

**Poster Presentations: Wednesday (Sept 30th, 2009)
Frontenac Room**



Proteomics Tool Box (P301 – P341)

P301 *Molecular Tool-Box For In Vivo Functional Biology and Proteomics: Application to DNA Topoisomerase*
G Budin, M Moune, S Meunier, L Brino, A Wagner

P302 *An Efficient Lentiviral Tagging System for the Affinity Purification of Human Protein Complexes*
Z. Ni, A.B. Mak, G. Zhong, J. Hewel, S. Smiley, E. Marcon, D. Roudevav, J. Li, J. Olsen, B. Cox, J. Rossant, A. Emili, J. Moffat, J. Greenblatt

P303 *Human Cell-Derived In Vitro Coupled Transcription/Translation Systems*
S Mikami, K Machida, S Yokoyama, and H Imataka

P304 *DeepQuanTR: A Software Package for the MALDI-Based Label-Free Quantification of Proteins*
T Fugmann, D Neri, and C Roesli

P305 *High Resolution Map of Prostaglandin E2-Dependent Signaling Networks*
Nikolaus G. Oberprieler, Simone Lemeer, Maria E. Kalland, Knut M. Torgersen, Albert J.R. Heck, Kjetil Taskén

P306 *Automated 2D Peptide Separation on a 1D Nano-LC-MS System*
Paul Taylor; Peter Nielsen; Morten B Trelle; Ole Horning; Michael Barrett Andersen; Ole Vorm; Michael Moran; Thomas Kislinger

P307 *Identification of Ub/Ubl Chains in an Integrated Mass Spectrometry/SpectraST/SUMmOn-Based Work-Flow*
T. Srikumar, S.M. Jeram, P.DA Pedrioli, H.Lam and B. Raught

P308 *Genetical and Chemical Proteomics*
Andrew Emili

P309 *Optimized Covalent Conjugation of Antibodies and Co-ImmunoPrecipitation Using Magnetic Beads*
D Gillooly, P Songe, E Breivold, H Lindstrom and E Ragnhildstveit

P310 *Design of Recombinant Antibody Microarrays Targeting Complex Proteomes*
M Kristensson

P311 *A Multi-Laboratory Study Assessing Reproducibility of a 2D-DIGE Proteomic Experiment*
J-J Bech-Serra, N. Colomé; ProteoRed, J-P Albar, A. Borthwick, M. Wells, F. Canals

P312 *Digital Microfluidics: An Automated, Integrated Platform for Protein Extraction and Processing*
V.N. Luk, M.J. Jebrail, A.R. Wheeler

P313 *Workflow for Maximizing Protein Identifications Using Multiple Re-Injections and Multiple Search Engines*
Cassandra Wigmore, Baoshen (Paul) Shan, Bernard Delanghe

P314 *Optimization of Peak Capacity in One- and Two-dimensional nanoLC*
Sebastian Eeltink, Evert-Jan Sneekes, Bas Dolman, and Remco Swart

P315 *Improving the Specificity of Peptide Identifications from MS/MS Spectra Using a Novel Transition-Based Correlation Algorithm (Tcorr)*
J. Liu, J. A. Hewel, V. Fong, A. Emili

P316 *A Red Line Not to Cross: Evaluating the Limitation and Properness of Gel Image Tuning Procedures*
HC Wu, CC Yen, WH Tsui, and HM Chen

P317 *Streamlined In-Gel Protein Digestion with a Mass Spectrometry-Compatible Surfactant*
Sergei Saveliev; Daniel Simpson; Becky Godat; Bill Daily; Grzegorz Sabat; Keith Wood

P318 *Efficient Methods for Avoiding Human Keratin Contaminations during Gel-Based Proteomics Analysis*
B. Xu; S, Shimada; Y, Zhang; S, Magdaldin; H, Fujinaka; Y, Yoshida; E, Yaoita; T, Yamamoto

P319 *High Throughput Antibody Development Platform*
P. Galéa, E. Du Paty, B. Beucher, L. Rubrecht, A. Blanc, S. Cobo, J. Rey, MC Mondon, D. Laune

P320 *New Developments in the ProteoWizard Open Source Software Library*
Darren Kessner, Matt Chambers, Brendan MacLean, Robert Burke, Kate Hoff, Brian Pratt and Parag Mallick

P321 *Characterization of Host Cell Protein Patterns to Increase Process Understanding*
Åsa Hagner McWhirter, Susanne Grimsby, Lena Kask, Maria Winkvist, Anneli Jorsback, Tomas Björkman, Lennart

Björkesten and Gunnar Malmquist

P322 *Functional Protein Analysis Using DNA Based Cell-Free Protein Synthesis Systems*

K.Q. Zhao, D. Leippe, D. Creswell, R. Hurst, J. Kinney, M.R. Slater, R.F. Bulleit, M. Urh and K. Wood

P323 *Increased Reproducibility and Resolution with the New Pre-Cast DIGE Gels*

Åsa Hagner-McWhirter, Erik Bjerneld and Peter Oliviusson

P324 *NCI's Antibody Characterization Pipeline*

M. Mesri, H. Rodriguez, C. Kinsinger, T. Hiltke and G. Whiteley

P325 *Comprehensive Analysis of Extracellular Growth Substrate Matrigel Reveals Diverse Protein Content*

Christopher Hughes, Suya Liu, Lynne Postovit, Gilles Lajoie

P326 *Exploration of the Phospho-Tyrosine Proteome Using SH2 Domains*

B. Kaboord, M. Major, S. Feuillerat, M. Schofield, M. Rosenblatt, J. Rogers, N. Haghdooost

P327 *Global Quantitative Proteomic Profiling Through 18O-Labeling and MS/MS Spectra Analysis*

C White, N Oey, and A Emili

P328 *SILVER: A Tool for the Stable Isotopic Labeling Quantitative Data Analysis in LC-MS Based Proteomics*

Jiyang Zhang, Hanchang Sun, Yunping Zhu, Hongwei Xie, Fuchu He

P329 *HUPO-PSI Transitions Markup Language (TraML) for Exchange of SRM Transition Lists*

E Deutsch; M Chambers; L Martens; B Maclean; J Shofstahl; P Mallick, D Kessner; F Levander; P-A Binz; R Aebersold; M Brusniak

P330 *Enhance Proteomic Detection Limitation by Random Nucleotide Library*

Hsien-Yu Tsai

P331 *Protein Profiling of Malignant B Cells Using Reversed Phase Protein Microarrays*

L Dexlin, S Ek, S Hober, M Erhart, C.A.K. Borrebaeck and C Wingren

P332 *Solubilization and Digestion of Integral Membrane Proteins in Ionic Liquid Solvent System*

Liangliang Sun, Bin Han, Dingyin Tao, Zhen Liang, Lihua Zhang, and Yukui Zhang

P333 *Middle Down Peptide Analysis Using an LTQ Orbitrap and ProSightPC 2.0*

Catherine Fenselau, Joe Cannon, Karen Lohnes, Colin Wynne and N.J. Edwards

P334 *Generating High Affinity Phage-Antibodies to Multiple SH2 Domain Proteins by Chain Shuffling*

J McCafferty, K Pershad, J Pavlovic, B Kay, MR Dyson

P335 *Improving the Human Protein Atlas Coverage by Re-Designing Protein Epitope Signature Tags*

A Skölleremo, B Amini, A Arokianathan, L Berglund, T Boström, M Cammenberg, H Eklund, J Fall, L Gong, M Hamsten, M Salahi and A Persson

