COMBINED PROTEOMIC AND METABOLOMIC ANALYSIS APPROACHES TO INVESTIGATE THE MODIFICATION IN THE PROTEOME AND METABOLOME OF IN VITRO MODELS TREATED WITH GOLD NANOPARTICLES (AUNPS)

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VARIABILITY OF 15N METABOLIC LABELING-BASED PROTEOMIC WORKFLOWS IN MOUSE SPECIMENS.

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EVALUATION OF MASS SPECTROMETER PERFORMANCES USED IN LARGE-SCALE PROTEOMICS

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SUCCESS VIA STANDARDISATION – BRINGING RELIABILITY TO CLINICAL PROTEOMIC BIOMARKER DISCOVERY

Ben Chaffey, Will Dracup, David Bramwell
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CONFIRMING THE REMARKABLE IMPROVEMENT IN LC-MS SENSITIVITY FOR PROTEOMICS BESTOWED BY DIMETHYLSULFOXIDE AS A LC SOLVENT ADDITIVE

Andrew Thompson, Amandeep Bhamra, Marcella Widya, Sarah Hanrahan
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MZQ LIBRARY -- AN OPEN SOURCE JAVA LIBRARY FOR SUPPORTING QUANTITATIVE PROTEOMICS STANDARD

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MASS SPECTROMETRY-BASED PROTEOMICS AS TOOL FOR THE QUALITY CONTROL OF INTRAVENOUS IMMUNOGLOBULIN.

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THE SEARCH FOR HEART SECRETORY PROTEINS AS HEART DISEASE BIOMARKERS

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HIGH-THROUGHPUT LC-MS MRM ANALYSIS OF CALCYCLIN IN PRE-ECLAMPSIA PATIENT SERA

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URINARY QUANTITATIVE PROTEOMIC REVEALS NEPHRIN 1 AS A MARKER OF SALT SENSITIVE HYPERTENSION IN HUMANS

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DIFFERENTIAL PROTEOMIC SIGNATURE IN CHRONIC CORONARY ARTERY DISEASE PATIENTS WITH AND WITHOUT A RECURRENT ACUTE EVENT

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ELUCIDATING THE RELATIONSHIP BETWEEN CALCIFIC AORTIC STENOSIS AND ATHEROSCLEROSIS: A COMPREHENSIVE PROTEOMIC STUDY IN AORTIC VALVE TISSUE

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PROTEOMIC CHARACTERIZATION OF HUMAN CORONARY THROMBUS IN PATIENTS WITH ST-SEGMENT ELEVATION ACUTE MYOCARDIAL INFARCTION: RIGHT TO THE EPICENTRE OF THE PATHOGENESIS

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ITRAQ: A STRATEGY FOR BIOMARKER PROFILING IN AORTIC STENOSIS DISEASE

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A CHARACTERISTIC PROTEOMIC AND METABOLOMIC PROFILE IN BLOOD PLASMA WITH UTILITY IN PREDICTING EVOLUTION OF PATIENTS WITH ARTERIAL HYPERTENSION TO ALBUMINURIA

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PROTEIN CONSTITUENCY OF LIPOPROTEINS DETERMINED BY RECONSTRUCTION OF SIZE FRACTION PROFILES COMBINED WITH SHOTGUN PROTEOMICS

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SIMPLIFICATION STRATEGIES FOR THE CARDIAC PROTEOME

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EXPLORING THE DYNAMICS OF THE ZEBRAFISH HEART PROTEOME

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SEPSIS ASSOCIATED GLYCOPROTEINS IN PLASMA

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VINNCARDIO: HIGH-THROUGHPUT SCREENING FOR PLASMA BIOMARKERS IN CARDIOVASCULAR DISEASE

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PROTEOMIC ANALYSIS OF LEFT VENTRICULAR TISSUES IN DILATED CARDIOMYOPATHY

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IDENTIFICATION OF A URINE MOLECULAR FINGERPRINT WHICH RESPONDS TO ALBUMINURIA CONDITION AND PROGRESSION IN HYPERTENSIVE PATIENTS CHRONICALLY RAAS SUPPRESSED

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MOLECULAR ALTERATIONS IN HUMAN URINE REVEAL ATHEROSCLEROSIS DEVELOPMENT AND CARDIOVASCULAR EVENT AT ONSET AND FOLLOW-UP.

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THE DIRECT EFFECT OF CORTISOL ON CA2+ REGULATORY PROTEINS IN THE HEART

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MULTIPLE PTMS PLAY A ROLE IN THE REGULATION OF PLATELETS IN HEALTH AND DISEASE

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ALTERED PHOSPHORYLATION PROFILE OF SCOTT SYNDROME PLATELETS REVEALED BY QUANTITATIVE PHOSPHOPROTEOMICS

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THE REGENERATIVE ABILITIES OF RESIDENT CARDIAC STEM CELLS DEPENDS ON SECRETED PARACRINE FACTORS

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CHARACTERIZING QUALITATIVE AND QUANTITATIVE GLOBAL CHANGES IN THE AGING HEART USING PSMART, A NOVEL ACQUISITION METHOD

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COMBINING MULTIPLE PROTEOMIC APPROACHES IN THE STUDY OF ATHEROSCLEROSIS: A NOVEL MECHANISM OF PLATELET-MONOCYTE INTERACTIONS

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THE ROLE OF BLOOD INTENSITY IN EXPRESSION AND GLYCOSYLATION OF LDLR IN ENDOTHELIAL CELLS

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SYSTEMATIC CHARACTERIZATION OF HUMAN PLATELETS IN CARDIOVASCULAR DISORDERS BY QUANTITATIVE PROTEOMICS

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ENDOMYOCARDIAL PROTEIN PROFILING OF DCM PATIENTS WITH DIFFERENT RESPONSE TO IMMUNOADSORPTION THERAPY

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PROFILING OF PLATELET PROTEIN IN CIRCULATION OF DIABETIC PATIENTS: IN VITRO EFFECT OF ISOLATED PLATELET-SPECIFIC PROTEIN MIXTURE ON ENDOTHELIAL CELLS

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A 2D-DIGE-BASED PROTEOMIC ANALYSIS REVEALS DIFFERENCES IN THE PLATELET RELEASATE DEPENDING ON THE PLATELET STIMULUS

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ESTABLISHMENT OF PROTEIN PROFILE-BASED STAGE CLASSIFICATION FOR AORTIC ANEURYSM

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INTEGRATED PROTEOMIC AND METABOLOMIC ANALYSIS REVEALS THE ROLE OF DYSSYNCHRONY IN METABOLIC REMODELING IN TACHYPACING-INDUCED HEART FAILURE

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MRM ASSAY DEVELOPMENT WITH APPLICATION TO BIOBANK SAMPLES FROM PATIENTS WITH ACUTE MYOCARDIAL INFARCTION

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THE COMPARATIVE SECRETOME OF HUMAN HEPATIC HUH7 CELLS IN THE PRESENCE OF B-ESTRADIOL AND ITS AFFECT ON THE SECRETED PCSK9 INTERACTOME

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QUANTITATIVE PROTEOME ANALYSIS OF SECTIONS OF FORMALIN FIXED-PARAFFIN EMBEDDED ARTERIAL SAMPLES FROM PATIENTS WITH TYPE 2 DIABETES: METFORMIN TREATMENT NORMALIZES ARTERIAL MATRIX COMPOSITION IN TYPE 2 DIABETES

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CARDIAC PROTEOMIC PROFILING IDENTIFIES NOVEL PLASMA MEMBRANE PROTEINS THAT REGULATE CARDIAC FUNCTION

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EXPLORING PROTEOMICS TOOLBOX TOWARDS HUMAN CARDIAC STEM CELLS CHARACTERIZATION

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QUANTITATIVE PROTEIN ANALYSIS OF ENDOTHELIAL PROGENITOR CELLS IN ATHEROSCLEROSIS

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PROTEOMIC PROFILING OF THE HUMAN VENOUS EXTRACELLULAR MATRIX REVEALS A ROLE FOR MAST CELL PROTEASES IN THE PATHOGENESIS OF VARICOSE VEINS

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PREDICTIVE BIOMARKERS FOR INCREASED RISK OF ARRHYTHMIC DEATH IN THE PREDICTION OF ARRHYTHMIC EVENTS IDENTIFIED BY LARGE-SCALE PLASMA PROTEOMICS PROFILING

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INNATE AND ADAPTIVE IMMUNE SYSTEM ALTERATIONS IN PRE-MANIFEST STAGES OF TRANSGENIC PORCINE MODEL OF HUNTINGTON'S DISEASE

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ALTERATIONS OF PROTEIN COMPOSITION ALONG THE ROSTRP-CAUDAL AXIS AFTER SPINAL CORD INJURY: PROTEOMIC ANALYSES

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DIFFERENTIAL PROTEOMICS OF HUMAN CSF FROM TRAUMATIC SPINAL CORD INJURY PATIENTS REVEALS PERTURBED MOLECULAR PATHWAYS IN SECONDARY INJURY PHASE

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QUANTITATIVE PROTEOMICS OF HUMAN LRRK2 (R1441C) DROSOPHILA MODEL OF PARKINSON DISEASE

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INDUCTION MECHANISM OF NEURAL DIFFERENTIATION OF HUMAN BONE MARROW MESENCHYMAL STEM CELLS BY ELECTROMAGNETIC FIELD

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A PROTEOMICS PERSPECTIVE ON NEURODEGENERATION IN AMYOTROPHIC LATERAL SCLEROSIS

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USE OF MULTIPLE REACTION MONITORING LC-MS FOR THE VERIFICATION OF PARKINSON'S DISEASE PROTEIN SIGNATURES

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RELATION BETWEEN CERVICAL CORD LESIONS AND DISK HERNIATION IN THE PATIENTS WITH MULTIPLE SCLEROSIS

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EPILEPSY IN THE PATIENT WITH MYASTHENIA GRAVIS, A CASE REPORT AND REVIEW OF THE LITERATURES

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PLASMA LEVELS OF IL-17 AND IL-23 IN THE PATIENTS WITH MULTIPLE SCLEROSIS

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ASSOCIATION OF PEROXISOME PROLIFERATORS-ACTIVATED RECEPTOR-GAMMA (PPAR T) ON PROGNOSIS OF MULTIPLE SCLEROSIS

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THE MONTH OF BIRTH AND THE INCIDENCE OF MULTIPLE SCLEROSIS IN THE IRANIAN POPULATION

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THE EFFECT OF FREE TESTOSTERONE ON COURSE, SEVERITY, DISEASE ACTIVITY AND DISABILITY IN MULTIPLE SCLEROSIS

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NEUROBRUCELLOSIS IN A PATIENT WITH MULTIPLE SCLEROSIS; A CASE REPORT

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PLASMA PROTEIN MARKERS IN MAJOR DEPRESSIVE DISORDER TREATED WITH ANTIDEPRESSANTS

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LOW-DOSE TOTAL BODY IRRADIATION IN NEONATAL MICE CAUSES LONG-TERM IMPAIRED COGNITIVE PERFORMANCE ASSOCIATED WITH CHANGES IN CREB / MIR-132-MEDIATED SYNAPTIC PLASTICITY

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CLINICAL WORKFLOW FOR ANALYSIS OF HUMAN CSF PROTEINS USING HIGH RESOLUTION MASS SPECTROMETRY PARALLEL REACTION MONITORING MULTIPLEX ASSAYS

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VALIDATION OF PROGNOSTIC BIOMARKERS FOR CONVERSION TO MULTIPLE SCLEROSIS IN PATIENTS WITH CLINICALLY ISOLATED SYNDROME

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STUDY OF THE EXPRESSION OF NUCLEOSIDE AND NUCLEOTIDE RECEPTORS IN MOUSE SPINAL CORD THROUGH MULTIPLE REACTION MONITORING.

