# Poster Presentations: Tuesday (Sept 29th, 2009)
# Frontenac Room

## Computational Approaches and Proteomic Datasets (C501 – C552)

**C501** *MacroSEQUEST: An Analysis of Candidate-centric Searching for Proteomics*
B. Faherty, D. Jewell, J. Milloy, and Scott Gerber

**C502** *Mesothelial Cell Stress Response to Peritoneal Dialysis Fluid – Potential Role of Glucose*
M Lechner, K Kratochwill, A Lichtenauer, P Perco, K Herkner, B Mayer, C Aufricht, and A Rizzi

**C503** *Gene-centric Knowledge-base of Human Proteins Coded in 18th Chromosome*
A.V. Lisitsa, A.L. Chernobrovkin, E.A. Ponomarenko and A.I. Archakov

**C504** *CPFP – The Oxford Central Proteomics Facility Pipeline*
D C Trudgian, S J McGowan, M Salek, B Thomas, O Acuto, B M Kessler

**C505** *Improving Transition Selection using Synthetic Peptide Database for TPM/MRM Pipeline*
V. Fong, J. A. Hewel, J. Liu, E. Ameis, X.Yang, S. Sureshkumar, A. Pun, A. Emili

**C506** *Variations of Peptide Ion Intensities in ESI LC-MS Experiments*
B Godugu, LE Kilpatrick, P Neta, PA Rudnick, SE Stein, DV Tchekhovskoi, X Yan

**C507** *Spectral Counting - An Easy To Use and Cost Effective Method for Label Free Proteomics.*
C. Stephan, M. Kohl, K. Podwojski, M. Turewicz, B. Sitek, S. Link, B. Korte, K. Stuhler, H. E. Meyer, M. Eisenacher

**C508** *Quantitative Toponome Analysis of KRAB ZNF Data Sets Present in the Proteinatlas Database*
P. Lorenz, Z. Qian, L. Kiseleva, B. Ziems, M. Kreutzer, C. Al-Khalili Szigyarto, Y. Li, M. Uhlén, H.-J. Thiesen

**C509** *Antibodypedia – A Portal for Sharing Antibody and Antigen Validation Data*
Kalle Jonasson, Lisa Berglund and Mathias Uhlen

**C510** *Modeling of Protein Networks in Complex Systems for the Optimization and Control of Bioprocesses*
M. Eisenacher, M. Kohl, K. Podwojski, M. A. Turewicz, H. E. Meyer, C. Stephan

**C511** *The Contaminant Repository for Affinity Purification (CRAP) project*
Alexey I. Nesvizhskii, Rob M. Ewing, and Anne-Claude Gingras

**C512** *Identification of Peptide PTMs and Allelic Changes using An Unbiased Search Algorithm*
B Halligan, S Parker, A Vallejos, S Twigger, A Greene

**C513** *ProHits: An Open Source Flexible Integrated LIMS and Analysis Platform for Interaction Proteomics*
F. Liu, J.P. Zhang, B. Larsen, A. Breitreutz, Z. Lin, A. Nesvizhskii, A.-C. Gingras, M. Tyers

**C514** *Possible Reasons of Ambiguity in Expression Study by Microarray and Ion Trap Proteomics*
TV Andreewski, VG Zgoda, LK Kurbatov, AT Kopylov, SA Moshkovskii, and AI Archakov

**C515** *InterPro: Deciphering the Human Proteome*
J. S. McDowall, S. Hunter

**C516** *Using the Global Proteome Machine Database to Define Protein Interaction Environments*
C Zhang, D Evans, R Beavis, J Kast

**C517** *A New Versatile File Translator for Proteomics Standards*
J.Alberto Medina-Aunon, S. Martinez de Bartolomeand J. Pablo Albar

**C518** *Computational Refinement of Post-translational Modifications Predicted from Tandem MS Data*
C Chung, J Liu, A Emili, and B Frey

**C519** *Analysis of Multiple Protein Marker Panels: Optimizing Sensitivity and Selectivity*
M. Athanas, A, Prakash, T. Rezai, B. Krastins, D. Sarracino, Kypros Nicolaides, Ramesh Kuppusamy, Mary F. Lopez

**C520** *Metabolic Llabeling Validation of Peptide MS/MS Spectral Library for Spectral Matching Strategy*
M. Xu, L. Li

**C521** *Analysis and Interpretation of Multiple Proteomic Datasets – Biologically Relevant Information Obtained in Less Than 3 Hours*
Christian Ingrell, Morten Bern, Alexandre Podtelejnikov, Ole Horning, Ole Vorm

**C522** *A Novel Protein Scoring Algorithm for Shotgun Proteomics*
N. Berntenis, S. Kux van Geijtenbeek, A. Ducret

**C523** *Automatic Alignment, Statistical Restoration and Quantification of Raw LC/MS and 2-DE Data*
AW Dowsey, G-Z Yang

**C524** *Pathway Analysis of Heart Disease Proteomic Profiles using Enrichment Maps*
R Isserlin, D Merico, A Gramolini, GD Bader, A Emili

**C525** *Peptide Detectability Prediction using Support Vector Machines with Novel Kernels*
E.Qeli, E. Brunner, K. Basler, C. Ahrens

**C526** *Integrated Time Alignment Application for Complex LC-MS Datasets*
C. Christin, A. Smilde, H. Hoefsloot, F. Suits, R. Bischoff, P. L. Horvatovich

**C527** *Towards a Better Understanding of Matrix Interferences in SRM*
T.Rezai, A. Prakash, B. Krastins, D. Sarracino, M. Athanas, M. F. Lopez, B.Domon

**C528** *Chromatographic peak centred approach improves phospho-peptide identification*
M.M. Savitsky, A.Scholten, G.Sweetman, T.Mathieson and M.Bantscheff

**C529** *Human Genome Re-annotation by Proteogenomic Mapping*
Jainab Khatun and Morgan C Giddings

**C530** *ITM Probe: Analyzing Information Flow in Protein Networks*
A. Stojmirovic and Y-K Yu

**C531** *Bioinformatics for Systems Biology: Directed Shotgun Proteomics & Deterministic Protein Inference*
E. Qeli, E. Brunner, M. Grobei, C. Panse, U. Grossniklaus, K. Basler, C.H. Ahrens

**C532** *Variability in Sample Preparation Protocols and LC-MS/MS Analysis*
L Kilpatrick, Y Mirokhin, J Roth, P Rudnick, X Yan, S Stein

**C533** *Searching Peptide Mass Spectral Libraries Using a "Target-Decoy" Strategy*
P. Rudnick, K. Clauser, L. Kilpatrick, Y. Mirokhin, J. Roth, D. Tchekhovskoi, S. Stein

**C534** *A Bayesian Approach to Distinguish Signal and Noise Peaks in Peptide Tandem Mass Spectra*
Wenguang Shao, Xin Zhang, Henry H. Lam

**C535** *Mass Spectrometry-Based Gene Annotation – A Study of Cell-Wall Surface Proteins from C. difficile*
MR Di Falco, V Forgetta, S LaBoissiere, L Roy, D Boismenu, R Blanchette, A Dascal and K Dewar

**C536** *DomPep - A Method for Predicting Modular Domain-linear Peptide Motif Recognition*
Lei Li, Bing Zhao, Jun Du, Xinfeng Jiang, Kaizhong Zhang, Carles X. Ling, Shawn Shun-Cheng Li

**C537** *Significant Improvements to the HUPO-PSI Mass Spectrometer Data File Standard mzML*
P-A Binz, M Chambers, L Martens, M Sturm, D Kessner, F Levander, J Shofstahl, W Tang, AD Pizarro, L Montecchi-Palazzi, N Tasman, M Coleman, P Souda, H Hermjakob, E Deutsch