P336 *Peptide Modification Strategy for Optimizing Electron Transfer Dissociation Fragmentation*

A. M. English, N. Udeshi, D. Allison, J. Shabanowitz, M. Mayo, D. F. Hunt

P337 *Improving the Reproducibility of Proteomics Using MassQC*

C. Roberts, C Mason

P338 *Simple Enrichment of Phosphopeptides Using TiO₂ Magnetic Beads*

A-M Nissfolk, Y Laurin, J Öhman, U Meyer, H Hedlund and M Albenius

P339 *Membrane Nanodiscs for Identification of Membrane-Protein Interactions*

J. Borch-Jensen, J. Møller-Jensen, P. Roepstorff

P340 *Parallel Isoelectric Trapping as a Rapid, Reproducible Method for Peptide Separation*

W. Kuhlman, D. Argoti, J. Dasch, S. Haralampu

P341 *Rapid Strategies for Sample Preparation and Complexity Reduction for Proteomic Analyses*

L. Bradbury, G. Kaur, M. Selladurai, C. Thangavel, S. Nagpal, T. Sanderson, H. Li

Proteomics and Epigenetics (P401 – P411)

P401 *Proteomic Analysis of a Novel HKMT and Its Role in Regulating Gene Expression*

M Abu-Farha, JP Lambert, F Elisma, and Daniel Figeys

P402 *Demethylation Increased the Expression and Transcription of SOCS-1 in Leukaemic Cell Lines*

MF Johan, AC Goodeve, JT Reilly

P403 *Mass Spectrometry Analysis of the Variants of Histone H3 and H4 of Soybean and Their Posttranslational Modifications*

T Wu, T Yuan, S Tsai, C Wang, S Sun, H Lam and Sai-Ming Ngai

P404 *Generation of Highly Specific Synthetic Antibodies Targeting Chromatin Remodeling Protein Domains*

J. Olsen, H. Persson, N. Economopoulos, N. Nady, C. Arrowsmith, S. Sidhu, A. Emili

P405 *Large-Scale Proteomic Characterization of Chromatin in Budding Yeast by mChIP*

Jean-Philippe Lambert, Leslie Mitchell, Kristin Baetz, Daniel Figeys

P406 *Differentiating Phenotypic Response to Environmental Stimuli from Individual Daphnia Microcrustacea by Two-Dimensional Gel Electrophoresis*

Gary B. Smejkal, Darren J. Bauer, W. Kelley Thomas, Myra Robinson and Winston P. Kuo

P407 *Proteomics Unraveling Honeybee Drone (Apis mellifera L.) Embryonic Development*

Jianke Li, Yu Fang, Mao Feng

P408 *Network Regulating of Antibiotic-Resistant Outer Membrane Proteome in Escherichia Coli*

Hui Li, Chao Wang, Bao-cheng Wang, Wen-jiao Xu, Xiang-min Lin, Xuan-xian Peng

P409 *Proteomic and Bioinformatic Identification of Hyperthermostable Proteins in Hyperthermophilic Archaeon Thermococcus onnurineus NA1*

Y.-H. Chung, S-O Kwon, S. H. Yun, S. G. Kang, J-H Lee, J. S. Choi, S. I. Kim

P410 *Histone Post Translational Modifications Associated with Transcription*

J.R. Chapman, K.W. Mulder, K.L. Rose, F.M.A.R. van Schaik, J. Shabanowitz, H.Th.M. Timmers, D.F. Hunt

P411 *Disruption of the Direct Interaction Between Pluripotent Protein Ctf with Y Box Binding Protein 1 (Yb-1) by Hpv Type 16 and 18 E7 Oncoprotein, Up-Regulates C-Myc Gene*

Venugopal Balakrishnan, Nor Hayati Othman and Shaharum Shamsuddin

Stem Cell Proteome Biology (S101 – S112)

S101 *Comparative 2-D Gel Analysis of Embryonic Carcinoma 2102Ep Cell Line and Three Human Stem Cell Lines*

Iolanda Vendrell, Lyn Healy, Lesley Young, Judit M. Nagy, Adrian Bristow, Glyn Stacey and Jun X. Wheeler

S102 *Applying FT-ICR MS in a Glycomics Approach Toward Understanding Cancer Stem Cell Differentiation*

H. He, C.L. Nilsson, M.R. Emmett, X. Wang, A.G. Marshall, R.A. Kroes, J.R. Moskal, H. Colman, F.F. Lang, C.A. Conrad

S103 *Quantitative Analysis of Surface Proteome in Mesenchymal Stem Cells Cultured With or Without Bfgf*

Sang Kwang Lee, Young Hye Kim, Yongtae Kim, Sung-Soo Kim, Jeong Hwa Lee, Kun Cho, Sang Sook Lee, Zee-Won Lee, Kyung-Hoon Kwon, Haeyoung Suh-Kim, Jong Shin Yoo and Young Mok Park

S104 *Glioma Stem Cell Quantitative Proteomics: A “Warburg Proteome-Metabolic” Dereglulation*

C Ramus, D Wion, JP Issartel, M F Nissou, F Berger

S105 *Quantitative Proteomic Analysis of Human Embryonic Stem Cells Using 8-plex iTRAQ Labeling*

M Jadhavi, Hyoung-Joo Lee, Mohammad Pakzad, Seul-Ki Jeong, Sang-Yun Cho, Hossein Baharvand, Ghasem Hosseini Salekdeh and Young-Ki Paik

S106 *SILAC Quantification to a Depth of 2500 Proteins from a Double Knockout GSK-3 of Mouse Embryonic Stem Cells*

Christopher Hughes, Brad Doble, Lei Xin, Clark Chen, Baozhen Shan, Suyu Liu, Bin Ma, Gilles Lajoie

S107 *Quantitative Proteomics of Leukemic Stem Cells Reveal Novel Regulators of Self-Renewal*

M. Trost, O. Herault, M. Sauvageau, A. Faubert, N. Mayotte, G. Sauvageau, P. Thibault

S108 *Quantitative Proteomic Analysis of hESCs by a Novel “Rare Cell Proteomic Reactor”*

Ruijun Tian, Shuai Wang, Lisheng Wang, Daniel Figeys

S109 *Proteomic Analysis of Human Embryonic Stem Cells in Hypoxic Conditions*

A Nuhn, C Hughes, L Postovit and GA Lajoie

S110 *Mass-Spectrometric Identification and Relative Quantification of N-linked Cell Surface Glycoproteins*

B. Wollscheid, D. Bausch-Fluck, C. Henderson, R. O’Brien, M. Bibel, R. Schiess, R. Aebbersold & JD Watts

S111 *Delineating the Cardio-Myogenic Hierarchy during Development*

C Yoon, D Bausch-Fluck, B Wollscheid, S Kattman, G Keller, P Zandstra

S112 *Phosphoproteomic Analysis of Human Embryonic Stem Cells*

Laurence M. Brill, Wen Xiong, Ki-Bum Lee, Scott B. Ficarro, Yue Xu, Alexey Terskikh, Andrew Crain, Evan Y. Snyder, and Sheng Ding

Structural Proteomics (S201 – S214)

S201 *Structural Mass Spectrometry of a Molecular Machine: ClpAP Protease Conformational Changes*
J Bohon, LD Jennings, CM Philips, S Licht, and MR Chance

S202 *Universal Integrative Approach to Study 3D-Proteomics*
L. Sennels, D. Ryan, T. Owen-Hughes, J. Rappsilber