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IDENTIFICATION OF POTENTIAL BIOMARKERS OF ISCHEMIC STROKE BY INTEGRATING 2D-DIGE AND LABEL FREE-MS/MS

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SEARCH FOR PERIPHERAL BIOMARKERS IN PATIENTS AFFECTED BY ACUTELY PSYCHOTIC BIPOLAR DISORDER: A PROTEOMIC APPROACH

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COMPARATIVE PROTEOMIC ANALYSIS OF DIFFERENT FRAGILE X SYNDROME CELL LINES

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PROTEOMIC CHARACTERIZATION OF CLUSTER SPOTS DOWN REGULATED IN PARKINSON DISEASE.

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DOWN REGULATION OF PLASMA APOLIPOPROTEIN A-IV IN SUICIDAL ATTEMPTERS: A MASS SPECTROMETRY BASED APPROACH

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AMYLOID-INDUCED TAU PHOSPHORYLATION AT MOUSE NEURONAL SYNAPSES ANALYZED BY QUANTITATIVE PHOSPHOPROTEOMICS

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CHARACTERIZING THE UNIQUE PROTEIN COMPLEXES FORMED BY PSD95 AND SAP102 IN THE POST-SYNAPTIC DENSITY OF THE BRAIN BY IP-LC-MS/MS

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KRABBE DISEASE: FIRST INVESTIGATION AT THE PROTEOMIC LEVEL

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QUANTITATIVE MASS SPECTROMETRY BASED COMPARISON OF THE VENTRICULAR AND LUMBAR CEREBROSPINAL FLUID (CSF) PROTEOME

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PPROD1 DOWNREGULATION: A MAJOR DEPRESSION BIOMARKER THAT REDUCES HIPPOCAMPAL NEUROPROTECTION THROUGH DECREASING AKT-NF¦ÊB PATHWAY ACTIVITY

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APPLICATION OF TRANSLATIONAL PROFILING METHOD FOR THE MOLECULAR CHARACTERIZATION OF LPS-STIMULATED BV2 MICROGLIA

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A PROTEOMICS INVESTIGATION TO UNDERSTAND THE ROLE OF SUBVENTRICULAR ZONE IN THE SURVIVAL OF GLIOBLASTOMA PATIENTS

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IDENTIFICATION OF ALTERED METABOLIC PROTEINS IN DISTINCT BRAIN REGIONS OF SCHIZOPHRENIA

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PHARMACO-PROTEOMIC ANALYSIS OF IPS-04001 IN ALZHEIMER'S DISEASE MOUSE MODEL

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EXPLORATIVE CLINICAL PROTEOMICS IN NEURODEGENERATIVE DISORDERS

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THE PROTEOMIC LANDSCAPE OF THE SUPRACHIASMATIC NUCLEUS CLOCK REVEALS LARGE-SCALE COORDINATION OF KEY BIOLOGICAL PROCESSES

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ANTIGEN AND PEPTIDE MICROARRAYS REVEAL AUTOANTIBODY TARGETS IN NARCOLEPSY

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PHYSICAL EXERCISE MODULATES HIPPOCAMPAL PROTEIN EXPRESSION WITH NEUROPROTECTIVE EFFECTS IN SENESCENCE-ACCELERATED SAMP8 MOUSE MODEL.

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EFFECT OF VITAMIN D ON MULTIPLE SCLEROSIS: NEUROCOGNITIVE IMPAIRMENT IMPLICATIONS

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A CHEMICAL PROTEOIMCS FOR SEARCHING DIAGNOSTIC MARKERS OF PARKINSON FS DISEASE.

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STUDY ON THE TREATMENT MECHANISM OF VITAMIN D IN MS/EAE

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QUANTITATIVE PROTEOMICS TO STUDY NEUROMUSCULAR DISORDERS

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PROTEOMIC ANALYSIS OF THE FRONTAL CORTEX AND THE HIPPOCAMPUS MITOCHONDRIA IN THE ANIMAL MODELS OF DEPRESSION

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APPLYING MASS SPECTROMETRY-BASED QUALITATIVE PROTEOMICS TO HUMAN AMYGDALOID COMPLEX

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QUANTITATIVE MASS SPECTROMETRY IDENTIFIES AGE-DEPENDENT CONTROL OF PROTEIN TRANSLATION BY FRAGILE X MENTAL RETARDATION PROTEIN

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HIPPOCAMPAL PROTEIN CONCENTRATION GRADIENTS – THE KEY TO AUTOIMMUNITY IN ALZHEIMER'S DISEASE?

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CROSS-LINKED SITES MS ASSIGNMENT IN A PHOTOCHEMICAL INDUCED-COVALENT AB DIMER

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VITAMIN D BINDING PROTEIN ISOFORMS AND APOLIPOPROTEIN E IN CEREBROSPINAL FLUID AS EARLY PROGNOSTIC BIOMARKERS OF DISEASE AGGRESSIVENESS IN MULTIPLE SCLEROSIS

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THE HUMAN TORSIN A IN DROSOPHILA ACTIVATES THE UPR AND INCREASES SUSCEPTIBILITY TO OXIDATIVE STRESS

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INVESTIGATING THE ROLE OF LG72 IN SCHIZOPHRENIA BY 2D-GEL ELECTROPHORESIS AND 15N METABOLIC LABELING

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DETECTION AND QUANTIFICATION OF TAU PROTEOFORMS IN THE CSF OF ALZHEIMER'S DISEASE PATIENTS USING HIGH RESOLUTION TARGETED MASS SPECTROMETRY

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MS STRATEGY FOR IDENTIFICATION OF ALPHA-SYNUCLEIN PROTEOFORMS

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ORBITRAP PROTEOMICS ANALYSIS OF CSF TO IDENTIFY NOVEL MARKERS FOR PROGRESSION AFTER A FIRST ATTACK OF DEMYELINATION

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CHANGES IN THE HUMAN HIPPOCAMPAL PROTEOME DURING ALZHEIMER'S DISEASE

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ITRAQ-BASED QUANTITATIVE PROTEOMICS STUDY ON THE NEUROPROTECTIVE EFFECTS OF BUYANG HUANWU DECOCTION IN CEREBRAL ISCHEMIC STROKE MICE MODEL.

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PROTEOMICS OF SYNAPTOSOMAL FRACTIONS TO MAP PREFRONTAL CORTEX PROTEINS DURING ANHEDONIA

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BIOMARKER IDENTIFICATION IN ALZHEIMER´S DISEASE BRAIN TISSUE AND RELATIONSHIP TO GENETIC RISK FACTORS

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AN ION MOBILITY MASS SPECTROMETRY APPROACH TO ELUCIDATE THE MOLECULAR MECHANISMS UNDERLYING AGGREGATION IN NEURODEGENERATIVE DISEASES

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VERIFICATION OF A PARKINSON'S DISEASE PROTEIN SIGNATURE IN T-LYMPHOCYTES BY MULTIPLE REACTION MONITORING

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SIMULTANEOUS PROTEIN DIGESTION AND 18O LABELING BY A GRAPHENE OXIDE BASED IMMOBILIZED ENZYMATIC REACTOR FOR HIGH THROUGHPUT QUANTITATIVE PROTEOME ANALYSIS

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SIMULTANEOUS PROTEIN DIGESTION AND 18O LABELING BY A GRAPHENE OXIDE BASED IMMOBILIZED ENZYMATIC REACTOR FOR HIGH THROUGHPUT QUANTITATIVE PROTEOME ANALYSIS

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IMMUNP-PROTEOMICS USING POLYCLONAL ANTIBODIES AND STABLE ISOTOPE LABELED AFFINITY-PURIFIED RECOMBINANT PROTEIN FRAGMENTS

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COMPOUND-CENTERED PROTEOMIC APPROACHES TO DEFINE THE PROTEIN TARGETS OF THE ANTITUMORAL NATURAL COMPOUND ORIDONIN.

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DEVELOPMENT OF ABSOLUTE QUANTIFICATION METHOD FOR DKK1 IN HUMAN SERUM USING LC-MS/MS

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HUMAN AORTIC VALVE STENOSIS ANALYZED BY MALDI-TOF IMAGING MASS SPECTROMETRY (MALDI-IMS) USING "LANGARTECH", A CUSTOM MADE MATRIX SPRAYER.

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REPRODUCIBLE PROTEIN SPOT COORDINATE DETECTION IN 2D-PAGE USING A PROTEIN MARKER GRID

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DETECTION OF BACTERIA AND COMPARATIVE PROTEOMIC ANALYSIS BY MASS SPECTROMETRY

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A PROTEIN BIOMARKERS PANEL TO DISCRIMINATE PROGRESSIVE FROM NON-PROGRESSIVE CHRONIC KIDNEY DISEASE USING A TARGETED PROTEOMICS METHOD

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OPTIMIZATION OF THE MALDI IMAGING LASER REPETITION RATES USING AN ORTHOGONAL MALDI MASS SPECTROMETER

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LIPID VISUALISATION AND IDENTIFICATION THROUGH COLLISION CROSS SECTION AIDED CORRELATION OF MALDI IMAGING AND MS/MS FRAGMENTATION DATA SETS

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EXPLORING IMPACT OF DYNAMIC ACCUMULATION FOR IMPROVING MS/MS QUALITY OF QQTOF DATA

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PRECISION AND NORMALIZATION STRATEGIES FOR LABEL FREE MRM ANALYSIS OF PLASMA PEPTIDES OVER AN 18 MONTH TIME COURSE STUDY

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RECONSTRUCTION OF HUMAN PROTEOME: REVIVAL OF TARGETED PROTEOMICS FROM SHOTGUN MASS SPECTROMETRY

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DEVELOPMENT OF A WORKFLOW FOR THE DETECTION OF DRUG-DERIVED ADDUCTS ON PROTEINS

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EVALUATION AND PROTEOMICS APPLICATIONS OF NEUTRON-ENCODED TMT10-PLEXING

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1 Cellzome GmbH • A GSK Company

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MALDI-TOF/TOF-IMS ON FORMALIN FIXED PARAFFIN EMBEDDED (FFPE) HUMAN BRAINSTEM TISSUE; EXAMINATION OF PEPTIDE EXPRESSION IN THE ROSTRAL (OPEN) MEDULLA

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PEPTIDE TISSUE IMAGING MASS SPECTROMETRY ON TISSUE MICRO ARRAYS FOR CANCER DIAGNOSTICS

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ELEVATING PROTEIN IDENTIFICATIONS PER MINUTE BY USING SPELC-MS/MS IN COMBINATION WITH ULTRA-SHORT GRADIENTS

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IMPROVED ANALYSIS OF PHOSPHOLIPIDS USING GRAPHENE OXIDE AS A MATRIX FOR MALDI IMAGING MASS SPECTROMETRY

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SINGLE-TUBE SAMPLE PREPARATION WORKFLOWS USING PARA-MAGNETIC BEADS FOR ULTRA-SENSITIVE PROTEOMICS

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A NOVEL MULTIPLE REACTION MONITORING METHOD OF QUANTITATIVE PROTEOMICS BY USING COMBINATION OF MULTIPLEX LABELING AND QCONCAT.