**C538** *Fingerprinting Bacterial Strains Utilizing LC/MS-based Profiling of Intact Proteins*
C. Miller, C. Carstens, B. Buehler, D. Horn and N. Kittagawa

**C539** *An Integrated Data Management Platform for Proteomics and Biomarker Discovery*
M. Dharsee, P.H. Nuin, P. Zhu, J. Bon, M. Sanders, R.M. Ewing, I.I. Stewart, T. Sills, K. Evans

**C540** *New Functionality for the Trans-Proteomic Pipeline: Tools for the Analysis of Proteomics Data*
Luis Mendoza, David Shteynberg, Natalie Tasman, Brian S Pratt, Henry Lam, Jimmy Eng, Alexey Nesvizhskii, Eric Deutsch, Ruedi Aebersold

**C541** *Efficient and Confident Identification of Protein Phosphorylation by Combining Dephosphorylation Reaction and High Mass Accuracy LC-MS Data*
HY Wu, VS Tseng, LC Chen, YC Chang, P Ping, YG Tsay, JS Yu, and PC Liao

**C542** *ICPL Meets ESI Platforms: ICPL-ESIQuant for Analyzing Stable Isotope Labeled Proteomic Data*
A Brunner, EM Keidel, D Dosch, J Kellermann and F Lottspeich

**C543** *Effective Mapping of Disulfide Bridges in Proteins Combining Informatics and $^{16}O/^{18}O$ Labeling*
Ya-Fen Chen and Yeou-Guang Tsay

**C544** *Bioinformatics Analysis of Quantitative Proteomics Datasets using Soft Clustering Algorithms*

M.Damsbo, C.Ingrell, A.Podtelejnikov, M.Trelle, M. Andersen

**C545** *Protein List Comparator (ProLiC): a Framework for Comparison of Protein Lists*
M Kohl, M Eisenacher, B Schonebeck, C. May, P Chartowski, F Brosseron, K Podwojski, M A Turewicz, H E Meyer, K Marcus and C Stephan

**C546** *Public Proteomics Data - of Carrots and Sticks*
Henning Hermjakob

**C547** *Deconvolution of Multiply Charged States of Intact Proteins*
N Belyaeva, T Pekar Second

**C548** *GeneMANIA: Gene Function Prediction using a Multiple Association Network Integration Algorithm*
SL Donaldson, GD Bader and QD Morris

**C549** *Protein Ontology (PRO) for Proteomics Data Integration*
CH Wu and PRO consortium

**C550** *APCF: a Large Proteomics Computational Resource and APCF UNITE for Launching and Viewing Data*
Robert L. Moritz, Simon Michnowicz and Jagan Kommineni

**C551** *ProteomeCommons.org Annotations and Project Management Resource*
JA Hill, BE Smith, M Gjukich, PC Andrews

**C552** *Recent and Upcoming Development in the Tranche Distributed Data Repository*
B Smith, J Hill, M Gjukich, P Andrews

**C553** *Homology Modelling of Salvia miltiorrhiza Lectin*
Edgar Antonio Reyes Montaño

## Environmental Proteomics (E101-E110)

**E101** *Proteome Analysis of Sulfur-reducing Hyperthermophilic Archaeon Thermococcus onnurineus NA1*
SO Kwon, SH Yun, CW Choi, SI Kim & JS Choi

**E102** *Proteomics of Bronchoalveolar Lavage Fluid: Adjuvant Effects of Ambient Particulate Matter*
X Kang, M Wang, N Li, P Boontheung, AE Nel and JA Loo

**E103** *Proteome Analysis of the Different Stages of the Biofilm Formation in Rhizobium etli*
Agustín Reyes-Pérez, Magdalena Hernández and Sergio Encarnación

**E104** *Development of Biomarkers for Pesticide Induced Carcinogenicity in Rodents: A Proteomic Approach*
George Jasmine, Mahmood Zafar and Shukla Yogeshwer

**E105** *Differential Expression of Proteins by LPA and ACI between Young and Senescent HDFs*
KE Yang, IC Kim, SH Kim, JS Choi, IS Jang

**E106** *Assessment of Chemical Effects in Neural Stem Cell using Proteomics and Cyclic Voltammetry*
Jeung Hee An, Chang- Mi Oh, Waleed Ahmed El-Said, and Jeong-Woo Choi

**E107** *Identification of PerR-Regulated Secreted Virulence Factors of Environmental Pathogen Streptococcus Pyogenes Using Comparative Proteomics Analysis*
Y. T. Wen, C. C. Tsou, J. J. Wu and P. C. Liao

**E108** *Mass Spectrometric Analysis of Protein Fatty Acyl Modifications in Membrane Signal Transduction*
Hongying Zhong, Jianjian Li, Yingxia Yue

**E109** *Environmental Proteomics, Tool to Search for Biological Effects of Emerging Pollutants*
Susana Cristobal

**E110** *Phosphoproteome Analysis of Pathogenic and Non-pathogenic Pseudomonas Species*
Ayshwarya Ravichandran, Naoyuki Sugiyama, Masaru Tomita, Sanjay Swarup, and Yasushi Ishihama

## Glycoproteomics (G101-G124)

**G101** *The Plasma Glycome: An Approach to the Early Detection of Cancer*
W. Hancock, M. Hincapie, M. Kullolli, and T. Plavina

**G102** *Fucosylated Glycoproteins as Biomarker Candidates for Heptocellular Carcinoma*
Y.S. Liu, J.T. He, X.L. Xie, C Li, D.M. Lubman

**G103** *Quantitative Analysis of N-glycoproteins in Search of the Disease Biomarker in HCC*
HJ Lee, K Na, H Kim, KS Kim, and YK Paik

**G104** *Characterization of Glycopeptides in Complex Systems Matrices Using LC-MSE*
C A Dorschel, R R Sprenger, J P C Vissers, and S J Geromanos

**G105** *Analysis of Sulfated Glycans by MALDI-Orbitrap and DHB/N,N-Dimethylaniline Matrix*
J Saba, P Drake, A Prakobphol, S Robinson, SJ Fisher, and R Viner

**G106** *Improved Analytical Strategy for Glycoproteome by Combined Enzymatic Deglycosylation*
Wei Zhang, Hong Wang, Mingqi Liu, Weiqian Cao, Liming Wei, Jing Cao, Pengyuan Yang

**G107** *Glycopeptides Analysis Using Cellulose-based Separation Cartridges and LTQ Orbitrap ETD*
RI Viner, J Saba, S Snovida, E. Bodnar, and Helene Perreault

**G108** *Glyco Chain Explorer: A Comprehensive Platform to Interpret Glycopeptides*
Yang Zhang, Mingqi Liu, Chengpin Shen, Yang Pengyuan, Fuchu He

**G109** *Membrane Glycoproteomics of Liver Inflammation in the Presence of a Distal Benign tumour*
A.Lee, J.M Chick, M. Tsoli, L. Jankova, D. Kolarich, P.A. Haynes, P.H Jensen, S.J Clarke, G.R. Robertson, N.H. Packer, M.S. Baker

**G110** *Automated N-Glycan Composition Analysis with LC-MS/MS*
H Peltoniemi, I Ritamo, J Rabina and L Valmu

**G111** *Glycoprotein Profiling using Tandem Mass Tags and Staudinger Ligation of Azido Sugars*
R Bomgarden, C Etienne, M Rosenblatt, A Deshpande, J Rogers, and B Kaboord

**G112** *Quantitative Proteomic Approach to Analyze Glycoprotein Regulation in Response to Hypoxia*
S Thaminy, Y Zhou, M Brusniak, N Zhang, Simon Letarte, Carey Sheu, Julian D. Watts and Ruedi Aebersold