S203 *Affinity Purification of Covalently-Linked Peptides Following CNBr Cleavage of Proteins*
T. Shi, R. Weerasekera, C Yan, W Reginold, H Ball, T Kislinger, G. Schmitt-Ulms

S204 *Probing Protein Dynamics and Higher Order Structure with a Novel ETD-FTICR*
R.R. Abzalimov, M. L. Easterling, D.A. Kaplan, I.A. Kaltashov

S205 *New Developments in Crosslinking Technologies for Structural Proteomics*
Evgeniy V. Petrotchenko, Christoph H. Borchers

S206 *Mass Spectrometric Identification of Recombinant Phosphoproteins Expressed in Escherichia Coli*
YM She, TD Cyr, L Xu, AF Yakunin, AM. Edwards, S Dhe-Paganon, CH Arrowsmith, DC Lee, Z Jia, L Donald, KG. Standing

S207 *Creation and X-ray Structural Analysis of TNFR1-Selective Mutant TNF with Antagonistic Activity*
Y.Abe, T. Nomura, H. Kayamuro, Y. Yoshioka, H. Kamada, S. Tsunoda, Y. Tsutsumi

S208 *Analysis of PTM Changes in EGFR under Normal and Hypoxic Conditions using Extended Range Proteomic Analysis*
Shiaw-Lin Wu, K. Moriyama, S. Dai, M. Sitkovsky, and B. L. Karger

S209 *Algorithms for Probing Biomolecular Surfaces using Structural Mass Spectrometry*
Parminder Kaur, Janna Kiselar, Mark R. Chance

S210 *Structural Determinants of SH2 Domain Specificity*
T. Kaneko, H. Huang, S. S-C Li

S211 *Isotopically Coded N-terminal Modification for Identification of Inter-Peptide Crosslinks*
J Serpa, EV Petrotchenko, CH Borchers

S212 *TGF-beta vs. BMP4: The Basis for Antagonistic Smad Signaling in Early Development*
Nithya BabuRajendran, Ralf Jauch, Prasanna Kolatkar, Paaventhana Palasingam

S213 *Top-down Analysis of Native and Crosslinked Proteins to Locate Modifications and Investigate 3-Dimensional Structures*
C. E. Costello, R. Théberge, G. Infusini, W. Tong, X. Xu, L. Han, C. Lin, M. E. McComb

S214 *Mass Spectrometry and its Role in Structural Biology*
Carol V. Robinson

Study Design and Standards for Clinical Proteomics (S301 – S311)

S301 *Deficient Triosephosphate Isomerase (TPI) Affect Micturition Dysfunction from Neurogenic Bladder*
Hyo Jin Kang, Hye Young Lee, Mei Hua Jin, Young Jae Im, Chang Hee Hong, Sang Won Han

S302 *Proteomics of Cerebellar Floccules during Vestibular Compensation of a Rat Vertigo Model*
M Fukasawa, K Okamoto, M Nakamura, K Nagai, M Arito, MS Kurokawa, K Masuko, N Suematsu, I Koizuka, T Kato

S303 *Thermal Inactivation Prior to 2DGE Stabilizes Brain Proteome*
Gary B. Smejkal, Alexander J. Trachtenberg, John Lindsay, Mats Borén, Winston P. Kuo

S304 *Identification and Characterization of Major ABO Blood Group-Carrying Proteins in Human Kidney*
M Tasaki, Y Yoshida, Y Zhang, E Yaoita, Y Nakagawa, K Saito, K Takahashi, T Yamamoto

S305 *Understanding Cross-Lab Reproducibility for SRM-Based Mass Spectrometry Clinical Assays*
T. Rezai, B. Krastins, D. Sarracino, M. Athanas, M. Ross, Paul Russo, H. Zhang, V. Kulasingam, I. Batruch, C. Smith, L. Liotta, E. Petricoin, E. Diamandis, D. Chan, Mary F. Lopez

S306 *Fixing Proteomics Initiative: A Global Quest for Reproducibility*
K. Bala, A. Borthwick, W.Dracup, P.Lavery, and H. Voshol

S307 *The Proteomic Profile of Endometriosis – A Comparative Study Between Endometrium and Serum*

C. Ng, M. J. Cooper, N. Andreadis, M. A. Kashem, R. Markham, I. S. Fraser

S308 *Proteomic Analysis of Small Intestinal Bacterial Overgrowth*

D. Ghosh, S.K. VenuGopal and U.C. Ghoshal

S309 *Building a Robust and Reliable Proteomics Biomarker Pipeline: NCI's CPTAC Network*

C. R. Kinsinger, M. Mesri, T. Hiltke, H. Rodriguez

S310 *AMT Tag Strategy for Bladder Cancer Biomarker Candidates Discovery in Urine*

C.D. Masselon, M. Court, M. Le Gorrec, M. Mellal, V. Brun, C. Bruley, V. Dupierris, E. Pereira, Y. Allory, Y. De Rycke, A. Savignoni, J. Garin

S311 *Shotgun Proteomics Identifies Protein Biomarkers Specific for Acute Renal Transplant Rejection*

T Sigdel, A. Kaushal, M Gritesenko, A. Norbeck, W. Qian, W. Xiao, D. Camp, R. Smith, and Minnie Sarwal

Poster Presentations: Wednesday (Sept 30th, 2009) Metro West

Quantification (Q101 – Q156)

Q101 *Quantitative Proteomic Analysis of Sulfolobus Solfataricus P2 under Different Temperatures*

T. K. Pham and P. C. Wright

Q102 *Progress in Label-Free Protein Quantification Tool Development T3PQ in Comparison with Superhirn, APEX and emPAI*

J Grossmann, B Roschitzki, C Panse, S Barkow-Oesterreicher, R Schlapbach

Q103 *Quantification of Total Peptide Amount by an Optimized Micro-LC/UV Method*

Y. Tang, N. Wang, L. Chen, A. Lo, L. Li

Q104 *Identification of miR-17-92 Targets in Lung Epithelial Cells Using a Quantitative Proteomic Approach*

Ryo Yokoyama, Ayumu Taguchi, Kiyoshi Yanagisawa, Takeshi Shibata, Masato Aoshima, Kenichi Kudo, Takuichi Tsubata, Sumie Ando and Takashi Takahashi

Q105 *Proteomics to Study the Roles of ROS and Src Kinase Inhibitor, PP1, in Ischemia Reperfusion Injury*

I-Wen Chen, Hsiu-Chuan Chou, Tian-Ren Lee, Hsin-Hsin Shen, John F. Timms and Hong-Lin Chan

Q106 *Toxicoproteomics: Clostridial Toxins Induce Changes Of Proteinprofiles In Colonocytes*

N Jochim, I Just, R Gerhard, A Pich

Q107 *Quantitative Phosphoproteomics of the Insulin and IGF-1 Signaling Pathways in Adipocytes*

Helle Moss, Blagoy Blagoev and Irina Kratchmarova

Q108 *A Simplified Method for microRNA Target Identification by Label-Free Mass Spec Analysis*

D.R. Boutz, Y.T. Lin, A.A. Bhinge, C.S. Sullivan, E.M. Marcotte

Q109 *A Label-free Quantitative Analytical Approach for Phosphopeptide Profiling*

X Xie, S Feng, H Vuong, Y Liu, S Goodison, and DM Lubman

Q110 *Relative Quantitation of Plasma Proteins Using Next Generation MALDI TOF/TOF Instrumentation*

L Ohlund, A Booy, D Smith, CL Hunter, CH Borchers

Q111 *An Efficient Label-free Strategy for Phosphoproteomics in Depicting Mechanisms of Cancer Invasion*