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TUNABLE ISOELECTRIC FOCUSING VIA MOVING REACTION BOUNDARY FOR HIGH RESOLUTION TWP-DIMENSIONAL GEL ELECTROPHORESIS AND PROTEOMICS

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INTEGRATING HEAT STABILIZION WITH MALDI IMAGING ENABLES MOLECULAR DISTRIBUTION IMAGES OF HIGH QUALITY TISSUE

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COMPREHENSIVE RELATIVE QUANTIFICATION OF THE CYTOCHROMES P450 USING SWATH(TM) ACQUISITION

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ULTRA-LOW FLOW ESI-MS FOR THE DETECTION OF POST TRANSLATIONAL MODIFICATION (PTM) SITES AND THE INCREASED SEQUENCE COVERAGE OF PROTEINS IN A SINGLE ANALYSIS

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CAN MRM-BASED SECRETOME PROFILING BE USED AS DRUG EVALUATION ASSAY?

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EXTENDING PROTEOME COVERAGE THROUGH AN ON-LINE 2D SCX-RP ULTRA-HIGH PRESSURE SYSTEM

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TARGETED PROTEOMICS WITH A HIGH-PERFORMANCE TRIPLE QUADRUPOLE MASS SPECTROMETER AND NEXT GENERATION ESI SOURCE

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QUANTIFYING CYTOCHROME P450 ENZYMES INVOLVED IN XENOBIOTIC METABOLISM – SCREENING OF DRUG-INDUCED PROTEIN EXPRESSION BY TXP-IMMUNOAFFINITY MASS SPECTROMETRY

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PNGASE F-CATALYZED 18P-LABELING FOR QUANTITATIVE GLYCOMICS AND GLYCOPROTEOMICS SIMULTANEOUSLY

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AN AUTOMATED DUAL-ONLINE MULTIFUNCTIONAL ULTRAHIGH PRESSURE LIQUID CHROMATOGRAPHY SYSTEM FOR HIGH THROUGHPUT AND EXTENSIVE PROTEOMICS ANALYSIS.

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SRM VS HR-MS QUANTITATIVE PROTEOMICS; MATRIX EFFECT AND LOQ IN SERUM

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AUTOMATED ISOFORM DETECTION BY CUSTOMIZED PEPTIDE IDENTIFICATION METHODS AND NOVEL HIGH THROUGHPUT LCMS INSTRUMENTATION

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PROBING PROTEIN STRUCTURAL TRANSITIONS IN COMPLEX BIOLOGICAL BACKGROUNDS ON A LARGE SCALE

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COMPARISON OF GROUP SPECIFIC IMMUNOAFFINITY MS BASED QUANTIFICATION OF PLASMA BIOMARKERS FROM DRIED BLOOD SPOTS, DRIED PLASMA SPOTS AND BLOOD PLASMA

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COMPARING ION THERMAL FOCUSING ELECTROSPRAY AND NANOSPRAY LC-MS/MS FOR CHARACTERIZING HUMAN EMBRYONIC STEM CELLS AND NEURAL PROGENITOR CELLS

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MASS DEFECT-BASED PSEUDP-ISOBARIC DIMETHYL LABELING METHODS FOR PROTEOME QUANTIFICATION

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ABSOLUTE QUANTIFICATION OF 26 CYTOCHROME P450 ENZYMES AND UDP-GLUCURONOSYLTRANSFERASES IN HUMAN LIVER MICROSOMES USING QCONCAT/MRM APPROACH

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EXPANSION OF ION LIBRARY FOR MINING SWATH DATA THROUGH FRACTIONATION PROTEOMICS

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USE OF MONOCLONAL ANTIBODY TO AID DIAGNOSIS AND PROGNOSTIC EVALUATION OF HEPATOCELLULAR CARCINOMA

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DEVELOPMENT OF A "UNIVERSAL" MASS SPECTROMETRY METHOD BRINGS THE END OF TIME-CONSUMING DATA-DEPENDENT METHOD OPTIMIZATION FOR ACHIEVING MAXIMAL IDENTIFICATIONS FROM ANY SAMPLE TYPE

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SIMS AND MALDI IMAGING METHODOLOGIES REVEAL LIPID MARKERS OF CHONDROGENIC DIFFERENTIATION

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A RIBONUCLEIC ACID BASED STRATEGY FOR RNA-BINDING PROTEOME ANALYSIS

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DIRECT TISSUE ANALYSIS BY MALDI-MASS SPECTROMETRY IMAGING (MSI) REVEALS A MOLECULAR PATTERN OF ARTERIAL LAYERS IN ATHEROSCLEROSIS DEVELOPMENT

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IMPROVED IONIZATION EFFICIENCY USING ACETONITRILE AS A DOPANT TO NANP-ELECTROSPRAY FOR THE ANALYSIS OF CLINICAL SAMPLES

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QUANTITATIVE EVALUATION OF GSTS IN MOUSE SERUM BY MRM

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INTERFACING SURFACE ACOUSTIC WAVE NEBULIZATION WITH LC-MS

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DEVELOPMENT OF SELECTED REACTION MONITORING (SRM) ASSAYS FOR QUANTIFICATION OF ANGIOTENSIN-II SIGNATURE PROTEINS IN HUMAN URINE

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DEVELOPMENT OF A HIGH-THROUGHPUT BINDER SELECTION AND SCREENING PLATFORM

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TARGETED ANALYSIS IN PRM MODE TOWARDS CLINICAL APPLICATION: OPTIMIZATION OF EXPERIMENTAL SETUP AND DATA PROCESSING FOR ACCURATE AMYLOID DIAGNOSIS

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LOCALIZING AND CHARACTERIZING DISULFIDE BONDS IN MS-BASED PROTEOMICS USING ONLINE LC–ELECTROCHEMISTRY–MS

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EXPLORING THE EFFECT OF DMSO AS A MOBILE PHASE ADDITIVE FOR IMPROVING PROTEIN IDENTIFICATION AND SWATH ACQUISITION BY NANOLC/MS/MS

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A NOVEL AND ROBUST WORKFLOW FOR PROTEIN QUANTITATION AND LARGE-SCALE BIOMARKER STUDY IN HUMAN PLASMA

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EVALUATION OF NEW KIDNEY INJURY BIOMARKERS USING ABSOLUTE QUANTITATIVE PROTEOMICS (PSAQ AND SRM)

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IMMOBILIZED MONOLITHIC ENZYMATIC REACTORS FOR ONLINE DIGESTION OF PROTEINS SECRETED BY DEVELOPING HUMAN EMBRYOS

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EVALUATION OF DATA-INDEPENDENT ACQUISITION APPROACHES FOR SPIKED PEPTIDES IN HELA DIGEST ON Q-OT-QIT MASS SPECTROMETER

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BARCDB: A NEW RESEARCH TOOL FOR THE ANALYSIS OF BIOSPECIMENS

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HIRIEF COUPLED WITH MS/MRM FOR ANTIBODY FREE PROTEIN QUANTIFICATION IN HUMAN PLASMA

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IELEMENT: NEW ULTRA-HIGH RESOLUTION MS (UHR-MS) UHRMS SIGNAL HANDLING APPROACH FOR MORE ACCURATE METABOLITE IDENTIFICATION

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MANIPULATION OF THE ISOTOPIC COMPOSITION OF PROTEINS AS A POWERFUL TOOL IN HIGH RESOLUTION HIGH SENSITIVITY MASS SPECTROMETRY ANALYSES

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ABSOLUTE AND MULTIPLEX QUANTIFICATION OF THERAPEUTIC MONOCLONAL ANTIBODIES IN SERUM SAMPLES BY LC-SRM USING PSAQ STANDARDS.

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CHARACTERIZATION OF AN IMPROVED ULTRA-HIGH RESOLUTION QUADRUPOLE TIME OF FLIGHT (UHR-TOF) INSTRUMENT FOR PROTEOMICS APPLICATIONS

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HIGH QUANTIFICATION EFFICIENCY IN PLASMA TARGETED PROTEOMICS WITH A FULL-CAPABILITY DISCOVERY Q-TOF PLATFORM

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A COMPARISON OF LABEL FREE DDA-HRXIC AND DIA ACQUISITION ON A BENCHTOP UHR-Q-TOF

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A SISCAPA IMMUNP-MASS SPECTROMETRIC ASSAY FOR QUANTIFICATION OF SOLUBLE TRANSFERRIN RECEPTOR (STFR) IN HUMAN SERUM

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NEW WORKFLOWS FOR IDENTIFICATION AND PROFILING OF DISULFIDE BONDS IN BIOPHARMACEUTICALS

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THE PAN-HUMAN LIBRARY: A REPOSITORY OF ASSAYS TO QUANTIFY 10 000 PROTEINS BY SWATH-MS

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ROBUSTNESS STUDY OF PEPTIDES IN PLASMA USING NOVEL TECHNOLOGIES IN AN LC-MS INSTRUMENT

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INCREASE OF SENSITIVITY WITH THE NANP-ESI CAPTIVESPRAY SOURCE ASSOCIATED TO NANOBOOSTER (BRUKER)

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ENRICHMENT OF CARBONYLATED PEPTIDES USING BIOTIN-LC (LONG CHAIN)-HYDRAZIDE

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IMPROVED SPATIAL RESOLUTION IN THE ANALYSIS OF FFPE TISSUE AFTER TRYPTIC DIGESTION

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LC-MS/SRM ASSAY FOR THE QUANTIFICATION OF PROTEINS INVOLVED IN CELLULAR LIFE AND DEATH PROCESSES – ELUCIDATING THE UNDERLYING MECHANISMS OF MITOCHONDRIAL DYSFUNCTION

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COMPARISON OF THREE MS2 BASED QUANTITATIVE METHODS FOR TARGETED PEPTIDE QUANTITATION

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IMPROVEMENT OF SELECTIVITY AND SENSITIVITY BY OPTIMIZED SWATH METHODS

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ANALYSIS OF POST-TRANSLATIONAL MODIFICATIONS IN HUMAN TRANSTHYRETIN ASSOCIATED WITH FAMILIAL AMYLOIDOTIC POLYNEUROPATHY BY TARGETED LC/MS AND INTACT PROTEIN MS

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MOTIF-TARGETING PHOSPHOPEPTIDE ENRICHMENT FOR QUANTITATIVE PHOSPHOPROTEOME ANALYSIS

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IN VIVO DEEP PROTEOME MICRO/NANP-HARVESTING EXPLORING INACCESSIBLE HUMAN TERRITORIES

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HIGHLY-MULTIPLEXED PROTEIN QUANTIFICATION FROM DRIED BLOOD SPOTS

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COMPARISON OF DRUG DISTRIBUTIONS IN IN-VIVO ANIMAL AND IN-VITRO EXPERIMENTAL MODELS BY MALDI-MS IMAGING

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DISTRIBUTION OF VEMURAFENIB IN MALIGNANT MELANOMA TISSUE BY MALDI MASS SPECTROMETRY IMAGING

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A SYSTEMS BIOLOGY APPROACH TO THE CHARACTERIZATION OF STRESS RESPONSE IN DERMACENTOR RETICULATUS TICK UNFED LARVAE.

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PROTEOMICS DISCOVERY OF PLASMA TEST-OF-CURE MARKERS FOR TRYPANOSOMA BRUCEI GAMBIENSE HUMAN AFRICAN TRYPANOSOMIASIS

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INCREASED ACUTE IMMUNE RESPONSE DURING THE MENINGP-ENCEPHALITIC STAGE OF TRYPANOSOMA BRUCEI RHODESIENSE SLEEPING SICKNESS COMPARED TO T. B. GAMBIENSE

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STRUCTURAL CHARACTERIZATION OF ECHINOCOCCUS GRANULOSUS IMMUNODOMINANT PROTEINS AND DEVELOPMENT OF A NOVEL IMMUNOASSAY FOR HUMAN CYSTIC ECHINOCOCCOSIS

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SCHISTOSOMIASIS INDUCES SIGNIFICANT CHANGES IN THE HOST BILE PROTEOME PROFILE.