**G113** *A Novel Human in vitro Translation System for Glycoprotein Expression*
K. Vattem, S. Mikami, K. Maas, E. Hommema, A. Morgan, M. Schofield, B. Webb, A. Deshpande and H. Imataka

**G114** *Analysis of Glycoproteins from Cancer Stem-Like Cells by a Lectin Affinity Approach*
J.T. He, Y.S. Liu, X.L. Xie, X. Fan, F. Xiang, D.M. Lubman

**G115** *Identification of Urinary Glycoprotein Biomarkers for Human Bladder Cancer by Multi-Lectin Affinity Chromatography and LC-MS/MS*
Na Yang, Shun Feng, Huy Vuong, Steve Goodison, Charles J. Rosser, Fan Xiang, David M. Lubman

**G116** *Tandem 18O Stable Isotope Labeling for Quantification of N-glycoproteome*
Ze Liu, Jing Cao, Yifeng He, Congjian Xu, Haojie Lu, and Pengyuan Yang

**G117** *A Novel Two-step Protease Digestion Approach for More Confirmed Glycoprotein Identification*
Yaohan Chen, Jing Cao, Pengyuan Yang

**G118** *Altered Glycoproteins in Distal Renal Tubular Cells upon Calcium Oxalate Dihydrate Crystal Adhesion*
Wararat Chiangjong, Supachok Sinchaikul, Shui-Tein Chen, and Visith Thongboonkerd

**G119** *Quantifying N-Glycosylation Distribution in Therapeutic Recombinant IgG using MRM Strategies and Triple Quadrupole Linear Ion Trap MS technology*
J. Albanese, C. L. Hunter, C. Fernandez-Metzler

**G120** *Beyond Proteomics: Everywhere We Look, The Sugars They are A-Changin ′*
Daniel Kolarich, Katherine Wongtrakul-Kish, Jenny Chik, Albert Lee, Miyako Nakano, Pia Hønnerup Jensen, Nandan Deshpande, Hiren Joshi, Jasmine Grinyer and Nicolle Packer

**G121** *Profiling the N-linked Glycome from Chicken Plasma to Identify Epithelial Ovarian Cancer Biomarkers*
D. C. Muddiman, R. B. Dixon, M. S. Bereman, A. M. Hawkridge, J. Petitte, and W.A. Cliby

**G122** *Comprehensive Analysis of Core-Fucosylated Glycoproteins from Mouse Embryonic Fibroblast (MEF)*
A Kurimoto, S Kitazume, Y Wada, and N Taniguchi

**G123** *Drug Resistance Inhibits Expression of $\alpha$2-6 Sialylated Glycans on Cell Membrane Proteins*
Miyako Nakano, Pia H. Jensen, Albert Lee, Rohit Saldanha, Daniel Kolarich, Maria Kavallaris , Nicolle H. Packer

**G124** *Protein O-GlcNAc Site Assignments by Electron Transfer Dissociation (ETD) Mass Spectrometry*
A.L. Burlingame, R. J. Chalkley, A. Ioanoviciu, A. Thalhammer and R Schoepfer

## Isotope-Dilution Mass Spectrometry (I301 – I303)

**I301** *Identification of the Target of an Innate Defense Regulator (IDR) using SILAC*
MM Guarna, Y Li, HB Yu, A Rozek, O Donini, BB Finlay and LJ Foster

**I302** *Proteomic Analysis of Programmed Genome Rearrangements in Tetrahymena thermophila using iTRAQ and LC-MS/MS*
X. S. Wang, O. Braguinets, R. E. Pearlman, and K. W. M. Siu

**I303** *Multiplex quantification of heart failure biomarkers using Protein Standard Absolute Quantification*
C. Huillet, A. Adrait, D. Lebert, M. Trauchessec, M. Jaquinod, A. Dupuis, J. Garin and V. Brun

# Poster Presentations: Tuesday (Sept 29th, 2009)
# Metro West

## Human Proteome Projects (H101 – H122)

**H101** *Russia on 18th Chromosome: Strategy and End-point*
A Archakov

**H102** *Evaluating the Impact of Salts on IEF protein separation*
SY Wu, HC Wu, TN Chen, and HM Chen

**H103** *A Human Plasma Proteome in the Peptide Atlas with Estimated Protein Concentrations*
T Farrah, E W Deutsch, N Zhang, D Shteynberg, H Lam, D Campbell, N Tasman, Z Sun, L Mendoza, G S Omenn, R Aebersold

**H104** *How Much is Enough? An Algorithm for Optimizing IEF Condition in 2-DE Experiments*
CY Lin, HC Wu, TN Chen and HM Chen

**H105** *Phosphoproteomic Study of Insulin Resistance in Type 2 Diabetes*
Tine E. Thingholm, Ole N. Jensen, Henning Beck-Nielsen, Michael Gaster

**H106** *Acetyl-Proteomics for the Investigation of Pathological Molecules in Rheumatoid Arthritis*
M Arito, M Kurokawa, K Masuko, K Okamoto, K Nagai, N Suematsu and T Kato

**H107** *Proteomics Analysis of Hepatocellular Carcinoma Caused by Hepatitis C Virus*
K Sugihara, Y Kuramitsu, T Tanaka, M Fujimoto, M Oka, and K Nakamura

**H108** *Atlas of Korean Plasma Proteome*
SK Jeong, EY Lee, JY Cho, HJ Lee, AS Jeong, SY Cho and YK Paik

**H109** *Global Detection of Human Protein Complexes by Fractionomic Profiling and Tandem Mass Spectrometry*
PC Havugimana and A. Emili

**H110** *Novel Proteins Associated with Uterine Receptivity in Fertile Women*
Tanu Bajaj, Geetanjali Sachdeva, Rajendra katkam, Lalita Savardekar, Pervin Meherji, Chander P Puri

**H111** *Novel Putative CRP and sFLT1 Sensors for the Point-of-Care Diagnostic*
H Dortay, B Mueller-Roeber and M Steup

**H112** *Sequential Proteome Profiles of Joint Inflammation in Arthritis Patients*
David S. Gibson, Margalit Rosenkranz, Raphael Hirsch, Caitriona Scaife, Stephen Pennington, Michael Dunn, and Madeleine Rooney.

**H113** *Semen Proteomics: Novel Technique to Identify Biomarkers of Reproductive Tract Disorders*
Ihor Batruch, Chris R. Smith, Eleftherios P. Diamandis, Robyn Halbot, Chang Han Ho, Brendan J. Mullen, Ethan Grober, Kirk C. Lo, and Keith A. Jarvi

**H114** *CrkRS/CDK12 Interacts with a Novel isoform of Cyclin K & Phosphorylates the C-terminal Domain of RNA Pol2*
S.-W.G. Cheng, M.A. Kuzyk, A. Moradian, J. F. Tien, S.E. Vollett, T. Ichu, E.K. Schaeffer, and G.B. Morin

**H115** *Understanding Innate and Adaptive Immunity: A Large Scale Proteomic Evaluation*
J Stephenson, C Whisnant, D Talley, N Garge, M Rowland, M Gardner, D Wagener, S Wu, G Page, H Staats, and P Majumder

**H116** *HT-Yeast Two-Hybrid for Generating Antibodies against the Human Proteome*
Michael P. Weiner, Dawn Alderman, Margaret Kiss and Daniel Gelperin

**H117** *Identification of Hypermethylated Genes in Lung Cancer Cell Line by Proteomics*
F Peng, T Tan, and ZQ Xiao

**H118** *Identification of Novel Biomarkers for Diabetic Retinopathy in Human Tears*
Terry Nguyen-Khuong, Valerie Wasinger, Anna Fitzgerald, Zhenjun Zhao, Mark DP Willcox, Bradley J Walsh,