YT Wang, CF Tsai, TC Hong, CC Tsou, PY Lin, TM Hong, PC Yang, TY Sung, WL Hsu and YJ Chen

Q112 *Quantitative Proteome Profiling of Obesity-induced Type-2 Diabetes Mice Using LTQOrbitrapXL*

D Rutishauser, H al Hasani, J Grossmann, and R Schlapbach

Q113 *Measurement of Phosphorylation Stoichiometry in Tumors by Mass Spectrometry*

L Jin, J Tong, P Taylor, J St-Germain, S Trudel, M Moran

Q114 *Protein Quantification in Label-Free LC-MS Experiments*

T. Clough, S. Braun, M. Key, I. Ott, S. Ragg, G. Schadow, O. Vitek

Q115 *Quantitative Profiling of the Secretome during Skeletal Muscle Cell Differentiation*

C.Y. Chan, J.C. McDermott, and K.W.M. Siu

Q116 *Targeted MRM Expression Profiling of 45 Proteins in a Cohort of 60 CVD Plasma Samples*

M.A. Kuzyk, D. Smith, T.J. Cross, J. Yang, A.M. Jackson, D.B. Hardie, J. S. Hill, and C.H. Borchers

Q117 *Quantitative Proteomic Changes by Activation of PPAR- γ with the Agonist Troglitazone.*

O Busk, L Halvorsen, T Lea, M Skaugen, and Morten Sorlie

Q118 *Quantification of Light-Regulated Proteins by ICPL Quadruplex Labeling*

L. Weigang, S. Heindl, A. Vogt, M. Ueffing, A. Brunner and F. Lottspeich

Q119 *Isotope Coded Protein Labels for Quantitative Analysis of Encephalitogenic CD4⁺ T Lymphocyte Cells*

J. O. R. Gustafsson, M. R. Condina, I. Comerford, S. R. McColl, P. Hoffmann

Q120 *The Development of Targeted MRM Assays from Multiplexed Discovery Phase Protein Results*

Therese McKenna, Christopher Hughes, Amy Bartlett and James Langridge

Q121 *Optimization of Sample Processing and LC/MS/MS Proteomic Analysis of Complex Field Samples*

N Stoynov, A. Tam, R. Parker, M.M. Guarna and L.J. Foster

Q122 *Unbiased Quantitation of Membrane Proteome Using Phase-Transfer Surfactants*

Y. Ishihama, T. Masuda, M. Iwasaki, M. Tomita

Q123 *A Common Processing and Statistical Framework for Label-free Quantitative Proteomics Analyses*

O. Riba Grognez, P. Waridel, F. Schutz, L. Long, M. Quadroni and I. Xenarios

Q124 *SILAC Based Quantitative Phospho-Proteomic Study of TGF- β Signaling in Colon Cancer Cells*

N. A. Ali, C. Chiu, M. P. Molloy

Q125 *Performance Factors of an Ultra-high Resolution API-Qq-TOF for Label-free Proteomics Studies*

Wolfgang Jabs, Markus Lubeck, Marina Behrens, Carsten Baessmann

Q126 *MatchRx – A Software Tool for Label-free Mass Spectrometry Protein Quantitation*

SJ. Foote, AJ. Barton, JF. Kelly and AS. Haqqani

Q127 *Comparison of Sample Preparation Methods in Amine-based Isotope Labeling for Quantitative Proteomics*

L. Chen, Y. Tang, A. Lo, L. Li

Q128 *Selected Reaction Monitoring Cubed (SRM3): A New Strategy for Validation of Putative Biomarkers*

J.-P. Charrier

Q129 *Identification of Molecular Pathways Underlying the Development of Psoriasis Using iTRAQ-2DLC-MS/MS*

I. Ruppen, H.B. Schonhaler, E.F. Wagner, and K Ashman

Q130 *The Quantitative Tyrosine Phosphoproteome Analysis of the IGF-1 Signaling Pathway in Glioma C6 Cells*

Qingsong Wang, Jintang He, Yashu Liu, Xuyang Zhao, Jianguo Ji

Q131 *Characterization of Cytokine-dependent Protein Stability by Comparative Pulse-Chase SILAC Analysis*

J Anthony, S Lin, V. Duronio, and J Kast

Q132 *Low Cost, Automated Chemical Derivatization for Relative Proteome Quantification*

A. Lo, J. H. Weiner, L. Li

Q133 *Endometrial Cancer Biomarker Discovery by a Drill-down Strategy Using iTRAQ and LC-MS/MS*

S. N. Voisin, O. Krakovska, L. V. DeSouza, A. D. Romaschin, T. J. Colgan and K. W. M. Siu

Q134 *Absolute Quantitation of Phosphorylation Dynamics in Breast Cancer Using MRM-MS Detection*

D Domanski, M Kuzyk, C Borchers

Q135 *Achieving pg/mL Peptide Sensitivity in Plasma Using Electrophoretic Enrichment and nanoLC-MS/MS*

Jeremy L. Norris, Gary A. Valaskovic, Mike Lee, James B. Harkins, III, Chuck Witkowski

Q136 *Quantitative Mass Spectrometric Analysis of PKA Phosphorylation of Purified CFTR*

S. Pasyk, P Taylor, M Ramjeesingh, M Moran, C Bear

Q137 *Application of an Immuno MALDI (iMALDI) Mass Spectrometry Assay for Diagnosis of Hypertension Related Diseases*

J.D. Reid, D. Holmes and C.H. Borchers

Q138 *Improving Fragmentation Efficiency of TMT Labeled Peptides Using Stepped Higher Energy Collisional Dissociation*

Terry Zhang, Lihua Jiang, Rosa Viner, Vlad Zabrouskov

Q139 *New Algorithm for Label-Free Protein Quantification*

W Chen, B Shan, E Bonnell, G Lajoie, P Thibault, B Ma

Q140 *Global Proteome Analysis of Leptospira Interrogans*

Azad Eshghi, Paul A. Cullen, Laura Cowen, Richard L. Zuerner and Caroline E. Cameron

Q141 *Quantitative Nano-Proteomics for Resolving Protein Complexes (QNanoPX) Related to Estrogen Transcriptional Action*

Pai-Chiao Cheng, Hsiang-Kai Chang and Shu-Hui Chen

Q142 *Protein Concentration Estimates from Mass Spectrometer Peptide Intensities*

B. Carrillo, Sylvie LaBoissiere, Line Roy, Daniel Boismenu, Nathalie Hamel, and R.E. Kearney

Q143 *The Effects of Ionizing Radiation and Radiprotectors on Lymphoblastoid Cells*

J Erde, AJ Ytterberg, RA Gatti, and JA Loo

Q144 *Hypopharyngeal Gland of Newly Emerged Honeybee Workers Could Secrete Royal Jelly: A Proteomic Analysis*

Mao Feng, Yu Fang, Jianke Li

Q145 *Modified Spectral Count Index (mSCI) for Estimation of Protein Abundance by Protein Relative Identification Possibility (RIPpro): A New Proteomic Technological Parameter*

Aihua Sun, Jiyang Zhang, Dong Yang, Handong Wei, Yunping Zhu, Ying Jiang, Fuchu He

Q146 *Development and Validation of a Multiplexed Panel of MRM Assays for Clinical Use*

M.T.McDowell, H.D.Soaes, Richard Jones, Michael Ford

Q147 *Quantitative Analysis of Lectin-enriched Aberrant Glycoprotein by Mass Analysis*

Yeong Hee Ahn, Ji Yeon Lee, Eun min Kim, Yong-Sam Kim, Jeong Heon Ko, and Jong Shin Yoo