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SCHISTOSOMIASIS: WORM-INDUCED CHANGES IN THE PROTEOME OF THE LUNG ENDOTHELIAL CELL SURFACE

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SHOTGUN ANALYSIS OF PLATELETS FROM DENGUE PATIENS: CONTRIBUTIONS TO THE PATHOGENESIS ELUCIDATION

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IMMUNP-COMPETITIVE CAPTURE MASS SPECTROMETRY FOR THE CHARACTERIZATION OF THE NS5A PROTEIN INTERACTOME IN A CELLULAR MODEL OF HEPATITIS C VIRUS REPLICATION

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ESSENTIAL AND NONREDUNDANT ROLES FOR DIAPHANOUS FORMINS IN CORTICAL MICROTUBULE CAPTURE AND DIRECTED CELL MIGRATION.

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STANDARD PROTEASOME AND IMMUNOPROTEASOME ASSOCIATE TO PREFERRED REGULATORS AS REVEALED BY LABEL-FREE QUANTITATIVE PROTEIN CORRELATION PROFILING

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PROTEIN INTERACTOMICS BASED ON DIRECT MOLECULAR FISHING ON PARAMAGNETIC PARTICLES: PRACTICAL REALIZATION AND FURTHER SPR VALIDATION

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MINIATURIZED CHEMOPROTEOMICS WORKFLOW ENABLES CHARACTERIZATION OF PATIENT SAMPLES

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CHARACTERISATION OF B-CATENIN CONTAINING PROTEIN COMPLEXES BY INTRACELLULAR CP-IMMUNOPRECIPITATION AND HIGH OUTPUT WESTERN BLOTTING.

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PROFILING OF CELLULAR SIGNAL TRANSDUCTION PATHWAYS USING A BEAD-BASED WESTERN BLOT

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TARGETING CANCER RELEVANT SUBCELLULAR SPECIES OF Β-CATENIN IN LIVING CELLS WITH NEW INTRACELLULAR FUNCTIONAL ANTIBODIES

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A COMPREHENSIVE PROTEOMICS SCREEN FOR SUBSTRATES OF THE SCFΒ-TRCP2 UBIQUITIN LIGASE

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PROTEOME-WIDE ANALYSIS FOR IDENTIFICATION OF FUNCTIONAL SNPS

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FUNCTIONAL INTERACTOMICS IN ALZHEIMER'S DISEASE

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DICER2-ARGONAUTE2-R2D2 NETWORK DYNAMICS DURING ANTIVIRAL RESPONSE IN D. MELANOGASTER CELLS.

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REVEALING DJ-1 FUNCTION UNDER OXIDATIVE STRESS THROUGH ITS INTERACTORS: IMPLICATIONS FOR PARKINSON'S DISEASE

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A CROSS-OMICS GLOBAL PHOSPHOPROTEOMICS AND METABOLOMICS ANALYSIS REVEALS A CONNECTION BETWEEN KINASE INHIBITION AND RNA PROCESSING IN BCR-ABL POSITIVE MYELOMA CELLS

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ANDSYSTEM: AUTOMATED LITERATURE MINING AND INTERACTOME NETWORKS RECONSTRUCTION IN THE AREA OF BIOLOGY

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MITOCHONDRIAL PROTEIN-PROTEIN INTERACTIONS REVEAL DIVERSE COMPLEXES AND DISEASE-RELEVANT FUNCTIONAL RELATIONSHIPS

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VIROTRAP: ABDUCTING PROTEIN COMPLEXES FROM MAMMALIAN CELLS

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TOWARDS MORE COMPREHENSIVE MODELING OF FUNCTIONAL REGULATION AND PATHWAY ENRICHMENT

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TOWARDS COMPREHENSIVE IDENTIFICATION OF PROTEIN-SPECIFIC INTERACTOMES VIA COMBINED USE OF AFFINITY MATRICES

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PATHOPHYSIOLOGICAL MECHANISMS IN COLLAGEN VI MYOPATHIES: CONTRIBUTION OF PROTEOMICS

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INVESTIGATION OF MOLECULAR MECHANISMS IMPAIRED IN WILSON

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GLYCOPEPTIDEID: WEB TOOL FOR N-GLYCOPEPTIDE IDENTIFICATION WITH CID MS2 SPECTRA

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A CURRENT PERSPECTIVE ON USING R AND BIOCONDUCTOR FOR PROTEOMICS DATA ANALYSIS

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A STATE-OF-THE-ART MACHINE LEARNING PIPELINE FOR THE ANALYSIS OF ORGANELLE PROTEOMICS DATA

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ANALYSIS OF LABELED AND NON-LABELED DIA AND DDA PROTEOMIC DATA USING 'PROGENESIS QI FOR PROTEOMICS'

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A SITE FOR DIRECT PROTEIN-PROTEIN INTERACTION FROM STRUCTURAL MODELLING AND DOCKING FOR INTEGRIN AVB6 AND UPAR

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UNLOCKING THE PUZZLING BIOLOGY OF THE BLACK PÉRIGORD TRUFFLE TUBER MELANOSPORUM

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NON-REDUNDANT PEPTIDES DATABASE FOR CHR18 ENCODED PROTEINS QUANTIFICATION

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CONSOLIDATING CHR 18 DATA USING KNOWLEDGEBASE OF PROTEIN AND TRANSCRIPT ANNOTATIONS

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CONSTRUCT: THREE-DIMENSIONAL VISUALIZATION OF SEQUENCE CONSERVATION

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PEPSHELL: VISUALIZING CONFORMATIONAL PROTEOMICS.

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RESPONSE OF PEPTIDE INTENSITY TO CONCENTRATION IN ESI¨CMS-BASED PROTEOME

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A SPATIALLY-AWARE PEAK PICKING METHOD FOR MALDI-IMAGING DATA FROM TOF AND FTICR MASS ANALYZERS

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APPLICATION OF NON-SELECTIVE PHOTOREACTIVE CROSS-LINKING IN MASS SPECTROMETRY-BASED STRUCTURAL PROTEOMICS

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AUTOMATED AND COMPREHENSIVE SITE-SPECIFIC CHARACTERIZATION OF GLYCOPROTEINS USING PROTEOLYTIC ENZYMES WITH HIGH AND LOW SPECIFICITIES

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AN HMSILAC-BASED ANALYSIS PIPELINE WHICH ENABLES ACCURATE ASSIGNMENT AND QUANTIFICATION OF METHYLATED SITES BETWEEN DISTINCT FUNCTIONAL STATES

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A SPATIALLY-AWARE PEAK PICKING METHOD FOR MALDI-IMAGING DATA FROM TOF AND FTICR MASS ANALYZERS

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INTEGRATED AND COMPARATIVE ANALYSIS OF 3-OMICS DATA TO IDENTIFY A PANEL OF DIFFERENTIALLY EXPRESSED MEMBRANE PROTEINS IN BENIGN AND METASTATIC PROSTATE CANCER CELLS LINES.

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IDENTIPY, AN OPEN-SOURCE MS/MS DATA SEARCH PLATFORM FOR SHOTGUN PROTEOMICS

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REANALYSIS OF PUBLIC DATA TO FIND NON-STANDARD PHOSPHORYLATIONS IN HUMAN SAMPLES

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MZJAVA: AN OPEN SOURCE MASS SPECTROMETRY LIBRARY

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THE SEAMASS PLATFORM: A NEW LC-MS SOFTWARE PIPELINE BASED ON IMAGE ANALYSIS AND BAYESIAN MODELLING

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OPTIMAL SELECTION OF SAMPLES FOR MULTIPLEX SEROLOGICAL ASSAY VALIDATION

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A COMPLETE WORKFLOW FOR ACHIEVING HIGH ACCURACY MULTIPLEXED N-TERMINOMICS DATA USING TMT10PLEX.

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LOCATING POST TRANSLATIONAL MODIFICATIONS THROUGH THE INTERROGATION OF SHOTGUN PROTEOMICS

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STATISTICAL CONFIRMATION OF MALDI-TOF MASS SPECTRA WITH R AND MASSUP CAN BE USED TO DISTINGUISH BETWEEN BACTERIA

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A STAND-ALONE VERSION OF MS AMANDA FOR INTEGRATION INTO PROTEOMICS WORKFLOWS

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PEPTIDE-CENTRIC DATABASE SEARCH ENGINES APPLIED TO DATA INDEPENDENT ACQUISITION UDMSE DATA

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ESTIMATION OF PROTEIN EXPRESSION PROFILES BASED ON PEPTIDE FEATURES AND QUANTIFICATION USING ISOBARIC LABELLING

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MZDB: A FILE FORMAT USING MULTIPLE INDEXING STRATEGIES FOR THE EFFICIENT ANALYSIS OF LARGE LC-MS/MS AND SWATH-MS DATASETS

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UNIPROT REFERENCE PROTEOMES FOR PROTEOMICS IDENTIFICATIONS

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ISOQUANT - AN INTEGRATED BIOINFORMATICS PIPELINE FOR EVALUATION AND REPORTING OF DATA INDEPENDENT (LC-MSE) LABEL-FREE QUANTITATIVE PROTEOMICS DATA

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NEW FUNCTIONALITY FOR THE TRANS-PROTEOMIC PIPELINE: TOOLS FOR THE ANALYSIS OF PROTEOMICS DATA

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CONCEPT OF JAPAN PROTEOME STANDARD REPOSITORY/DATABASE (JPOST)

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COLIMS: AN OPEN SOURCE LIMS SYSTEM TO AUTOMATE AND EXPEDITE PROTEOMICS DATA MANAGEMENT, PROCESSING AND ANALYSIS

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SOFTWARE-SUITE FOR INTELLIGENT PROTEOME ANALYSIS AND BIOMARKER SEARCH ADAPTED TO AN AUTOMATED HIGH THROUGHPUT WORKFLOW

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SIMULTANEOUS LOCALIZATION AND ASSIGNMENT OF DIFFERENT POST-TRANSLATIONAL MODIFICATIONS USING PTMRS

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MYMRM: A SOFTWARE TOOL FOR DESIGNING AD-HOC MRM EXPERIMENTS

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MQRUN — INTEGRATING MAXQUANT INTO A LINUX CLUSTER-BASED WORKFLOW SYSTEM

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ORGANIZE & ANALYZE YOUR MASS-SPECTROMETRY DATASETS ACCORDING TO YOUR EXPERIMENTAL DESIGN WITH PROLINE.

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DIRECT QUATITATIVE ANALYSIS OF NATIVE HUMAN PEPTIDES IN COMPLEX SECRETOME SAMPLES

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FROM DATA NORMALIZATION TO STATISTICAL SIGNIFICANCE: QUANTITATIVE PERFORMANCE OF LABEL FREE LC-MS PLATFORMS EVALUATED

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SIMULATED LINEAR TESTS APPLIED TO QUANTITATIVE PROTEOMICS

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23 - Human Proteome Project

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CABA IN ISSUE IN NEPAL

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MASS SPECTROMETRY BASED DRAFT OF THE HUMAN PROTEOME

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TERMINI ORIENTATED PROTEOMICS-HUMAN AMINO TERMINOME (TOP-HAT) FOR THE HUMAN PROTEOME PROJECT: N TERMINI AND NA-ACETYLATION STATUS DIFFERENTIATE STABLE CLEAVED PROTEIN SPECIES FROM CLEAVAGE REMNANTS

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SIZE OF HUMAN PROTEOME: EXAMPLE OF CHR 18

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PROTEOMIC EVALUATION OF LOW- AND HIGH-FLUX HEMODIALYSIS

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PROTEOME OF THE HUMAN FULL TERM PLACENTA

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THE HUMAN DIABETES PROTEOME PROJECT (HDPP): 13TH HUPO WORLD CONGRESS IN MADRID

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THE HUMAN SURFACEOME

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SUBCELLULAR FRACTIONATION ANALYSIS OF PLACENTAL TISSUE MEMBRANE PROTEINS FOR IDENTIFICATION OF MISSING PROTEIN.