**H119** *The Protein Production Pipeline in the HPR-project*
H Tegel, M Uhlén, S Hober and J Ottosson

**H120** *The Effect of Transforming Tobacco Leaves with a Gene Expressing the Heavy and Light Chain of Rabies Antibody on the Proteome*
P Mathabe, S Stoychev, D Mancama, T Stark, E Chakauya and R Chikwamba

**H121** *A Human Protein Atlas for Profiling Cells, Tissues and Organs*
Mathias Uhlen

**H122** *Mapping and Measuring Proteomes*
Ruedi Aebersold

## Innovation in Peptide & Protein Separation Technologies (I101 – I133)

**I101** *A New protocol for High-Yield Purification of Recombinant Human CXCL8(3-72)K11R/G31P Expressed in Escherichia coli*
Jya-Wei Cheng, Hsi-Tsung Cheng, Bak-Sau Yip, Hui-Yuan Yu, Xixing Zhao, Fang Li, Jennifer Town, John R. Gordon, and Kuo-Chung Huang

**I102** *Quantification of Predictive Toxicoproteomic Biomarkers of Inflammatory Diseases by Immunoaffinity Capillary Electrophoresis*
Norberto A. Guzman

**I103** *3D-Gel Electrophoresis, a New Approach to Protein Analysis*
Robert Ventzki, Sjouke Hoving, Jorg Bernhardt, Jan van Oostrum, and Josef Stegemann

**I104** *RPLC Proteome Fractionation for Shotgun Proteome Mapping of MCF-7 Cell Membranes*
X Ye, N Wang, and L Li

**I105** *Identification and Absolute Quantitation of Clostridium Acetobutylicum Proteins using 2D RP/RP LC MS*
Thérèse McKenna, Joanne B. Connolly, Chris Hughes, Jim Langridge, Philippe Soucaille and Gwenaelle Bestel-Corre

**I106** *Simultaneous Detection of Posttranslational Modifications of Proteins with Quantum Dot Technology*
M Oh-Ishi, T Isobe, Y Kodera, T Maeda

**I107** *Investigating Reproducibility of LC-MS Analysis of Complex Peptide Mixtures using FFPE Tissue*
C.J. Hughes, T. McKenna, J. Langridge, N. Nirmalan, R. Banks

**I108** *SRM to Identify Low Abundant Olfactory Receptors from Human Spermatozoa*
Kathrin Bartho and Dirk Wolters

**I109** *Analysis of Proteins Secreted by Cultured Cells in Serum-Containing Media*
M. Colzani, P. Waridel, J. Laurent, E. Faes, C. Ruegg, M. Quadroni

**I110** *The Interaction Network of the Phosphatase PP1 through optimized LCMS for gelfree AP-MS samples*
B Larsen, ZY. Lin, A.-C. Gingras

**I111** *Highly Reproducible Data from a Microfluidic Separation Platform for Proteomics*
R. van Soest, J. B. Young, N. Hebert, D. Wyrick, E.Lin

**I112** *Protease Substrates Discovery Using Terminal Amine Isotope Labeling of Substrates (TAILS)*
Alain Doucet, Kleifeld O., auf dem Keller U., Schilling O., Foster L., Kizhakkedathu J., Christopher M. Overall

**I113** *Ultra-high-performance nanoLC-MS/MS Analysis of Complex Proteomic Samples*
Evert-Jan Sneekes, Bjorn de Haan, Sebastiaan Eeltink and Remco Swart

**I114** *Design of Monolithic nanoLC Columns for Ultra-High-Efficiency LC-MS Peptide Mapping*
Sebastiaan Eeltink, Evert-Jan Sneekes and Remco Swart

**I115** *Protein Equalizer Based on scFv Displaying M13 Phage Library for Serum Proteome Analysis*
Peng Zhao, Lihua Zhang, Zhen Liang and Yukui Zhang

**I116** *Optimization of the Sample Preparation in Urinary Proteomics*
H Loftheim, TD Nguyen, H Malerod, E Lundanes, A Asberg and L Reubsaet

**I117** *Specific Enrichment of Multiply Phosphorylated Peptides in Aliphatic Hydroxy Acid-Modified Metal Oxide Chromatography (HAMMOC)*
Y.Kyono, N.Sugiyama, M.Tomita, Y.Ishihama

**I118** *Mapping the Trypsin-Resistant Proteome by Targeted Multi-Enzyme Digestion of Large Tryptic Peptides*
B. Tran, C. Hernandez, P. Waridel, M. Quadroni

**I119** *Simple Immunoprecipitation of Phosphorylated Proteins from CHO Cells Using Magnetic Beads*
G Risberg, M Sjodahl, N Norrman, G Glad, H Hedlund, J Ohman

**I120** *Comparative Peptide Separations by on-line MudPIT and IPG-IEF in an Off-gel Set-up*
Sarah Elschenbroich, Vladimir Ignatchenko, Parveen Sharma, Anthony O. Gramolini, Thomas Kislinger

**I121** *Automated High Sensitivity Platform for Multidimensional LC/MS Analysis of Phosphopeptides*
Scott Ficarro, Yi Zhang, Jignesh Parikh, Manor Askenazi, and Jarrod A. Marto

**I122** *Quantitative Study of the Yield and Recovery of Proteomics Fractionation Methods*
Y. Fang, D.P.Robinson, L.J. Foster

**I123** *Characterization of a Novel Rapid Fluorescent Gel Stain*
T Berkelman

**I124** *GELFREE: Molecular Weight Based Fractionation with Liquid Phase Recovery*
Nghia Chiem, Chuck Witkowski, Jay Harkins, Christopher Dill, Jeremy Norris

**I125** *Enrichment of Phosphorpeptides by a Ceramic Hydroxyapatide Micro Spin Column with Stepped Elution for Mass Spectrometric Analysis*
N. Liu, K. Academia, J. Walker II, T. Wehr and A. Paulus

**I126** *High Efficient Proteome Analysis with Gel Free Protein Prefractionation and Peptide Separation*
Dingyin Tao, Lihua Zhang, Zhen Liang and Yukui Zhang

**I127** *Parallel Electrophoretic Peptide Enrichment System for High Throughput Quantitative MRM Analysis*
Chuck Witkowski, Nghia Chiem, Jay Harkins, Jeremy Norris

**I128** *Comparative Proteome Study on Midbrains of Normal and PD Rats Using 2D-HPLC with Fluorescence Detection*
Xiaoqiang Qiao, Lihua Zhang, Zhen Liang, and Yukui Zhang

**I129** *A Global Isolation and Identification Method for Blocked N-Terminal Peptides by DITC-Mnps and MS*
Yangjun Zhang, Liyan Zhao, Junying Wei, Dong Cao, Xiaohong Qian

**I130** *Novel separation and identification techniques for proteome study*
Yukui Zhang

**I131** *Novel Mass Spectrometry Approaches to Characterize Ubiquitin-Like Protein Function*
S.M. Jeram, T. Srikumar, Y. Sydorskyy, J. Wan, S. Wheaton and B. Raught

**I132** *Novel Proteomic Approaches for Biomarker Discovery in Clinical Samples*
S Saxena

**I133** *Exploring the Complexity of Post-Translational Modifications on Salivary Basic Proline-Rich Proteins*
F Amado, R. Ferreira, R Vitorino

## Integration and Storage of Proteomics Data (I201 – I207)

**I201** *Omicshub, A New Generation of Data Standards Oriented LIMS Integrating Analysis Workflows*
T Lloret, JF Elvira, J Alberto Medina-Aunon, JM Carazo, JP Albar and E Gonzalez Couto

**I202** *OpenFreezer LARISA: An Enterprise Application for Reagent Tracking and Workflow Automation*
M. Olhovsky, A. Pasculescu, J.P. Lee, J.G. Park, C. Wells, K. Williton, A. Dai, M. Goudreault, R. Linding, T. Pawson, and K. Colwill