Q148 *Optimizing the Peptide Quantitation Workflow from Biomarker Discovery to Validation*

K. Waddell, N. Tang and C. Miller

Q149 *Multiplexing Proteomic Quantification: Application to Autism biomarkers evaluation*

L.Canelle, T.Pawlowski, R.Huttenhain, M.Huentelman, R.Aebersold and B.Domon

Q150 *An Hsp90 Dependent Folding Defect in CFTR NBD1 Contributes to Cystic Fibrosis*

J Copping, D Hutt, A Koulov, S Pankow, W Balch, and JR Yates III

Q151 *Method Development for Quantification of Bacterial Integral Membrane Proteins*

Benjamin Fränzel and Dirk Wolters

Q152 *Proteolytic 18O-Labeling For Quantitative FSHD Biomarker Discovery Using PALeO Strategy*

Min Du, Charles P. Emerson Jr., Markus Hardt

Q153 *Proteomic Analysis of Microtubule Associated Proteins during Macrophage Activation*

P.C. Patel, K.H. Fisher, E.C.C. Yang, C.M. Deane and R.E. Harrison

Q154 *The Membrane Proteome of Leishmania Mexicana*

D. Lamasudin, C. Naula, R. Burchmore

Q155 *Driving Biological Discovery Using Quantitative Mass Spectrometry*

John R. Yates

Q156 *Rapid Quantitative Metabolome Profiling by Differential ¹³C-/¹²C-Isotope Labeling and Fast LC FT-ICR MS*

K. Guo, L. Li

Systems Approach to Biomarker Discovery (S401 – S444)

S401 *Proteomics of Invasive and Metastatic Human Breast Carcinoma*

Kah-Wai Lin, Serhiy Souchelnytskyi

S402 *Proteomic Profiling of Prostate Cancer and Benign Prostatic Hyperplasia from 1ml of Urine*

Taha Haj-Ahmad, Moemen Abdalla, Yousef Haj-Ahmad

S403 *Gene-Centric View to the Proteins of 18th Chromosome Identified in Blood Plasma: Potential Biomarkers*

SA Moshkovskij, VG Zgoda, SA Melnik, AL Chernobrovkin, TV Andreewski, EA Ponomarenko, AV Lisitsa, and AI Archakov

S404 *Discovery of KPNA2 as a NSCLC Potential Biomarker by Integration of Cancer Cell Secretome and Tissue Transcriptome*

Chun-I Wang, Chih-Liang Wang, Chi-De Chen, Chih-Wei Wang, Chih-Ching Wu, Ying-Huang Tsai, Yu-Sun Chang, Jau-Song Yu, and Chia-Jung Yu

- S405** *New Screening Method for Autoantigen Protein Based on Biotinylated Protein Library*
Kazuhiro Matsuoka, Hiroaki Komori, Masato Nose, Yaeta Endo, Tatsuya Sawasaki
- S406** *Pancreatic Cancer Cell Line and Pancreatic Juice Proteomics: A Search for Biomarkers*
S Makawita, C Smith, A Soosaipillai, I Batruch, F Ruckert, EP Diamandis
- S407** *Proteomic and Bioinformatic Analysis of Cancer-cell Secretome for Biomarker Identification*
Chih-Ching Wu, Chia-Wei Hsu, Chi-De Chen, and Jau-Song Yu
- S408** *Proteome Profiling of Invasive Ductal and Lobular Carcinomas*
Olena Zakharchenko, C Greenwood, Louise Alldridge, Serhiy Souchelnyskiy
- S409** *Proteomics of Serum and CSF of Monozygotic Twins Discordant for Schizophrenia*
LC Gillet, RH Yolken, FE Torrey, A Panagiotidis, R Aebersold, B Domon
- S410** *Building Tools for the Analysis and Visualization of Metabolomic Data*
A. Karnovsky, J. Gao, G. Tarcea, C. Beecher, C. Burant, B. Mirel, H.V. Jagadish, G. S. Omenn
- S411** *High-speed Proteomic Signature by Informatics-Assisted Label-free Quantitation*
CF Tsai, PY Lin, CC Tsou, YT Wang, CP Wu, TY Sung, WL Hsu, YJ Chen
- S412** *Metabonomic and Proteomic Research for Discovering New Biomarkers of Liver Failure Caused by HBV*
Lijun Zhang, Xiaofang Jia, Xia Peng, Chao Qiu, Qiang Ou, Yamin Yao, Fang Shen, Hua Yang, Xiuhua Peng, Zhenghong Yuan
- S413** *SNU4 KO Mice is Resistant to Diet-induced Obesity*
Il Yong Kim, Yo Na Kim, Kyung Jin Roh, Jae Hoon Shin, Ji Won Choi, Yu Hee Lee, Mi Ra Sohn, Yun Soo Bae and Je Kyung Seong
- S414** *Analysis of Acyl-CoA dehydrogenase (ACAD) Deficiency Products in Human Urine*
A Zuniga, L Li
- S415** *A Streamlined Pipeline for Plant Metabolomics by FTMS*
J Han, RM Danell, R Datla, J Bahlmann and CH Borchers
- S416** *A Proteomics Approach to Understanding Cryptococcus Gatti Infection*
B.Herbert, C. Hill, M. Sivell, M. Padula, K. Bala, Dee Carter, M Krockenberger
- S417** *Mitochondrial Fatty Acid Oxidation (FAO) Enzyme Deficiencies: A Urinary Acylglycines Study*
A Lewis, L Li
- S418** *Immuno-proteomic Approach for Antigenic Characterization of Clonorchis sinensis*
Myoung-Ro Lee, Yu Jeong Kim, Shin-Hyeong Cho, Jae-Ran Yu, and Jung-Won Ju
- S419** *Secreted Protein Expression from HepG2 Cells Exposed to Benzyl butyl phthalate*
Seonyoung Choi, Zhi Zheng, So-Young Park, Sohee Phark, Min Lee, Donggeun Sul
- S420** *The Identification of Antigenic Proteins in Clonorchis sinensis Using by Multi Dimensional Fractionation System*
Jung-Won Ju, Myoung-Ro Lee, Yu Jeong Kim, Shin-Hyeong Cho, Jae-Ran Yu
- S421** *Quantitative and Qualitative Screening of Urinary Biomarkers by Selected Reaction Monitoring*
Mariette Matondo, Nathalie Selevsek, Ruedi Aebersold, Yves Allory, and Bruno Domon
- S422** *Secreted Protein Expression from HepG2 Cells Exposed to Di-2-ethylhexyl phthalate*
Seonyoung Choi, Zhi Zheng, So-Young Park, Sohee Phark, Min Lee, Donggeun Sul
- S423** *Translating Protein Expression Results into Targeted MRM Assays to Study Kidney Osmotic Regulation.*
Aaron Booy, Patrick Pribil, Joan Ferraris, Maurice Burg, and Brigitte Simons
- S424** *Improvement of 2D-PAGE Resolution of Mammalian Follicular Fluid*
S Fahiminiya, V Labas, JL Dacheux, N Gerard
- S425** *Comparative Secretome-based Identification of Novel Pancreatic Cancer Biomarker*
J-S Yu, M-H Tsai, C-C Wu, Y Liang, I-M Shyr, and T-L Huang
- S426** *Cell Secretome Analysis Using a Hollow Fiber Culture System Leads to the Discovery of CLIC1 Protein as a Novel Plasma Marker for Nasopharyngeal Carcinoma*
Y.H. Chang, C.C. Wu, K.P. Chang, J.S. Yu, P.C. Liao
- S427** *Quantitation of Carbonyls in Biofluids Using 14N-/15N-dansylhydrazine Labeling and LC/FTMS*
M Dawe, K Guo, and L Li
- S428** *Lipidomics in a Systems Biological Approach to Cancer Research: Response, Targets and Biomarkers*