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SIMULTANEOUS TARGETED ANALYSIS OF FIVE OSTEOARTHRITIS BIOMARKER CANDIDATES RELATED TO CHROMOSOME 16 BY LIQUID CHROMATOGRAPHY-MULTIPLE REACTION MONITORING MASS SPECTROMETRY

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SERUM BIOMARKERS OF ERYTHROPOIETIN RESISTANCE: ESTABLISHING AN OPTIMAL MULTIDIMENSIONAL LIQUID CHROMATOGRAPHY WORKFLOW COMPATIBLE WITH HEXAPEPTIDE-BEAD LIBRARY AND ISOBARIC PEPTIDE TAGGING REAGENTS

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DEVELOPMENT OF IMPROVED SUBCELLULAR FRACTIONATION PROCEDURES OF THE PLACENTAL MEMBRANE PROTEINS FOR DISCOVERING DISEASE BIOMARKERS AND MISSING PROTEINS

Jong-Sun Lim[1], Seul-Ki Jeong[1], Keun Na[1], Min-Jung Lee[1], Jin-Young Cho[1], William Stephen Hancock[2], Young-Ki Paik[1]
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2 Northeastern University, Boston, MA, USA

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GENOMEWIDEPDB V 2.0: UPDATE ON THE TRANSCRIPTOMIC AND PROTEOMIC EXPRESSION DATA WITH ALTERNATIVELY SPLICED PRODUCTS LAYERED IN A GENOME-WIDE MANNER

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UNRAVELING THE PROTEOME OF NUCLEUS BASALIS OF MEYNERT

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1 Navarrabiomed-Miguel Servet Foundation

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IDENTIFICATION PROTEINS OF CARDIOVASCULAR SYSTEM IN HEALTHY SUBJECTS' URINE DURING "DRY" IMMERSION

Liudmila Pastushkova[1], Igor Dobrokhotov[1], Olga Obraztsova[1], Aleksey Kononikhin[1,2], Eugene Tiys[3], Igor Popov[2,4], Eugene Nikolaev[2,4], Irina Larina[1]
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2 Institute for Energy Problems of Chemical Physics RAS, Moscow, Russia
3 Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
4 Emanuel Institute of Biochemical Physics RAS, Moscow, Russia

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BIOLOGICAL PROCESSES IN COSMONAUTS AFTER LONG DURATION SPACE FLIGHTS BY STUDYING URINE PROTEOME

Irina Larina[1], Luidmila Pastushkova[1], Aleksey Kononihin[1,2], Eugene Tiys[3], Olga Obraztsova[1], Igor Dobrohotov[1], Igor Popov[2,4,5], Kirill Kireev[6] Vladimir Ivanisenko[3] Eugene Nikolaev[2,4]
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3 3Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
4 Emanuel Institute of Biochemical Physics RAS, Moscow, Russia
5 Moscow Institute of Physics and Technology, Moscow, Russia
6 Gagarin Cosmonauts Training Center, Star City, Moscow region, Russia

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HIGH-THROUGHPUT EVALUATION OF ANTIBODIES ON WESTERN BLOT WITHIN THE HUMAN PROTEIN ATLAS PROJECT

Klas Linderbäck[1], Marica Hamsten[1], Jenny Ottosson Takanen[1], Annelie Cajander[1], Anna Johansson[1], Delaram Afshari[1], Atefeh Mohsenchian[1], Mona Moradi[1] Camilla Ohlsson[1] Mattias Uhlén[1]
1 Royal Institute Of Technology/School Of Biotechnology

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INFLUENCE OF EXPERT TEST WITH LARGE RADIUS CENTRIFUGE ROTATION ON URINE PROTEOM OF COSMONAUTS

Kirill Kireev[1], Luidmila Pastushkova[2], Vladimir Pochuev[1], Aleksey Kononikhin[2,3], Irina Larina[2]
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2 Institute For Biomedical Problems Of RAS, Moscow,Russia
3 Institute for Energy Problems of Chemical Physics RAS, Moscow,Russia

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CELL TO GEL WORKFLOW: A STREAMLINED PROTEOMICS WORKFLOW FOR MINIMIZING SAMPLE PREPARATION AND MAXIMIZING PROTEIN SAMPLE UTILIZATION.

Kenneth Oh[1], Ning Liu[1], Matthew Hammond[1], Jonathan Kohn[1], Anton Posch[2], Nancy Braun[2]
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2 BiP-Rad Laboratories, Munich, Germany

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PROTEOMIC BIOMARKER ANALYSIS OF MATERNAL SERUM FOR IDENTIFICATION OF PRETERM LABOUR

Arlene D'Silva[1], Jon Hyett, Jens Coorssen
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2 Obstetrics, Gynaecology and Neonatology, Central Clinical, Royal Prince Alfred Hospital, University of *Sydney, Sydney. NSW, Australia*
3 School of Medicine Nanoscale Organisation & Dynamics Group School of Science & Health University of Western Sydney NSW, Australia

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ANTIBODY RANKER

Tadashi Yamamoto[1], Naohiko Kinosita[1, 2]
1Niigata University
2Niigata University of Health and Welfare

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MITOCHONDRIAL PROTEOME OF CYBRID CELLS HARBOURING A TRUNCATIVE MITOCHONDRIAL DNA MUTATION IN RESPIRATORY COMPLEX I

Clara Musicco[1], Antonella Cormio[2], Maria Antonietta Calvaruso[3], Luisa Iommarini[3], Giuseppe Gasparre[3], Anna Maria Porcelli[3], Anna Maria Timperio[4], Lello Zolla[4]
Maria Nicola Gadaleta[1]
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3 University of Bologna, Bologna, Italy
4 Tuscia University, Viterbo, Italy

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QUANTITATIVE HUMAN TEARS PROTEOME IN SHORT-TERM DECORATIVE CONTACT LENS WEAR

Jingfang Bian[1], King Kit Li, Chi-ho To, Carly S. Lam, Thomas Chuen Lam
The Hong Kong Polytechnic University, Hong Kong

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PROTEOMIC ANALYSIS OF THE SPERM CELL: TOWARDS THE COMPLETE SPERM CELL PROTEOME AND IDENTIFICATION OF PROTEINS INVOLVED IN MALE INFERTILITY

Carla Paiva[1,2], Claudio Attardo Parrinello[1], Judit Castillo[1], Ruben Azpiazu[1], Alexandra Amaral[1, 2], Orleigh Bogle[1], Montserrat Codina[1], Josep Maria Estanyol[3] Josep Lluís Ballescà[4] Rafael Oliva[1]

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2 Hospital Clinic From Barcelona
3 PhD Programme in Experimental Biology and Biomedicine, CNC-Center for Neuroscience and Cell
4 Biology and Institute for Interdisciplinary Research, and Biology of Reproduction and Stem Cell Group, 5CNC, University of Coimbra, Coimbra, Portugal
6 Proteomics Unit, Scientific and Technical Centers of the University of Barcelona (CCiTUB), Barcelona, Spain
7 Institute of Obstetrics, Gynecology and Neonatology, Hospital Clinic, Barcelona, Spain

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MEASURING SUCCESS A PRIORI? THE REGULATION OF RESEARCH BY TRANSLATIONAL TENSIONS

Mavis Jones[1], Christina Holmes[2], Fiona McDonald[3]

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2 St. Francis Xavier University, Antigonish, Nova Scotia, Canada
3 Queensland University of Technology, Brisband, Queensland, Australia

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URINE PROTEOMICS FOR THE DISCOVERY OF NON-INVASIVE DIAGNOSTIC BIOMARKERS FOR PEDIATRIC DISEASES

Hanno Steen[1], Alex Kentsis[1], Susan Kim[1], Rebekah Mannix[1], Richard Bachur[1]

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MITOCHONDRIAL PROTEOMICS INVESTIGATION OF A CELLULAR MODEL OF IMPAIRED DOPAMINE HOMEOSTASIS, AN EARLY STEP IN PARKINSON'S DISEASE PATHOGENESIS

Tiziana Alberio[1], Heather Bondi[1], Luisa Pieroni[2], Andrea Urbani[2], Mauro Fasano[1]

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2 University of Roma "Tor Vergata", Roma, Italy

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CHARACTERIZATION OF CANCER-ASSOCIATED PROTEINS RELATED TO CHROMOSOME 16

J. Ignacio Casal[1], Oriol Bachs[1], Francesc Canals[1], Josep M. Estanyol[1], Manuel Fuentes[1], Alberto Medina[1], Javier Muñoz[1], Fernando J. Corrales[1] Juan P. Albar[1]

1 ProteoRed-ISCIII. Plataforma De Recursos Biomoleculares Y Bioinformáticos. Spain

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DISECTING CHROMOSOME 16 PROTEOME

Fernando J. Corrales[1], Concha Gil[1,] Francisco Blanco[1], Manuel M. Sánchez Del Pino[1], Jesús Vázquez[1], Javier Muñoz[1], Enrique Santamaría[1], Félix Elortza[1] Eliandre Oliveira[1] Francesc Canals[1] Alberto Pascual-Montano[1] Jesús M. Arizmendi, Josep Mª Estanyol, Silvia Barceló, Irene Orera, M. González-Barderas, Jaime Sancho, Fernando Vivanco, Manuel Fuentes, Eduard Sabidó

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THE SPANISH BIOLOGY/DISEASE INITIATIVE WITHIN THE HUMAN PROTEOME PROJECT

Juan P. Albar[1], Oriol Bachs[1], Francesc Canals[1], Ignacio Casal[1], Fernando Corrales[1], Manuel Fuentes[1], Concha Gil[1], Javier Muñoz[1] Fernando Vivanco[1] Francisco Blanco[1]
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TARGETING PROTEINS OF CHROMOSOME 16

Letizia Odriozola[1], Nuria Colomé[1], Francesc Canals[1], María L. Hernáez[1], Felipe Clemente[1], Concha Gil[1], Patricia Fernández[1], Cristina Ruiz[1] Irene Orera[1] Silvia Barceló[1] Miguel Marcilla[1] Severine Gharbi, Fernando Vivanco, Eduard Sabido, Eva Pérez, Manuel M. Sánchez del Pino, Joaquín Fernández, Juan P. Albar, Fernando J. Corrales
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Spanish Consortium of C-HPP (Chr-16)

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SUBCELLULAR FRACTIONATION ENHANCES CHROMOSOME 16 PROTEOME COVERAGE

Irene García-Palmero[1], María López-Lucendo[1], J. Alberto Medina-Aunon[1], Kerman Aloria[1], Jesús M. Arizmendi[1], Francesc Canals[1], Montserrat Carrascal[1], Felix Elortza[1] Josep Mª Estanyol[1] Joaquín Fernández[1] Anabel Marina[1] Javier Muñoz, Eliandre Oliveira, Alberto Pascual-Montano, Manuel Sánchez Del Pino, Jesús Vázquez, Fernando J. Corrales, Juan P. Albar, J. Ignacio Casal
1 ProteoRed-ISCIII. Plataforma De Recursos Biomoleculares Y Bioinformáticos. Spain.