**I203** *Accurate mass tag retention time data base for urine proteome*.
Evgenij N Nikolaev, I.A. Popov, A.S. Kononikhin, I.A. Agron, D.M. Avtonomov, S.A. Moshkovsky, I.M. Larina, I.A. Zamulaeva, C. Masselon, A.I.Archakov

**I204** *Salivary Proteome Wiki: A Collaborative Environment to Share and Annotate Proteomics Data*
W Lau, L Shum, C Johnson

**I205** *MS Repo: Organizing, Analyzing and Sharing Proteomics Data*
Matthias Berth, Christian Scharf, Leif Steil, Uwe Völker

**I206** *Improving Untargeted Differential Analysis of Mass Spectrometry Data by Recursive Feature Extraction*
N. Kitagawa, S. Fischer, T. Sana, D. Peterson, X. Li and E. Darland

**I207** *Comparison of Human Glomerulus Proteome using Antibody-based and Mass Spectrometry-based Proteomics*
M. Nameta, M. Uhlen, Y. Yoshida, B. Xu, Y. Zhang, E. Yaoita, and T. Yamamoto

## Kinase-Protein Substrate Networks (K101 – K112)

**K101** *Integrated Proteomic Analysis Uncovers the Activity State of the Intracellular Signaling*
K. Nagano, T. Shinkawa, N. Yabuki, N. Inomata, Y. Watanabe, S. Nagahashi, N. Ishii, Y. Aoki, and M. Haramura

**K102** *PtpA, a Mycobacterium tuberculosis Protein, Blocks Macrophage ' s Signaling Pathways*
Valérie Poirier, H. Bach, Y. Av-Gay

**K103** *Exploring Signaling Pathways by Combining APMS and Phosphorylation Enrichment*
Z.-Y. Lin, B. Larsen, A. Breitkreutz, M. Tyers, A.C. Gingras

**K104** *The Human Sh2 Project: T-Cell Receptor Mediated Protein-Protein Interaction Signaling Network Via Sh2 Domains*
T k J Dayarathna, G A Lajoie and S C Li

**K105** *Selective Reaction Monitoring (SRM) Reveals Coordinated Phosphorylations and Protein Interactions Associated with EGFR Endocytosis*
MF Moran, P Taylor, A Prakash, SM Peterman, and J. Tong

**K106** *Characterizing NPM-ALK Phosphorylation using Tandem Affinity Purification-Mass Spectrometry*
P Wang, F Wu, L Young, R Lai, L Li

**K107** *Easy Identification and Quantitation of Phosphorylation Sites: An Example Using MEF2 Transcription Factors*
D M Cox, N B Nowacki, B Simons, X Guo, J C McDermott

**K108** *Identification of ATP Binding Proteins and Its Application to Insulin Signaling*
Ja-Hye Park, Daehee Hwang and Moon-Chang Baek

**K109** *Evaluation of Kinase Inhibitors by Phosphoproteomics-based Phosphorylation Profiling*
N, Sugiyama, Y. Kyono, K. Imami, S, Ohnuma, M. Tsukahara, M. Tomita, Y. Ishihama

**K110** *Building A Targeted Selected Reaction Monitoring (SRM) Assay of Phosphopeptides by Utilizing Discovery Information*
B. Krastins, A, Prakash, T. Rezai, S. Peterman, D. Sarracino, M. Athanas, Paul Taylor, Mike Moran, Mary F. Lopez

**K111** *The FGFR3 Network in Multiple Myeloma: A Phospho-Proteomic Profile*
JR St-Germain, P Taylor, J Tong, LL Jin, S Trudel, and MF Moran

**K112** *Network Analysis of Cell-Specific Eph/Ephrin Bidirectional Phospho-Tyrosine Signaling in Co-Culture*
C. Jorgensen, A. Sherman, G.I. Chen, A. Pasculescu, A. Poliakov, M. Hsiung, R. Linding, T. Pawson

## Mass Spectrometry Innovations (M101 – M126)

**M101** *A New Rapid and Comprehensive Peptidome Analysis by One-Step Direct Transfer Technology for 1-D Electrophoresis/MALDI Mass Spectrometry*
K. Tanaka, L. Lee, T. Hashiguchi, and I. Maruyama

**M102** *Increased Quantitative Throughput and Selectivity for Triple Quadrupole Mass Spectrometer Based Assays Using Intelligent SRM (Isrm)*
Reiko Kiyonami, Alan Schoen, Amol Prakash, Huy Nguyen, Scott Peterman, Vlad Zabrouskov, Nathalie Selevsek, Andreas Huhmer, Bruno Domon

**M103** *Relieving Experimental Artifacts in Proteomic Analysis of J774 Cells for Relative Potency of PMs*
P. Kumarathasan, D. Das, S. Mohottalage, Y. Siddiqui, S. Karthikeyan and R. Vincent.

**M104** *Identification and Quantification of Protein Pathways using MS/MS-Assays built with Synthetic Peptide Arrays*
J. A. Hewel, J. Liu, V. Fong, S. Chandran, P. Havugimana, J. Kwan, H. Wenschuh, M. Schutkowski, L. Eckler, A. Emili

**M105** *Intact Protein Sequencing Using ETD-PTR in Linear Ion Trap*
Zhiqi Hao, Jae C Schwartz and Andreas F Huhmer

**M106** *qPAcIFIC: How to Quantify Deeper into the Proteomics Ocean*

A Panchaud, SA Shaffer and DR Goodlett

**M107** *MALDI-Immuno Screen (MiSCREEN)™: A new method for selection of high affinity anti-peptide monoclonal antibodies*
M. Razavi, M. E. Pope, N. L. Anderson and T. W. Pearson

**M108** *Comprehensive Proteomic Studies Leveraging a Novel SRM Technique*
Bruno Domon, Reiko Kiyonami, Alan Schoen, Amol Prakash, Paola Picotti, Nathalie Selevsek, Scott Peterman, Ruedi Aebersold, Andreas Huhmer

**M109** *Overcoming Undersampling in Proteomic Experiments using a New Linear Trap-Orbitrap Mass Spectrometer*
E Damoc, K Scheffler, E Denisov, J Blethrow, T Pekar Second, V Zabrouskov, J Griep-Raming, A Makarov, and Thomas Moehring

**M110** *Proteomics based Diagnostic and Prognostic Biomarkers for Head-and-Neck Cancer: Challenges and Opportunities*
Ranju Ralhan, Leroi V. DeSouza, Ajay Matta, Satyendra C. Tripathi, Jatinder Kaur, Shyam S. Chauhan, Siddartha DattaGupta, Nootan K. Shukla, Terence J. Colgan, Christina MacMillan, Ian Witterick, Iona Leong and K.W. Michael Siu.