M.R. Emmett, H. He, C.L. Nilsson, A.G. Marshall, R.A. Kroes, J.R. Moskal, M. Groves, C.A. Conrad

S429 *Comparison of Protein Subcellular Location in Normal and Cancerous Tissues*
E. Glory, J. Newberg, R. F. Murphy

S430 *2D-LC Fractionation and Dansylation Labeling Combined with FT-MS and NMR for Human Urine Metabolome Identification*

R Zhou, J Peng, K Guo, L Li

S431 *Understanding Pathogenesis of Down Syndrome by Quantitative Proteomics Analysis of Amniotic Fluid*
C.-K. J. Cho, E.P. Diamandis

S432 *Examination of the Human Plasma Phospholipid Profile of Patients with Metabolic Syndrome*
R Kozłowski, J Han and CH Borchers

S433 *Extending the Dynamic Range for Multiplexed Plasma Proteomics based Biomarker Discovery*
M. Sethuraman, M. Paniagua, M. Lynch, S. Booth, J. Campbell and P. Juhasz

S434 *Protein Signatures in Plasma for Stratification of Ovarian Cancer Subtypes*
R Huettenhain, D Dinulescu, V Heinzelmann-Schwarz, and R Aebersold

S435 *Discovery of RbAp46 as a Novel Prognostic Marker for Distant Metastasis in NSCLC*
Chih-Liang Wang, Chun-I Wang, Pao-Chi Liao, Ying Liang, Chi-De Chen, Wen-Yu Chuang, Ying-Huang Tsai, Hua-Chien Chen, Jau-Song Yu, Chih-Ching Wu and Chia-Jung Yu

S436 *Quantitative Proteomics for Metastatic Biomarker Discovery in the Microdissected Oral Cancer Tissues*
Lang-Ming Chi, Kun-Yi Chien, Kai-Ping Chang, Chien-Wei Lee, Jau-Song Yu

S437 *Establishing Sera Metabolic Fingerprinting and Recognition Models of NPC*
DJ Li, LZ Yi, JH Deng, SP Liang, ZQ Xiao, ZC Chen

S438 *DBP as a Potential Biomarker for Multiple Sclerosis (MS) Research*
Shilian Liu and Zhaoyu Qin

S439 *Development of the Platform for Comparative Analysis of the Tear Proteome based on the AMT Approach*
A Bugrova, T Shevchenko, A Kononikhin, A Zhiryakova, I Popov, N Khristenko, I Agron, D Avtonomov, G Kalamkarov, E Nikolaev

S440 *A Blood Protein Signature for Hepatotoxicity – Systems Strategy for Organ-specific Biomarker Discovery*
Z. Hu, C. Lausted, S Qin, X. Yan, H. Yoo, A. Brightman, L. Hood

S441 *Six Protein Molecular Signature to Diagnose Tuberculosis from Human Serum.*
R K Nanda, K V S Rao, R Singla, V S Chauhan

S442 *Combining Methods Improves Plasma Proteomic Analyses in Patients with Coronary Artery Disease*
J B. Béland, P Maurice, L Roy, P Comtois, S LaBoissière, A Bonnefoy, P Thérour

S443 *Possibility of Neuroprotection to Toxic-induced Retinal Damage by Synuclein-beta*
R Sano and S Suzuki

S444 *Secretome-based proteomic analysis reveals proteolytic modulation of the extracellular matrix during epithelial-mesenchymal transition*
D.W. Greening, and R.J. Simpson.

Poster Presentations: Wednesday (Sept 30th, 2009) Harbour Ballroom

Systems Biology (S501 – S528)

S501 *Phosphoproteome Dynamics Reveals Heat Shock Protein Complexes Specific to the Leishmania Infectious Stage*
G.F. Spath, M.A. Morales, R. Watanabe, P. Chaffey, J. Osorio y Fortea, P. Lenormand, and J.C. Rousselle

S502 *Global Functional Atlas of Escherichia coli Encompassing Previously Uncharacterized Proteins*
JJ Diaz-Mejia, P Hu, SC Janga, M Babu, G Butland, W Yang, O Pogoutse, X Guo, S Phanse, P Wong, S Chandran, C Christopoulos, A Nazarians-Armavil, N Karimi Nasser, G Musso, M Ali, N Nazemof, V Eroukova, A Golshani, A Paccanaro, JF Greenblatt, G Moreno-Hagelsieb, A Emili

S503 *A Targeted Protein-Protein “Interact-ome” of the Insulin Signaling Pathway in Drosophila and Compared to Human Cells*
J.M. Asara, A.A. Friedman, X. Yang, M. Kulkarni, P. Hong, J.A. Engelman, N. Perrimon

- S504** *Cellular Proteome of Aspergillus Fumigatus Reactive with Sera of Rabbits after Experimentally Induced Aspergillosis*
AR, Asi, M, Oellerich, VW, Amstrong, U, Gross and U. Reichard
- S505** *Comparative Semi-quantitative Proteome Analysis of Five Species*
M. Weiss, S. Schrimpf, C. von Mering and M. Hengartner
- S506** *Molecular Systems Biology of Aging and Anti-Aging*
V.I. Titorenko, A. Goldberg, P. Kyryakov, S. Bourque, T. Boukh-Viner, A. Beach, M. Burstein, G. Machkalyan, V. Richard, S. Rampersad, and S. Milijevic
- S507** *A Structured Syntax for Minimotifs*
J. Vyas, M. R. Gryk, Martin R. Schiller
- S508** *Signatures of Human Protein and mRNA Expression Levels – Lessons on Translation and Protein Degradation*
C Vogel, RS Abreu, D Sandhu, TL Burton, SC Burns, S Yun, B Shapiro and LF Penalva
- S509** *Integrating Genomics and Proteomics Data Using Cross-Linking Databases*
S.-J. Lee and R.E. Kearney
- S510** *pSILAC in the Zebrafish as a Tool to Study Posttranslational Regulation by microRNAs in vivo*
M Kirchner, M Renz, S Seyfreid, M Selbach
- S511** *Cytoprotective Effects of Glutamine in Mesothelial Cells after Exposure to Peritoneal Dialysis Fluid*
K. Kratochwill, M. Lechner, R. Herzog, A. Lichtenauer, B. Mayer, A. Rizzi, C. Aufricht
- S512** *Identification of Proteins Regulated by dDAVP and ANG II in Kidney IM Using Systems Biology*
MiNa Song, JeongEun Lee, Pyong-Gon Moon, Hyo-Jung Choi, MinHyung Kim, Daehee Hwang, Tae-Hwan Kwon, Moon-Chang Baek
- S513** *Endoplasmic Reticulum (ER) Targeting of Phospholamban: The Diarginine Motif in ER Retention*
Parveen Sharma, Vladimir Ignatchenko, Thomas Kislinger, and Anthony O. Gramolini
- S514** *System-wide In Depth Analysis of Protein Half-lives in Mammalian Cells*
B Schwanhaeusser, N Li, W Chen, M Selbach
- S515** *A Novel Method to Characterize the NuA4 Lysine Acetyltransferase and its Substrates*
L Mitchell, J-P Lambert, H Zhou, D Figeys, K Baetz
- S516** *Quantitative Proteomic Profiling of the Interaction of Francisella Tularensis LVS with Macrophages*
A.Hartlova, M. Link, J. Stulik
- S517** *Proteomic Profiling of Protein Kinases*
U Kusebauch, J Malmstroem, O Rinner, R Aebersold
- S518** *A Systems Biology Approach to Dissecting Host-pathogen Interactions*
JN Adkins, CK Ansong, RN Brown, JE McDermott, L Shi, H Yoon, G Niemann, S Porwollik, M McClelland, F Heffron, and RD Smith
- S519** *Proteomics to Interactomics: A Streamlined Approach to Identify High-yield Hits*
Satish P. RamachandraRao, Priti Talwar, Timothy Ravasi & Kumar Sharma
- S520** *The Chromatin Proteome and a Systems Approach to Understanding Genetic Stability*
Guennadi A.Khoudoli, Iain M. Porter, Sandra C. Moser, Peter J. Gillespie, Graeme X. Stewart, Jens S. Andersen, Jason R. Swedlow and J. Julian Blow
- S521** *Towards a Systems Approach to Understanding Breast Cancer*
N Bertos, G Finak, R Lesurf, F Pepin, S Shahalizadeh, B Schade, W Muller, M Park, M Hallett
- S522** *An Integrated Pipeline for Identification and Quantitation of Metabolites from Accurate Mass LC-MS Data*
R Danell, J Han, C Borchers
- S523** *Network Dynamics during Embryo Development in Canola and Arabidopsis*
R Datta, D Xiang, E Wang, P Venglat, C Tibiche, H Yang, W Keller and G Selvaraj
- S524** *High-Resolution Mapping of the Protein Interaction Network for the Human Transcription Machinery Identifies Novel Complexes That Regulate RNA Polymerase Biogenesis*
B Coulombe, P Cloutier, R Al-Khoury, M Lavallée-Adam, D Faubert, C Poitras, A Bouchard, M Blanchette, D Forget
- S525** *Global Interaction Atlas of Escherichia coli Encompassing Previously Uncharacterized Proteins*
JJ Díaz-Mejía, P Hu, SC Janga, M Babu, G Butland, W Yang, O Pogoutse, X Guo, S Phanse, P Wong, S Chandran, C Christopoulos, A Nazarians-Armavil, N Karimi Nasser, G Musso, M Ali, N Nazemof, V Eroukova, A Golshani, A