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TRANSCRIPTOMIC PROFILING TOWARDS THE LOCALIZATION OF THE MISSING PROTEINS

Elizabeth Guruceaga[1], Fernando J. Corrales[1], V. Segura[1]
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MISSING PROTEINS IN CHROMOSOME 16. SPANISH HPP

Manuel Fuentes, Felipe Clemente, María Luisa Hernáez, María Gonzalez-Gonzalez, Fernando Corrales, Juan Pablo Albar, Concha Gil,
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3 National Center of Biotechnology. CSIC. Madrid.
4 Center For Applied Medical Research (CIMA).Pamplona. SPAIN

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THE CHROMOSOME 19 STRATEGY TO CHARACTERIZE NOVEL PROTEOFORMS AND MISSING PROTEINS USING ENCODE RESOURCES

Carol L. Nilsson, Ekaterina Mostovenko, Cheryl F. Lichti, Kelly Ruggles, David Fenyö, Roger A. Kroes, Sophia Hober, Ákos Végvári, Melinda Rezeli, Per E. Andrén, Erik P. Sulman, Frederick F. Lang, Manuel Fuentes, Elisabet Carlsohn, Joseph R. Moskal, Jill A. Opsahl, Frode S. Berven, Thomas E. Fehniger, György Marko-Varga*
Lund University, Sweden

24 - Late Break Abstract

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2D PROTEOME EXPRESSION PATTERN IN ORAL SQUAMOUS CELL CARCINOMA OF EXTRACTS FROM AGRIMONIA PILOSA LEDEBROOT

Yeon Ju Kwak[1], Park Kyoung Eun[2], Hye Ock Jang[2]

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2 Department of Dental Pharmacology and Biophysics, School of Dentistry and Research Institute For Oral Biotechnology, Yangsan Campus of Pusan National University, Beomeo-Ri, Mulgeum-Eup, Yangsan-Si, Gyeongsangnam-Do, 626-870, Korea

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DIMETHYL LABELING AFFECTS RECOVERY OF SINGLY PHOSPHORYLATED PEPTIDES IN TIO2 CHROMATOGRAPHY

Philipp Spät[1,2], Karsten Krug[2], Boris Macek[2], Mirita Franz-Wachtel[2]

1 Institute of Microbiology, Organismic Interactions, University Tübingen, Germany,

2 Proteome Center Tübingen, University Tübingen, Germany

GENERAL INFORMATION

REGISTRATION TO THE CONGRESS

	Until July 8th, 2014	From July 1st to September 22, 2014	From September 23, 2014 (onsite)
HUPO member *	450 €	550 €	650 €
HUPO non member	550 €	650 €	750 €
HUPO member Student **	200 €	250 €	300 €
HUPO non-member Student **	275 €	325 €	375 €
Accompanying person ***		100 €	

VAT Included

Registration fee includes:

- Access to the Opening Session and the Welcome Reception
- Access to the scientific sessions
- Bag with Congress materials
- Coffee during breaks
- Certificate of attendance
- FREE WIFI at the congress venue

Accompanying person fee includes:

- Access to the Opening Session
- Attendance to Welcome Cocktail
- Access to the Commercial Exhibition area
- Coffee during breaks

COURSES

	Date	Fee *(VAT Included)*
Pre Congress Course	3th and 4th October 2014	200 €
Clinical Day Course	5th October 2014	75 €
Educational Day Course	5th October 2014	75 €

SOCIAL PROGRAM

OPENING CEREMONY (18:00-19:30) AND OPENING RECEPTION (19:45 - 21:30)

SUNDAY 5 OCTOBER 2014

The Opening Ceremony will be held in the Auditorium, on the 1st floor of the North Congress Centre, IFEMA.

The Opening Ceremony will be provided with choreography of stylized dance based on the Albéniz music that brings us near to the purity and the roots of the Spanish dance. With this dance we can enjoy the Spanish elements such as the castanets, the fan and the footwork, all of these with a style that makes us travel into the past with the modern language of the Spanish dance. Mariemma School of Dance: “Por Derecho”. Choreography: Antonio Pérez. Music: Isaac Albeniz. Team “Larreal”.

The welcome reception will take place in the Pavilion 10 and it is included in the Registration Fee.

The welcome reception will be provided with a jazz quartet. The VT quartet will present selection of favorite all-time standards and songs that will surely please the senses and souls of any audience. Four accomplished musicians blend their talents and years of professional experience. Their goal is no other than to share their love for classy melodies, dear to our ears and memories. We sincerely hope that you enjoy them as much as we do.

CONGRESS DINNER

TUESDAY 7 OCTOBER 2014, 21:00.

A sitting dinner, proceeding by a string quartet on the Glass Gallery, will be held in Cibeles Palace. His large glass dome, irregular in shape, serves as a roof to the over 2,400 m2 of this new space which constitutes an intrinsic component of the Madrid City Council’s new headquarters. It was part of the Retiro Royal Palace in the 17th century, and in the 19th century it housed a leisure garden. From 1904 to 1919, it was officially incorporated as a passageway and loading area for the Communications Palace which was designed by architects Palacios and Otamendi. The gallery, which as undergone extensive work, is now part of the Madrid City Council’s headquarters and is used to host both institutional acts and celebratory events. It has two entrances: Calle Alcalá, 50, and Calle Montalbán,1.

We have the satisfaction to present the wonderful artists that form the group “Cuarteto Madrid”. The quartet is compound by the following musicians: Anne Marie North, Antonio Cárdenas, Iván Martín y John Stokes. This group has been together since 2003 and even though they interpret music from all times and composers, their repertoire is based mainly on Spanish composers.

After dinner a live rock´n roll concert will be offered by the group Gate Doors.

GENERAL INFORMATION

SCIENTIFIC ABSTRACTS ON USB KEY

The HUPO 2014 Abstracts will be available on a USB key. Participants will receive it in his Congress Bag.

BADGES

Name badges must be visible and used at all times, anywhere at the Congress Centre.

CERTIFICATE OF ATTENDANCE

Certificate of Attendance can be collected at the Registration Area (Self-Badge Printing desk) during Tuesday, 7 October 2014. The other types of certificates will be send by email.

CONGRESS BAG

Participants will receive a congress bag voucher with all the congress documents at the Registration Area (Congress Bags desk).

CONGRESS SECRETARIAT

HUPO 2014

TILESA KENES SPAIN
C/Londres, 17
28028, Madrid
Tel: + 34 91 361 26 00
Fax: +34 91 355 9208
E-mail: hupo2014@kenes.com
Website: http://www.hupo2014.com/

EXHIBITION AREA INFORMATION

The HUPO 2014 Exhibition, featuring commercial displays of International Organizations, Pharmaceutical Companies, Media Publishers and Scientific Societies, will be located in Pavilion 10 of the North Congress Centre, IFEMA. Catering facilities and Poster Sessions will also be located in the Exhibition hall.

EXHIBITION AREA SCHEDULE

Sunday 5 October 17:30h - 21:30h
Monday 6 October 08:00h - 20:00h
Tuesday 7 October 08:00h - 20:00h
Wednesday 8 October 08:00h -16:00h

COFFEE BREAKS

Coffee breaks are included in the Registration Fee.
They will be served in the Exhibition Hall in the Pavilion 10, from Monday 6 to Wednesday 8 September.

INTERNET

Free WIFI is provided in Pavilion 10 and the North Convention Center, IFEMA.

HUPO OFFICE

The Technical Secretariat will be located in the hall of the North Convention Center, IFEMA.

LANGUAGE

The official language of the 13th Human Proteome Organization World Congress is English.

POSTER SESSIONS

Posters will be displayed for the duration of the poster session. Poster presenters have been scheduled to be by their poster according to the program times. Odd numbers will be presented on Monday 6 October; even numbers will be presented on Tuesday 7 October. Wednesday 8 October remains for free presentations.

TECHNICAL SECRETARIAT

The Technical Secretariat at North Convention Center will be open as follows:

Sunday 5 October 08:00h - 19:30h

Monday 6 October 07:30h - 20:00h

Tuesday 7 October 07:30h - 20:00h

Wednesday 8 October 07:30h - 19:30h

RULES

Smoking Policy - The HUPO 2014 Congress is a non-smoking event. Participants are kindly requested to refrain from smoking in the Congress venue, including the Exhibition Area.

Mobile Phones - Delegates are kindly requested to keep their mobile phones in the off position in the rooms where scientific and educational sessions are being held, as well as during poster sessions.

TRANSPORTATION

By Metro:
Access to IFEMA is possible from anywhere in the city by means of Campo de las Naciones station on Line 8, whose exit is at the South Entrance of the complex. Line 8 also connects the exhibition complexes with the different terminals of Barajas International Airport.

By Bus:
A wide bus network provides access to Feria de Madrid from different points in the city:
Route 112-Mar de Cristal-Feria de Madrid-Bº Aeropuerto.
Route 122-Avda. de América-Campo de las Naciones-Feria de Madrid.
Route 828-Universidad Autónoma-Alcobendas-Canillejas-Feria de Madrid.

By Taxi:
With ranks at each entrance to the exhibition complex, more than 15,000 taxis are available to visitors to Feria de Madrid.

By car:
Feria de Madrid is linked by road to Madrid's major access routes and ring roads: the M11 (Exits 5 and 7), the M40 (Exits 5, 6 and 7) and the A2 (Exit 7). The South, North and East Entrances to the exhibition complex provide direct access to the various parking areas.

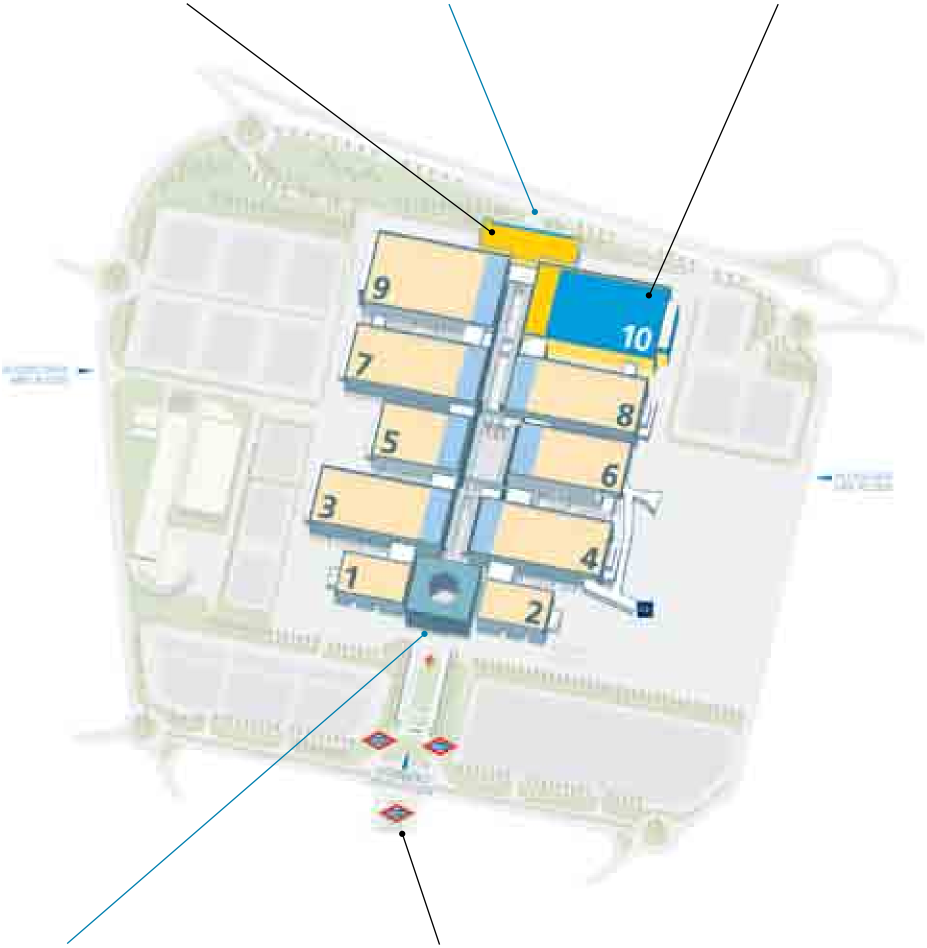
SPEAKER PREVIEW ROOM

Please ensure that you have visited the Speaker Preview Room to confirm your audiovisual requirements at least 2 hours prior to the start of your session. However, it is recommended speakers register with the Speaker Preview Room the day before their presentation. The Speaker Preview Room is located at the entrance of the Congress Centre.