**M111** *Liquid Chromatography - Electron Transfer Dissociation and Ion Mobility Studies on a QTOF Mass Spectrometer*
James Langridge, Jeffery M Brown; Steven D Pringle; Iain D G Campuzano; Richard C Chapman

**M112** *12-Plexed Quantitation: Combining Tandem Mass Tags with SILAC*
MM Rosenblatt, K Rampalli, RG Biringer, J Saba, M Major, S Feuillerat, N Haghdoost, B Kaboord, J Rogers, and P Haney

**M113** *Novel Software Approach to Building, Processing, and Scoring Large Targeted Peptide Assays using Intelligent SRM Transitions*
S. Peterman, R. Kiyonami, A. Prakash, D. Sarracino, B. Krastins, T. Rezai, M. Athanas, and M. Lopez

**M114** *Differential Protein Expression throughout the Life Cycle of Parasitic African Trypanosomes*
Brett Eyford, T. Sakurai, D. Smith, N. Inoue, C. Hertz-Fowler, T.W. Pearson

**M115** *PTM Finder Based on PEAKS De Novo Sequencing Result*
L Xin, B Shan, G Lajoie, B Ma

**M116** *High Throughput Global Proteome Profiling of Mammalian Tissue using Hybrid Triple Quadrupole / LIT Technology*
Xu Guo, Brigitte Simons, Feng Zhong, Jason Hoffert

**M117** *Modeling ETD Fragmentation with Bayesian Network for Peptide Identification*
X. Liu, B. Shan and B. Ma

**M118** *Exploring Proteome Responses of Alkalimonas Amylolytica N10 to Different External pHs*
Q Wang, Z Qian, B Meng, Z Wang, C Zhou, W Tong, F Peng, and S Liu

**M119** *Combining Chip-based Enrichment of Phosphopeptides with Specific Analysis using ETD Mass Spectrometry*
N. Tang, D. Lin, C. Miller and K. Waddell

**M120** *On The Usage of The Number of Carbon Atoms for Peptide Mass Fingerprinting*
D.M. Avtonomov and E.N. Nikolaev

**M121** *Increased Proteome Definition Exploiting a New Linear Ion Trap Mass Spectrometer*
Tonya Pekar Second, Justin Blethrow, Jae C. Schwartz, Vlad Zabrouskov

**M122** *Generating Products of All ions with an Experimental Trap-TOF*
S. Tate, Nic Bloomfield, Igor Chernushevich, Alexandre Loboda

**M123** *Innovative Mass Spectrometry Technology for the Identification of Cancer Immunotherapeutics*
Donald F. Hunt

**M124** *Of Bears and Birds Genome Free de novo Sequencing by A Combination of LysN Protein Digestion and Electron Transfer Dissociation*
A.F. Maarten Altelaar, Nadia Taouatas, Shabaz Mohammed, Albert J.R. Heck

**M125** *Lys-N and Trypsin Cover Complementary Parts of the Phosphoproteome in a Refined SCX-Based Phosphoproteomics Approach*
Shabaz Mohammed, Sharon Gauci, Andreas O. Helbig, Nadia Taouatas, Maarten Altelaar, and Albert J.R. Heck

**M126** *Optical Fibres as Multi-channel Electrospray Emitters*
GTT Gibson, S Su, SM Mugo, DM Marecak, and RD Oleschuk

# Poster Presentations: Tuesday (Sept 29th, 2009)
# Harbour Ballroom

## Mass Spectrometry Based Molecular Imaging (M201 – M206)

**M201** *Determination of Oxaliplatin Distribution in rat kidney during HIPEC: a Mass Spectrometry Profiling*
A. Boussilmani, C. Hirtz, N. Bec, B. Lopez, and C. Larroque

**M202** *Tracking the Distribution of Tiotropium in Rat Lung Using MALDI Imaging Mass Spectrometry*
A Nilsson, Thomas Fehniger, Lena Gustavsson, Malin Andersson, Kerstin Kenne, György Marko-Varga, Per E. André

**M203** *Neuropeptidome Alterations in an Experimental Model of Parkinson Disease*
N Schintu, A Nilsson, M Fälth Savitski, P Svenningsson, PE Andrén

**M204** *A Novel Statistical Approach to Interpret Complete MALDI Mass Spectrometry Datasets*
Roy Martin, Emmanuelle Claude, Pr. Chen, Keith Richardson, Thérèse Mckenna, Jim Langridge

**M205** *MALDI-Tissue Imaging at High Resolution and Speed: Towards its Applications in Histology*
Sören-Oliver Deininger, Michael Becker, Martin Schürenberg, Arne Futterer, Armin Holle, Jens Höhndorf, Detlev Suckau

**M206** *Expression of Human Vitreous Humor Proteins in Retinal Detachment*
A.Noureen, A.Ahmed

## Nanotechnologies and Cell Imaging (N101 – N104)

**N101** *Optical and Optico-Acoustical Biosensor Application for Protein-Protein Interaction in Proteomics*
Yu.D. Ivanov, T.O Pleshakova and A.I. Archakov

**N102** *AFM/MS Irreversible Fishing Technology for Detection of Low- and Extra-Low Copied Proteins*
A Archakov, Yu Ivanov, V Zgoda

**N103** *Optico- acoustic biosensor technology for express analysis of proteins*
T.O Pleshakova, Yu.D. Ivanov, Krohin N.V. and A.I. Archakov

**N104** *Nanozeolite-Driven Approach for Enrichment of Secretory Proteins in Human Hepatocellular Carcinoma Cells*
J Cao, Y Hu, C Shen, J Yao, L Wei, F Yang, Y Liu, Y Zhang, Y Tang and Pengyuan Yang

## Neurodegenerative Biology and Medicine (N201 – N224)

**N201** *Proteome Analysis of Carbonyl Proteins in Cerebrospinal Fluid by Cy5-Hydrazyde labeling*
T Toda, M Nakamura, F Shibasaki, T. Yoshizawa

**N202** *Biomarkers in animal model of Parkinson ' s disease- Relationship of cerebrospinal fluid and plasma*
S. Argüelles, JL Venero, S. Garcia-Rodriguez, M. Tomas-Camardiel A. Ayala, J. Cano and A. Machado

**N203** *Profound Protein Expression Changes Precede Phenotype Onset in a Mouse Model of Huntington Diseases*
C Zabel, L Mao, B Woodman, A Koppelstatter, G Nebrich, O Klein, S Grams, D Hartl, J Klose and GP Bates

**N204** *Proteome Wide Peptide Libraries for MS/MS Identification of Human Protease Cleavage Sites*
PF Huesgen, O Masson, E Liaudet-Coopman and CM Overall

**N205** *Discovery and Validation of Human African Trypanosomiasis Staging Markers*
Natalia Tiberti, Alexandre Hainard, Xavier Robin, Veerle Lejon, Dieudonné Mumba Ngoyi, Enock Matovu, John Enyaru, Catherine Fouda, Joseph Mathu Ndung'u, Markus Mueller, Frédérique Lisacek, Alexander Scherl, Loïc Dayon, Natacha Turck, Jean-Charles Sanchez

**N206** *Comparative Proteomic and Digital Transcriptomic Investigation of Parkinsons Disease Related Cell Lines*
AD Knudsen, D Otzen, PH Jensen and A Stensballe

**N207** *Proteomic Analysis of Parkin Ubiquitin Ligase*
CH Pu, and T Mayor

**N208** *Development of a Protocol for a Rat Spinal Cord Proteome*
F. Gil Dones, S. Alonso Orgaz, G. Davila, T. Martin-Rojas, F. Vivanco, J. Scott Taylor and M.E.G. Barderas

**N209** *Quantitative Analysis of Brain Proteins in an Animal Model of Multiple Sclerosis*
R. Daniels, A. Vanheel, K. Baeten, J. Hendriks, D. Dumont, J. Robben, J-P. Noben, P. Stinissen and N. Hellings

**N210** *FTMS Reveals Tissue Transglutaminase Induced Crosslinking and Deamidation of Amyloid-beta*
Yury O. Tsybin, Luca Fornelli, Patrice Waridel, Manfredo Quadroni, and Adrien W. Schmid

**N211** *Proteomic Analysis Reveals the Effect of Dot1 Silencing on Neuro-2a Cells*
Chun Mei Wang, Sau Na Tsai, Sai Ming Ngai

**N212** *Quantitative Study of Phosphorylated Brain Proteins in a Model of Multiple Sclerosis*
A. Vanheel, R. Daniels, K. Baeten, J. Hendriks, J-P, Noben, P. Stinissen and N. Hellings

**N213** *Identification of Novel Protein-Protein Interactions Linked to Alzheimer's and Parkinson's Disease*
D. Dewar-Darch, J-P. Lambert, F. Elisma, D. Figeys