Paccanaro, JF Greenblatt, G Moreno-Hagelsieb, A Emili

S526 *Interactome Mapping – Where Are We and How to Move Forward?*
Pascal Braun

S527 *Computational Methods for AP/MS Protein-protein Interaction Data*
Alexey I. Nesvizhskii

S528 *Family Reunion - Encounter of Molecular Cousins Uncovers Founder and Ancient Function of Prion Gene Family*
Gerold Schmitt-Ulms, Joel Watts, Sepehr Ehsani, Hairu Huo, Yu Bai, Holger Wille, David Westaway

S529 *A Bayesian Statistical Approach to Peptide Identification by Accurate Mass and Time Tags*
C. M. Yanofsky, A. W. Bell, S. Lesimple, B. Carrillo, R. E. Kearney

Tissue Proteomics (T101-T144)

T101 *Differential Proteomics Approach Yields Inventory of Domain Specific Epididymal Sperm Proteins*
A R Suryawanshi, S A Khan and V V Khole

T102 *Large-Scale Proteomic Study of Chronic Kidney Allograft Rejection from Tissue Biopsies*
Aleksy Nakorchevsky, Johannes A. Hewel, Sunil M. Kurian, Tony S. Mondala, Daniel Campbell, Steve R. Head, Christopher L. Marsh, John R. Yates III and Daniel R. Salomon

T103 *A Study of the Liver and Pancreas Post Mortem Degradome*
Karl Sköld, Birger Scholz, Kim Kultima, Celine Fernandez, Sofia Waldemarson, Mikhail Savitski, Mats Borén, Marcus Svensson, Roman Zubarev, Per Andrén and Peter James

T104 *Heat Stabilization Prior to Shot-gun Proteomics Improve Quantification & Reduce Non-tryptic Peptides*
Mats Borén, Kim Kultima, Carina Sihlbom, Marcus Svensson, Karl Sköld, Per Svenningsson

T105 *Phosphoproteomic Pattern in Normozoospermic and Infertile Teratozoospermic Men*
A. M. Ardekani, S. Jabbari, M.R. Sadeghi, N. Amirjanati, A. E.Habibi, N. Lakpour, M. Hodjat, M.M. Akhondi

T106 *Heat Stabilization of the Tissue Proteome for Improved Proteomics*
Marcus Svensson, Mats Borén, John Lindsay, Maria Fälth, Per E. Andrén, Per Svenningsson, Karl Sköld

T107 *Development of Off-line 2D-LC Tandem Mass Spectrometry for Comprehensive Tissue Proteome Analysis*
N. Wang and L. Li

T108 *Interrogating the Proteome of Formalin-Fixed Paraffin-Embedded Tissues*
Timothy Veenstra

T109 *Pancreatic Cancer Serum Detection Using a Lectin/Glyco-Antibody Array Method*
C Li, E Zolotarevsky, MA Anderson, DM Lubman

T110 *Quantitative Proteomics Analysis of Alcohol-induced Cardiomyopathy Using Label Free LC-MS Approach*
E. Yohannes, H. Anni, G. E. Gonye, S. Ilchenko, E. Rubin, M. R. Chance

T111 *Apis mellifera Proteomics of Innate Resistance (APIS): Quantitative Proteomic Analysis of Honey Bee Populations within Canada.*
R. Parker, M Guarna, A Tam, N Stoynov, A Melathopoulos, S F. Pernal and L J. Foster

T112 *Detection of Novel Biomarkers of Liver Cirrhosis by Proteomic Analysis*
B Sitek, C Mölleken, G Poschmann, C Henkel, B Sipos, S Wiese, B Warscheid, M Reiser, SL Friedman, U Holmskov, A Schlosser, G Klöppel, W Schmiegel, HE Meyer, K Stühler

T113 *The Effect of Inflammation on the Human Visceral Adipose Tissue Secretome*
E. Szalowska, D. Weening, M. de Vries, A. Hoek, R. J. Vonk, H. Roelofsen

T114 *Optimisation of Protein Extraction from Tissue*
Susanne Schwonbeck, Nathanael Lemonnier, Ivo G. Gut

T115 *Biological Significance of a Novel Mechanism of Protein Modification*
M Boucher, P Rawson, L Peng, TW Jordan

T116 *Analysis of Infected Tissues by Laser Microdissection and LC-MS/MS*
M Hubalek, V Jedlickova, J Pejchal, A Macela, J Stulik

T117 *Comprehensive Analysis of Wild and AQP 8 Knockout Mouse Colon by Nanoflow Lc-Ms/Ms*
S Magdeldin, Y Yoshida, H Li, Yokoyama, B Xu, H Fujinaka, Y Zhang, E Yaoita, T Yamamoto