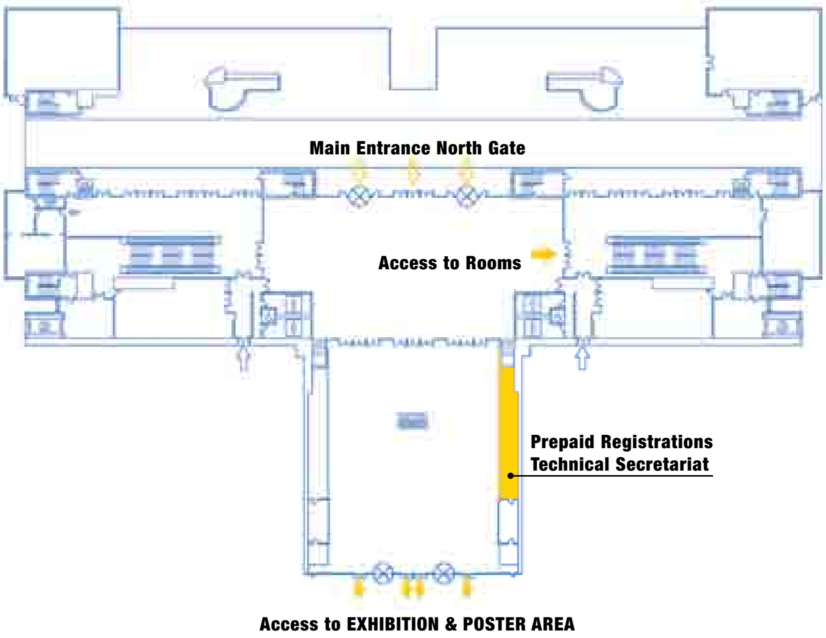
Opening times are as follows:

Sunday 5 October 08:00h - 19:30h
Monday 6 October 07:30h - 20:00h
Tuesday 7 October 07:30h - 20:00h
Wednesday 8 October 07:30h - 19:30h

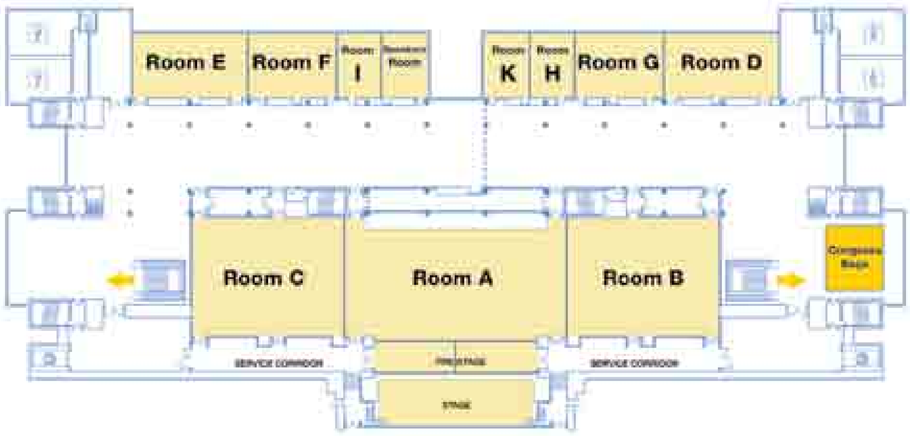
LOCATION MAP



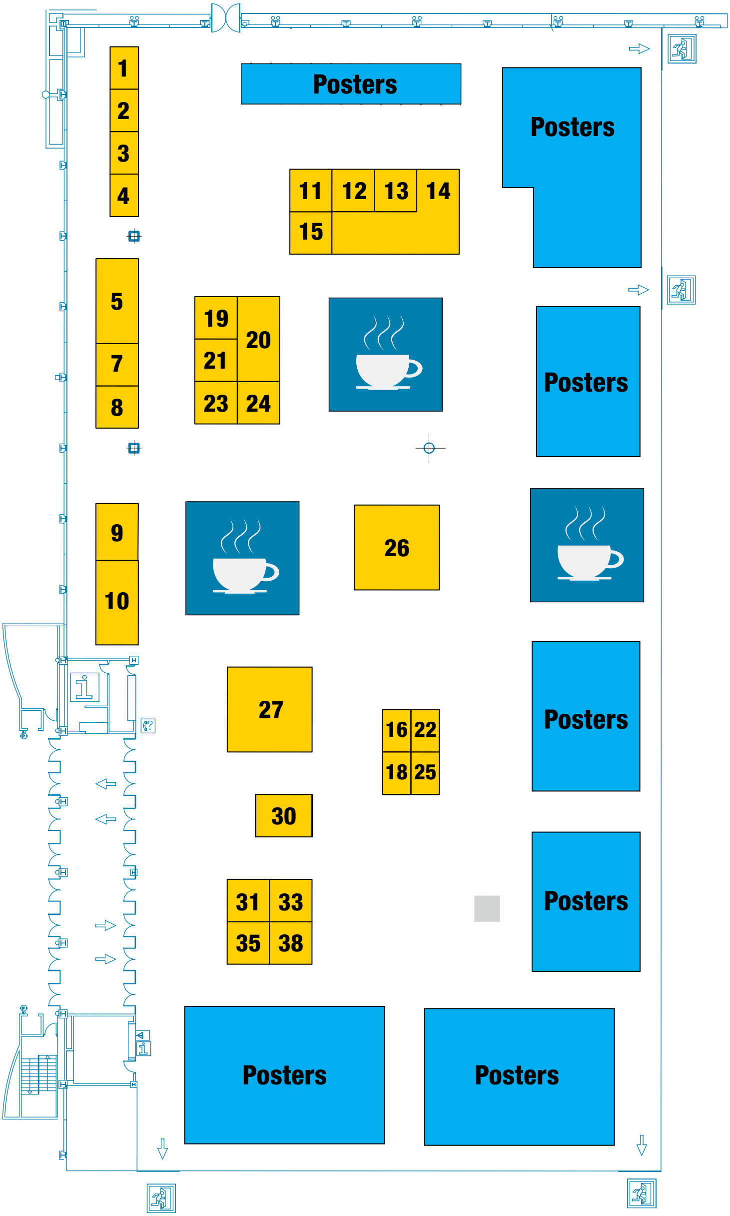
NORTH GATE - FLOOR 0



FLOOR 1 - MEETING ROOMS



EXHIBITION FLOOR PLAN



Exhibitor List

COMPANY	BOOTH Nº
ABCAM	4
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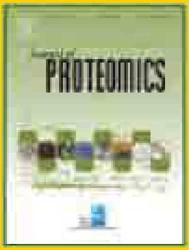
Luminex	9
Media Corner	5
MyCartis	19
Pressure Biosciences	38
Protein Simple	11
ProteoRed	22
PTM Biolabs	12
SEProt	25
Sigma Aldrich	31
Silantes	1
Thermo Fisher	14
Total Lab LTD	2
Waters S.A.S	20
Wiley	7

CALL FOR PAPERS



http://ees.elsevier.com/jprot/

Journal of Proteomics: Special Issue:

HUPO 2014

Guest Editors: Fernando J Corrales, Juan Calvete, Concha Gil

Submission Deadline: December 1st, 2014

The Scientific Committee is pleased to announce that a Special Issue containing selected papers from the **HUPO 2014** will be published in the **Journal of Proteomics**. All manuscripts will be refereed according to the scientific standards of the journal.

Those wishing to submit a review article, full-length article or technical reports for publication in the Special Issue, will have the option to do so online as of **1 October 2014**. Please note that the deadline for submission is **1 December 2014**.

In order to avoid delays in publication of the special issue, only papers requiring no or minor revision will be accepted for the special issue. Papers requiring major revision can be considered for later regular issues. The scientific quality of papers clearly falling within the scope of the Issue will be the only criteria for manuscript acceptance.

The use of colour is free in your article. Illustrations enhance the educational value of your article; the journal will publish a high resolution version of your artwork in the html version of your article, for easy downloading into PowerPoint slides shows. There are no page or figure restrictions – scientific quality and relevance are the main criteria.

Upon publication the corresponding author will at no cost, be provided with a personalized link providing 50 days free access to the final published version of the article on ScienceDirect. This link can also be used for sharing via email and social networks. The corresponding author will also receive 1 free copy of the issue.

Instructions for submission:

All manuscripts and any supplementary material should be submitted through the online submission system http://ees.elsevier.com/jprot Please select article type **"HUPO 2014"**. The covering letter of the article should be addressed to the Guest Editors and clearly indicate if the submission is a review, original article or technical report.

Further information regarding preparation and submission can be found in the Guide for Authors at
http://www.elsevier.com/journals/journal-of-proteomics/1874-3919/guide-for-authors
For more information please contact: **Jasmin Bakker** ja.bakker@elsevier.com

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Continuing what has become a tradition at HUPO meetings, Agilent Technologies is pleased to host the "Meeting of the Minds" on 7th October. This event allows young scientists to meet with established leaders in Proteomics in a social environment.

Company Profiles

AVACTA LIFE SCIENCES

Booth Nº21

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Fahrenheitstrasse 4 - 28359 Bremen - Germany
Phone: +49 (0)421-2205-0 - Fax: +49 (0)421-2205-104 - sales@bdal.de

Bruker Daltonics provides a broad range of high performance, easy to use Mass Spectrometry (MS) and analytical separation systems. Bruker delivers a series of innovative, fully integrated solutions for Proteomics, Metabolomics and Clinical Research areas, including:

- Biomarker Discovery & Characterization
- Qualitative and Quantitative Proteomics
- PTM Analysis
- Top-down Protein Characterization
- Molecular Imaging in Tissue
- Drug Research and Development
- Microorganism Identification
- Metabolite Discovery and Identification

By utilizing a product and technology portfolio which includes MALDI-TOF, UHR-QTOF, Ion Traps, FTMS as well as LC and GC systems, Bruker provides best solutions for the latest analytical questions.

CAMBRIDGE ISOTOPES

Booth Nº23

www.isotope.com

Cambridge Isotope Laboratories, Inc. (CIL) is the world leader in the manufacture of stable isotope-labeled compounds (13C, D, 15N, 17O, 18O) used for quantitative MS-based proteomic applications. Key innovative products include MouseExpress® Lysine 13C6 mouse feed and MouseExpress® Lysine 13C6 mouse tissue, MouseExpress® Spirulina 15N mouse feed and MouseExpress® 15N mouse tissue, 99% enriched amino acids, SILAC reagents and kits, amino acids for peptide synthesis, dimethyl labeling reagents, 18O water for enzymatic labeling and intact heavy labeled proteins, and an INLIGHT™ Glycan Tagging Kit for the relative quantification of N-linked glycans by mass spectrometry.