**N214** *Alzheimer's Disease Proteomics: Expression of Membrane Proteins in Different Brain Regions*
S. Zahid, R. Khan, AR Asif, N. Ahmed

**N215** *Evolutionary descent of prion family genes from a ZIP metal ion transport ancestor*
S Ehsani, JC Watts, H Huo, D Westaway, H Wille, G Schmitt-Ulms

**N216** *Quantitative analysis of Membrane Proteins and Glycoproteins in Activated Brain Cells using Label-Free LC-MS-Based Proteomics*
A.S. Haqqani, C.E. Delaney, J. Mullen, P. Couraud, W. Zhang, J Kelly, D.B. Stanimirovic

**N217** *Proteomic Analysis of Stress Responses Associated to the Ubiquitin Proteasome System*
N. Fang, M. Brack, I. Wilde, E. Gies and T. Mayor

**N218** *Comprehensive Analysis of Lipid Extracts from Hippocampus of Human Brain*
W Hou, LA Swayne, H Zhou, SAL Bennett, D Figeys

**N219** *A Proteomics Based Investigation of the Insoluble Proteins Implicated in Degenerative Neuropathy*
J.N. Agar, M.L. Easterling, and C.J. Thompson

**N220** *Investigation of the Role of Tau Gene Transcriptional Regulation in Neurodegeneration*
F Anaya, J Vandrovcova, A Lees and R de Silva

**N221** *Characterization of TTR-Cys10 isoforms in CSF from AD patients by immunoaffinity – MS and ETD MS/MS*
K Poulsen, JMC Bahl, AH Simonsen, G Waldemar, MR Larsen and NHH Heegaard

**N222** *Protein expression variations in Cornelia de Lange Syndrome*
L. Bianchi, A. Gimigliano, C. Landi, M. Puglia, T. Serchi, L. Mannini, A. Musio, L. Bini

**N223** *Proteomic Analysis of CSF from Methamphetamine Abusers and Meth Treated Neural Stem Cells Shows Profound Effects on Oxidative Stress Pathways and Growth Factors*
Arun Venkatesan, Dawn Chen, Linda Chang, Ute Feger, Robert Cotter, Avindra Nath

**N224** *Proteomic Analysis of Human Brain Microdialysates of Stroke Patients*
L Dayon, N Turck, A Vilalta, J Montaner, JC Sanchez

## Organelle Proteomics (O101 – O125)

**O101** *Proteomic study of Endoplasmic Reticulum from Jurkat Cells during Heat Stress*
X-L. Zhang, T. Tanaka, Y. Kuramitsu, M. Fujimoto, K, Nakamura,

**O102** *Phosphoproteome Analysis Reveals Regulatory Sites In Major Pathways of Cardiac Mitochondria*
N Deng, Y Wang, J Zhang, P Doran, CN Zong, P Korge, JN Weiss and P Ping

**O103** *Proteomics of Mouse Liver Microsomes: Performance of Different Protein Separation Workflows for LC-MS/MS*
A.Melnik, V.G.Zgoda, S.A.Moshkovskii, A.T.Kopylov, E.A.Ponomarenko, E.Y.Fomchenkova, A.I.Archakov

**O104** *Analysis of exosome-like vesicles from rat urine as model for biomarker discovery*
J Conde-Vancells, E Rodriguez-Suarez, E Gonzalez, A Berisa, D Gil, N Embade, M Valle, F Elortza, SC Lu, JM Mato and JM Falcon-Perez

**O105** *Strategies for Membrane Proteomes: The AOHUPO Membrane Proteomics Initiative*
Lifeng Peng, Eugene A. Kapp, David Fenyo, Min-Seok Kwon, Pu Jiang, Songfeng Wu, Ying Jiang, Mibel Aguilar, Mark Baker, Zongwei Cai, Phan Van Chi, Maxey Chung, Fuchu He, Kazayuki Nakumura, Sai Ming Ngai, Young-Ki Paik, Tai-Long Pan, Terence Poon, Ghasem Hosseini Salekdeh, Nikhat Ahmed Siddiqui, Richard J. Simpson, Ravi Sirdeshmukh,

Chantragan Srisomsap, Jisnuson Svasti, Yu-Chang Tyan, Florian Dreyer, Daniel Klotz, Danyl McLauchlan, Pisana Rawson and T. William Jordan

**O106** *The Human Proteome Project #X: Differential Proteomic Analysis of DRM (Detergent Resistant Microdomains) Proteins in Cystic Fibrosis.*
C Guerrera, F Borot, DL Vieu, F Guillonneau, A Edelman and M Ollero

**O107** *Membrane Proteome of Cyanobacterium Synechocystis sp. PCC 6803*
HJ Park, G Park, JH Oh, JS Choi, and Young Hwan Kim

**O108** *New Insight into Peroxisome Membrane Interaction Networks by Quantitative Proteomics*
S Oeljeklaus, B Reinartz, I Michels, S Merich, M Kohl, C Stephan, HE Meyer, W Schliebs, R Erdmann, C Brocard, B Warscheid

**O109** *Subcellular proteome analysis discovering annexin A2 related to liver fibrosis caused by HBV*
Lijun Zhang, Xia Peng, XiaoFeng Jia, YanLing Feng, Zhanqin Zhang, Hua Yang, Lianguo Shi, Xiaonan Zhang, and Zhenghong Yuan

**O110** *Organelle based proteomics of the caudate nucleus in simian immunodeficiency virus infected and methamphetamine treated rhesus macques*
G Pendyala, SA Trauger, P Ciborowski, HE Gendelman, G Siuzdak, and HS Fox

**O111** *Phosphoproteome Analysis of Calcium-Dependent Cell Adhesion Dynamics in Mouse EpH4 Cells*
Takeshi Masuda, Masaru Tomita, Yasushi Ishihama

**O112** *Subcellular Fractionation in a Fluidic Microsystem by Dielectrophoresis (DEP)*
A Posch, A Paulus, M Hausmann, N Kunz, M Stelzle, M Moschallski, TT Duong, and G Blankenstein

**O113** *Acetylation of Lysine, Serine and Threonine Residues in Mouse Liver Detected by Liquid Chromatography-Mass Spectrometry*
Bing Zhang, Chao Zhao, Kaixuan Luo, Guoquan Yan, Yingyin Wang, Huizhi Fan, Pengyuan Yang

**O114** *Organelle proteomics of endosomal compartments in Arabidopsis thaliana*
A.J. Groen, P.G. Sadowski and K.S. Lilley

**O115** *The Protein Composition of Mitotic Chromosomes by Multidimensional Quantitative Proteomics*
J. Rappsilber, S. Ohta, J.-C. Bukowski-Wills, F. de Lima Alves, Z. Chen, D. F. Hudson, W. C. Earnshaw

**O116** *Altered Proteins in Subcellular Compartments of Human Endothelial Cells during Dengue Virus Infection*
Sa-nga Pattanakitsakul, Jesdaporn Poungsawai, Rattiyaporn Kanlaya, Supachok Sinchaikul, Shui-Tein Chen, and Visith Thongboonkerd

**O117** *Analysis of IMPs Based on Heat Gel-embedment and Improved In-gel Digestion Strategies*
J Zhou, S Huang, D Bi, H Zhang, JL Li, Y Lin, P Chen, XC Wang, and SP Liang

**O118** *Differentiation and activation of myeloid cells, as viewed by proteomics*
T Rabilloud, M. Chevallet, C. Villiers, Hélène Diemer, A. Van Dorssealer

**O119** *iTRAQ Reagent-Based Quantitative Proteomic Analysis of Age-Related Changes in Mitochondrial Proteome from Mouse Liver and Kidney*
H.Amelina, J. Bergquist, and S. Cristobal

**O120** *Low Levels of Collapsin Response Mediator Protein1 (CRMP1), as Detected by iTRAQ Analysis, Promotes Invasion of Human Gliomas Expressing Mutant EGFRvIII*
J. Mukherjee, L.V. DeSouza, J. Micaleff, Z. Karim, S. Croul, K.W. M. Siu, A. Guha

**O121** *Organelle Mapping of the Human Proteome – Towards a Subcellular Atlas*
E Lundberg, M Hjelmare, M Skogs, C Stadler, M Wiking, H Brismar, M Uhlén

**O122** *Proteome Analysis of RER from Acute Pancreatitis Models*
Xuequn Chen, Maria Dolors Sans, John R. Strahler, Nancy Vogel, Stephen A. Ernst, George Michailidis, John A. Williams, and Philip C. Andrews2

**O123** *Proteomic Characterization of Rat Gastrocnemius Subsarcolemmal and Intermyofibrillar Mitochondria*
R Ferreira, R Vitorino, R Alves, JA Duarte, F Amado

**O124** *Proteomic Investigation of Leishmania containing phagosomes*
Martin E. Barrios-Llerena, Daniel Paape, Thierry Le Bihan and Toni Aebischer

**O125** *Proteomic Imaging of Endothelium and Caveolae for Targeted Penetration into Single Organs and Solid Tumors*

## Other (O201 – O207)

**O201** *Application of an Intact Protein Separation Space for PTM Characterization*
M. E. McComb, D. H. Perlman, W. Ying, L. Li, G. Infusini, V. Bhatia, W. Tong, C. E. Costello

**O202** *Effect of High Dose Thiamine on the Levels of Protein Biomarkers in Diabetes Mellitus Type 2*
Samreen Riaz, Saadia Shahzad Alam, Naila Rabbani, Paul J Thornalley and M. Waheed Akhtar

**O203** *A label-free Method Identified Differentially Abundant Proteins in Related M.tuberculosis Beijing Strains*
Gustavo A. de Souza, Suereta Fortuin, Chris R McEvoy, Roghelio Hernandez Pando, Christian J. Koehler, Bernd Thiede, Robin M Warren and Harald G. Wiker

**O204** *Global Analysis of Small Molecule-Protein Interactions*
Xiyan Li and Michael Snyder

**O205** *A thiol Reactive Alkylhydroquinone Exhibits Cytoprotective Effect via Keap1-Nrf2-ARE Signaling*
TY Lin, CP Huang, YR Chen, RYY Chiou, WC Tang, and ShwuBin Lin

**O206** *Phylogenetic analysis of Hepatitis B virus*
Naaz Abbas, Zainulabedin and Talat Afroze

**O207** *Proteome Responses of Human Oral Epithelial Cell to HIV/AIDS and Drug Abuse*
E. Yohannes, Santosh Gosh, Gaurav S.J.B. Rana, Thomas S. Mccormick, Aaron Weinberg, Mark R. Chance

## Plant Proteomics (P101 – P105)

**P101** *Proteomics Analysis of Rice Shoot Treated with Gibberellic Acid and Salt*
YH Pan, FP Wen, ZH Zhang, T Bai, and Q Xu

**P102** *In-Depth Analysis of the Arabidopsis thaliana Proteome Using a Novel Hybrid Linear Trap-Orbitrap Mass Spectrometer*
K Scheffler, E Damoc, E Denisov, A Makarov, J Blethrow, V Zabrouskov, J Griep-Raming, T Moehring

**P103** *Comparative Tuber Proteome in Wild-Type and Transgenic Potato Expressing a Seed Albumin*
L Agrawal, N Chakraborty, A Datta, and S Chakraborty

**P104** *Proteome Analysis of Differentially Displayed Proteins in Extracellular Matrix of Rice*
A Pandey, U Rajamani, J Verma, A Datta, S Chakraborty, and N Chakraborty

**P105** *Proteome Analysis of Apoplastic Proteins in Rice Shoot Respond to Salt*
Yi Guo, Yun Song, And Alma Burlingame

## Proteomics of Macromolecular Complexes (P201 – P224)

**P201** *Membrane Complexome of F. tularensis and its Response to Iron Restriction Studied by BN-PAGE/DIGE*
J Dresler, J Klimentova, and J Stulik

**P202** *Proteome-wide Identification of Poly(ADP-ribose)-binding Proteins and Poly(ADPribose)-associated Protein Complexes.*
J-P Gagné, M Isabelle, S Bourassa, MJ Hendzel, VL Dawson, TM Dawson and GG Poirier

**P203** *Interaction Network Analysis: Cross-Comparison of Methodologies, Species and Cell Types for the PP2A Interactome*
M Mullin, M Goudreault and AC Gingras

**P204** *Molecular Dissection by AP/MS of a Signaling Complex Linked to Cerebral Cavernous Malformations*
MJ Kean, D Ceccarelli, L D'Ambrosio, M Goudreault, M Sanches, F Sicheri, and AC Gingras

**P205** *Identification of Novel Interactors of Protein Phosphatase 4 using Quantitative Proteomics*
G.I. Chen, A.-C. Gingras

**P206** *Benchmarking Affinity-Purification/Mass Spectrometry to Define Probability Values for Protein-Protein Interactions*
A-C Gingras, B Larsen, Z Lin, B Gonzalez-Badilllo, M Goudreault, B Raught, S Angers, A Pawson, J Wrana, P Braun, B Coulombe, A Nesvizhskii

**P207** *Nested Partition Clustering Algorithm for AP/MS-derived Protein Interaction Data*
Hyungwon Choi, Sinae Kim, and Alexey I. Nesvizhskii

**P208** *Systematic Interrogation of the Budding Yeast Kinome*
A. Breitkreutz, H. Choi, J. Sharom, L. Boucher, V. Neduva, B. Larsen, Z. Lin, C. Stark, B.J. Breitkreutz, R. Almeida, X. Tang, D. Dewar, A. Pawson, A.-C. Gingras, A. Nesvizhskii, M. Tyers

**P209** *Development of a Selected Reaction Monitoring (MRM) Assay for the Adaptor GRB2 Proteome*
N Bisson, L Taylor, A James, B Larsen, S Tate and T Pawson

**P210** *Proteomic Screen for Multi-protein Complexes in Synaptic Plasma Membrane from Rat Hippocampus*
Xuanwen Li, Chunliang Xie, Xianchun Wang, Ping Chen, Songping Liang

**P211** *Systems Analysis of Networks and Complexes Containing Poly(ADP-Ribose)-Metabolizing Enzymes*
M Isabelle, Gagne JP, Rouleau M, Ethier C, Moreel X, Gagne P and Poirier GG

**P212** *HMGA Oncoproteins in Double Strand Break Repair Network*
E Maurizio, R Sgarra, S Zammitti, L Arnoldo, S Costantini, A Lo Sardo, S Pegoraro, V Giancotti, A Vindigni and G Manfioletti

**P213** *LC-MS Analysis to Identify Ryanodine Receptor 1 (RyR1) Protein-Protein Interactions*
Tim Ryan, Parveen Sharma, Alex Ignatchenko, David H. MacLennan, Anthony O. Gramolini,* and Thomas Kislinger

**P214** *Four and a Half LIM domains protein 1 (FHL1) Interactions in Mammalian Tissue*
T. Shathasivam, P. Sharma, A. Ignatchenko, T. Kislinger, and A. O. Gramolini

**P215** *MRJP1-Binding Proteins from Honey Bee Brain*
G.C. N. Cruz, L. Garcia, C. A. O. Ricart and M. Valle de Sousa

**P216** *Quantitative Analysis of the Effect of Methylation Inhibitors on Messenger Ribonucleoprotein Complexes*
APL Snijders and M.J. Dickman,

**P217** *Studying Integrin _1 Complexes by Formaldehyde Cross-Linking and Mass Spectrometry*
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