Company Profiles

CELL SIGNALING

Booth Nº34

www.cellsignal.com

Founded by research scientists in 1999, Cell Signaling Technology (CST) is a private, family-owned company with over 400 employees worldwide. Active in the field of applied systems biology research, particularly as it relates to cancer, CST understands the importance of using antibodies with high levels of specificity and lot-to-lot consistency. It's why we produce all of our antibodies in house, and perform painstaking validations for multiple applications. And the same CST scientists who produce our antibodies also provide technical support for customers, helping them design experiments, troubleshoot, and achieve reliable results. We do this because that's what we'd want if we were in the lab. Because, actually, we are www.cellsignal.com.

DENATOR

Booth Nº24

www.denator.com

Denator produces instruments and consumables, based on the company's proprietary sample preservation technology, within the life science and clinical research markets.
The Stabilizor™ T1 enables scientists to ensure the quality and in vivo profile of biological samples, by immediate and complete inactivation of enzymatic activity otherwise causing sample change and degradation. Its additive free, and enables reliable analysis and quantification of proteins, peptides and their modifications. It can be used for all tissue types, fresh or frozen, allowing secure analysis also of stored samples. Stabilized samples have improved signal-to-noise ratio, enabling detection of low abundant molecules such as potential biomarkers.

Company Profiles

EuPa

Booth Nº16

www.eupa2015.org

The European Proteomics Association (EuPA) is the federation of European national proteomics societies. It has been established to coordinate and integrate national initiatives within the proteomics field. The main objectives are to strengthen and promote fundamental research and applications, as well as education and training in all areas of proteomics throughout Europe. EuPA is a non-profit organisation.

EURISO-TOP

Booth Nº3

www.eurisotop.com

Euriso-top is the European leading provider of stable isotope-labeled compounds (13C, 15N, 18O, D) for Mass spectrometry (MS) based proteomics which has become over the last decade an essential tool for biologists. L-Arginine, L-Lysine, MouseExpress®, Mouse Feed and Tissue, Spirulina, Cell Growth Media, Labeled Proteins are among a large variety of reagents which will help you in the quantification of your proteins. Suitable with various applications like SILAC, SILAM, Peptide Synthesis Reagents, Protein expression, Chemical tagging.

With over 20 years of experience, Euriso-top offers full satisfaction to its customers through a comprehensive technical and commercial support.

Company Profiles

IBA GmbH

www.iba-lifesciences.com

Rudolf-Wissell-Str.28
37079 Göttingen
Tel.: +49-551-50672-0
Fax: +49-551-50672-181

IBA GmbH is covering with its proprietary products and services the entire production process of recombinant proteins. The combination of IBA´s proprietary Strep-tag® affinity purification technologies and StarGate® combinatorial cloning system provide optimal solutions for cloning, protein expression and purification as well as detection and immobilization of proteins.

HUPO

www.hupo.org

The Human Proteome Organization (HUPO) is an international scientific organization representing and promoting proteomics through international cooperation and collaborations by fostering the development of new technologies, techniques and training.

HUPO2015

Booth Nº18

www.hupo2015.com

Join us in Vancouver next year for the 14th HUPO World Congress September 27-30, 2015.
More information available at www.hupo2015.com

Company Profiles

JPT PEPTIDE TECHNOLOGIES

Booth Nº15

www.jpt.com

Innovative Peptide Solutions

JPT Peptide Technologies is the leading provider of innovative peptide tools and services for applications in discovery and targeted proteomics, peptide biomarker discovery, proteome spanning T-cell epitope discovery and enzyme profiling. JPT is the inventor of the SpikeTides and SpikeMix concepts for low cost provision of small scale, isotopically labeled and quantified peptides & peptide pools for the development of high-thoughput SRM/MRM assays and absolute quantification of protein expression levels. These approaches have been translated into a variety of ready to use, heavy labeled proteotypic peptide collections related to Cytokines, Tumor Associated Antigens, Kinase Activations Loops, Cross Species Standards and more.

LUMINEX

Booth Nº9

www.luminexcorp.eu

Luminex Corporation develops, manufactures and markets innovative biological testing technologies with applications throughout the clinical diagnostic and life science industries.
The company's open-architecture xMAP® and xTAG® Technologies enable large numbers of biological tests (bioassays) to be conducted and analyzed quickly, cost-effectively and accurately. Systems using xMAP technology perform discrete bioassays on the surface of color-coded beads known as microspheres, which are then read in a compact analyzer. Further information on Luminex Corporation or xMAP can be obtained at www.luminexcorp.eu.

MY CARTIS

Booth Nº19

www.mycartis.net

"Evalution™ is Mycartis' multiplex analysis platform tailored to the clinical research and pharmaceutical markets and designed to analyze a broad range of protein and nucleic acid-based biomarkers, delivering superior data quality and rapid results. Evalution™ provides an integrated reaction and detection environment and simultaneous analysis of large numbers of analytes per assay."

Company Profiles

PRESSURE BIOSCIENCES

Booth Nº38

www.pressurebiosciences.com

Pressure BioSciences, Inc. (“PBI”) (OTCQB: PBIO) develops and sells proprietary laboratory instrumentation and associated consumables based on Pressure Cycling Technology (“PCT”). PCT is a patented, enabling platform that uses cycles of hydrostatic pressure between ambient and ultra-high levels. PCT has proven applications in enhanced proteomic research, biomarker discovery, bio-therapeutics characterization, vaccine development, histology, and in many other fields. PBI will feature its new Barozyme HT48 for high throughput accelerated enzymatic digestion and its MicroPestle System for protein extraction from minute samples. In addition, PBI will showcase Constant Systems cell disruptors for small to pilot-scale protein extraction from yeast, bacteria, and other organisms.

PROTEIN SIMPLE

Booth Nº11

www.proteinsimple.com

Our goal is simply to help researchers gain a better understanding of proteins and their role in disease. We develop and commercialize proprietary systems and consumables for protein analysis that ultimately help reveal new insights into the true nature of proteins. Our goal is to make protein analysis simpler, more quantitative and affordable. Our comprehensive portfolio of tools includes Simple Western systems that quantify protein expression and Biologics systems that probe the structure and purity of protein-based therapeutics.

PROTEORED

Booth Nº22

www.proteored.org

The main objective of ProteoRed consortium is to coordinate and integrate activities of the Spanish proteomic facilities and services in a common network with a nodal structure, so they will support the whole development of the proteomic research in our country. For this purpose, ProteoRed has been constituted as a technological platform composed by six nodes, supporting 17 + 2 proteomic facilities placed all over Spain.

Company Profiles

PTM BIOLABS

Booth Nº12

www.ptm-biolab.com

PTM Biolabs, Inc is the only organization specifically for providing superior proteomics services and manufacturing antibodies targeting to protein post-translational modifications (PTMs) and epigenetics. Our technology and products help to explore the most comprehensive PTM pathways, including acetylation, methylation, phosphorylation, ubiquitination, glycosylation, crotonylation, succinylation, malonylation, etc.

Our proteomics services provides customer-orientied analysis utilizing the integrated platform with premium PTM reagents, high-end mass spectrometry and unrivaled software application. This superior technology can be applied for PTM identification, global screening of enzyme substrates, quantification of PTM dynamics, and discovery of biomarker and drug targets in biomedical and pharmaceutical pre-clinical research.

Our PTM antibodies are the most comprehensive PTM reagents collection worldwide, offering unparalleled advantages for PTM proteomics.

SEPROT

Booth Nº25

www.2.cbm.uam.es/seprot/

The Spanish Proteomics Society (SEProt) was founded in 2004 and it currently has about 200 members .The main objective of SEProt is "to promote the development of Proteomics in Spain". This is to be done by encouraging scientific and technical research in the field of Proteomics, by promoting training, learning and formation in this field, and by sponsoring and facilitating the organization and/or participation of their members in national or international activities, courses, workshops and meetings and any kind of cooperation and interchange with other societies.

Company Profiles

SIGMA ALDRICH

Booth Nº31

www.sigma-aldrich.com

SIGMA® Life Science offers a wide portfolio of innovative technologies, products and services spanning cell biology, proteomics, protein biochemistry, genomics, functional genomics, biomolecules and epigenetics. Through continued investment in innovation and quality we are the leading destination for life science researchers to access deep biological information and market leading products that improve the quality of life.

SILANTES

Booth Nº1

www.silantes.com

Silantes activities are focused on the production and marketing of compounds labelled with stable isotopes (SI: 2H, 13C and 15N) used in NMR structural analysis and quantitative mass spectrometry. Silantes is specialized on SILAC-products.

Silantes SI-platforms are:

- Heteronuclear NMR providing

- SI-labelled growth media for E.coli and yeast;
- SI-labelled nucleotides (d/rNTP, NMPs);

- Quantitative proteomics providing

- SI-amino acids;
- kits for cell culture-labelling (SILAC);
- kits for in vivo-13C-lys-labelling of SILAC-mouse, SILAC-fly, SILAC-zebrafish etc.
- Service for in vivo proteomics in mice

Company Profiles

THERMO FISHER

www.thermoscientific.com

Booth Nº14

Thermo Fisher Scientific is the world leader in serving science, enabling you to make the world healthier, cleaner and safer. With annual sales of more than $17 billion and 50,000 staff, we serve our customers worldwide within a broad range of markets and sectors.

With four premier brands we help solve analytical challenges from routine testing to complex research and discovery. Thermo Scientific is the leading brand for technology innovation and offers customers a complete range of high-end analytical instruments as well as laboratory equipment, software, services, consumables and reagents to enable integrated laboratory workflow solutions across all fields of proteomics research".

TOTAL LAB LTD

www.totallab.com

Booth Nº2

The Phoretix family of software for electrophoresis analysis was first produced in 1991. TotalLab was first released in 1999 representing a breakthrough in levels of automation and ease of use. Both were developed by Nonlinear Dynamics Ltd.

In 2002 ImageQuant TL™ (IQTL) was created for GE Healthcare by the TotalLab team based on TotalLab v2.

TotalLab Ltd was spun-off from Nonlinear in 2007 taking with it the Phoretix and TotalLab product ranges and, in 2009, a new management team was created to push forward new development projects required to satisfy changing market needs.

Now in 2013 SameSpots for 2D Gel analysis has moved over to TotalLab Ltd from Nonlinear Dynamics.

Nonlinear Dynamics continues to develop their leading-edge Progenesis range of software for LC-MS, Metabolomics and MALDI.

Company Profiles

WATERS S.A.S **Booth Nº20**

www.waters.com

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™

Waters is a leading resource for tailored analytical solutions to meet the demands of leading proteomics and biomarker discovery research laboratories. Building on more than 50 years of experience, our advanced systems provide the gold standard in data quality and efficiency for protein discovery, characterization, quantification, and validation.

Waters' patented innovations in UltraPerformance LC (UPLC), Ion Mobility Separation (IMS), and High Definition Mass Spectrometry (HDMS) provide uniquely powerful tools unmatched by conventional LC/MSbased strategies for the best qualitative and quantitative proteomics

Our Publishers

Science
AAAS

CLINICAL PROTEOMICS

ELSEVIER

european pharmaceutical review

IOS Press

Journal of proteome research

GEN
Genetic Engineering & Biotechnology News

MCP MOLECULAR & CELLULAR PROTEOMICS

PS PROTEOME SCIENCE

ROYAL SOCIETY OF CHEMISTRY

AUTHORS INDEX

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14TH HUMAN PROTEOME ORGANIZATION WORLD CONGRESS

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BCProteomicsNetwork

Translating Proteomics and
Allied -Omics to the Clinic

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