- T118** *Overexpression of Prothymosin alpha in Oral Premalignant Lesions*
SC Tripathi, A Matta, J Kaur, SS Chauhan, L DeSouza, NK Shukla, S DattaGupta, KWM Siu, R Ralhan
- T119** *Nano LC-MS/MS for Oocyte and Early Embryo Proteome Profiling with Minute Sample Amounts*
M Demant, T Frohlich, E Wolf, GJ Arnold
- T120** *Molecular Dissection of Spinal Cord Injury Using a Refined Proteomic Approach*
R.Hussain Butt, T.A. Pfeifer, J.M. Lubieniecka, J. Liu, T.A. Grigliatti, L.J. Foster, W. Tetzlaff and J.R. Coorsen
- T121** *A Label-free Quantitation Strategy for Personalized Membrane Proteomics Signature in Colorectal Cancer*
Chien-Peng Wu^{1\}, Jinn-Shiun Chen, Chia-Li Han, Kuei-Tien Chen, Chia-Feng Tsai, Chih-Wei Chien, Pei-Yi Lin, Err-Cheng Chan, Jao-Song Yu, Yu-Ju Chen
- T122** *Multicenter Analysis of Proteome and Transcriptome of Liver Cancer Showing Dysregulated Catabolism*
Terence C.W. Poon, Paul B.S. Lai, Leung Hing Ho, Ronald T.K. Pang, Nathalie Wong, Sai-Ming Ngai, Siu Tim Cheung, Joseph J.Y. Sung
- T123** *Comparative Analysis of Sialome and Salivary Gland Proteome from Vectors of Tropical Diseases*
Almeras Lionel, Fontaine Albin, Belghazi Maya, Villard Claude, Briolant Sébastien, Bourdon Stéphanie, Orlandi-Pradines Eve, Pophillat Matthieu, Fourquet Patrick, Pradines Bruno, Fusai Thierry, Rogier Christophe.
- T124** *Proteomic Analysis to Identify Proliferation-Specific Factors using Cultured Amniocytes*
K Lakshmi Rao, T Raseswari, D. Tosh, P Gautam, R Sirdeshmukh, L Singh
- T125** *Optimum Method Designed for 2D-DIGE of Arterial Intima and Media Isolated by Laser Microdissection*
F. de la Cuesta, G. Alvarez-Llamas, A.S. Maroto, A. Donado, I. Zubiri, R. Juarez-Tosina, L. Rodriguez- Padial, A. G. Pinto, M. G. Barderas and F. Vivanco
- T126** *Characterization of Zebrafish Gill Proteome Changes after Naphthenic Acid Exposure*
A.G. De Souza, T.J. MacCormack, A. Lo, G.G. Goss, and L. Li
- T127** *Quantitation of Her2 in FFPE Breast Cancer Tissue by Mass Spectrometry MRM Analysis*
Marlene Darfler, Michael Ford, Richard Jones, Albert Kovatich, Brian Hood, Jeff Zhang, Timoth Veenstra, Thomas Conrads, David Krizman
- T128** *Digital Pathology: Quantifying Barretts' Markers in Tissue Samples Using LCM-MS*
A. Prakash, T. Rezai, B. Krastins, D. Sarracino, M. Athanas, Brian Hood, Melanie Flint, Jon Davison, Mary F. Lopez, Thomas P. Conrads
- T129** *Enrichment of Low Abundance Proteins in Tissue and Cell Line Samples Using ProteoMiner™ Protein Enrichment Technology*
S. Freeby, K. Smith, N. Liu, K. Academia, J. Walker II, T. Wehr and A. Paulus
- T130** *Identification of Periostin as an Invasion Promoter Protein in the Stroma of Nasopharyngeal Carcinoma by Proteomic Analysis*
Li Meixiang, Li Guoqing,, Peng Fang, xiao Zhiqiang, Li Maoyu, Zhang Pengfei, Chen Zhuchu
- T131** *3D Liver Co-Culture Proteome as a Model for Functional Tissues*
R. Isbrucker, D. Smith, T. Cyr
- T132** *Development of Protein Extraction Methods for Deer Antler Proteome Research*
Liang Gao, Zhen Liang, Lihua Zhang, Yushu Huo, Yukui Zhang
- T133** *Local Snakebite Pathophysiology Induced By Jararhagin Injection: A Tissue Proteomics Approach*
R M S, Terra, A F M Pinto, T Escalante, J M Gutierrez, J A Guimaraes and J W Fox
- T134** *Identification of Lipids in Placentas from Control and Preeclamptic Pregnancies*
NJ Carruthers, VKM Han, and G Lajoie
- T135** *Detection and Quantification of Potential Markers in FFPE Tissue and Plasma Samples*
Leroi V. DeSouza, Declan Williams, Marlene M. Darfler, David B. Krizman, Casimir Eitner, Alexander D. Romaschin, Terence J Colgan, K.W. Michael Siu
- T136** *An Integrated Platform For MALDI Imaging*
E.J. Clemis, D. Smith and C.H. Borchers
- T137** *Quantitative Proteomics of Glutathione S-Transfereases in Mouse Liver Mitochondria*
Haidansun, Yuan Wang, Fuli Peng, Yawei Ru, Xishu Chen and Siqi Liu
- T138** *MRM Assay to Identify Biomarkers for Lung Carcinoma of Large-cell Neuroendocrine (LCNEC)*

Toshihide Nishimura, Masaharu Nomura, Tetsuya Fukuda, Kiyonaga Fujii, Takeshi Kawamura, Hiroko Hamasaki, Hiroshi Hike, Yasuhiko Bando, Harubumi Kato

T139 *Comparatively Proteomic Analysis to Drosophilatreated with/without Hypoxia*
Songyue Yin, Yuan Wang, Haidan Sun, Yawei Ru, Xishu Chen and Siqi Liu

T140 *Collection and Characterization of Human Liver Cell Secretome Using a Hollow Fiber Bioreactor Culture System Coupled with Tangential Flow Filtration Enrichment*
Y.T. Wen, Y.C. Chang, L.C. Lin and P.C. Liao

T141 *Thermal Treatment Stabilizes the Brain Proteome during Sample Preparation*
A.A. Robinson, J.A. Westbrook, J.A. English, M. Boren, M.J. Dunn

T142 *Proteomic Analysis of a Transgenic Mouse Model of Heart Failure Resulting from Cardiac Hypertrophy*
S. Chugh, N. Bousette, T. Kislinger, R. Isserlin, P. Liu, DH MacLennan, A. Emili, AO Gramolini

T143 *Role of Corneal Epithelial Proteins in Re-epithelialization*
S. Mushtaq and N, Ahmed

T144 *Skin Pathology Induced by Snake Venom Metalloproteinases: Analysis of the Hemorrhageome*
Solange M.T. Serrano, Adriana F. Paes Leme, Ana K. Oliveira, Marina T. Assakura, Antonio C.M. Camargo, David M. Smalley, Nicholas E. Sherman, Jay W. Fox

Yeast Proteomics, Sparks for New Biology (Y101 – Y106)

Y101 *Optimized Protein Extraction from Thermotolerant Probiotic Yeast (S. Cerevisiae OBV-9) for 2-D Gel Electrophoresis*
B Bhima, T Anjana Devi², M Sudhakara Reddy, Y Ramana Reddy¹ and L Venkateswar Rao

Y102 *Heat-Shock Induced Misfolded Cytoplasmic Proteins Are Ubiquitinated by a Network of Ubiquitin E3 Ligases in Saccharomyces cerevisiae*
N, Fang, T. Mayor

Y103 *Proteomic Analysis of Aspergillus fumigatus to Identify Molecular Targets of Artemisinin*
P Gautam, W Hasan, T Madan, R Sirdeshmukh, C S Sundaram, W N Gade, P U Sarma

Y104 *Building a global map of Rub1 function in S. cerevisiae*
Y. Sydorsky, T. Makhnevych, B. Raught

Y105 *Proteome Analysis of Aspergillus ochraceus*
M. Rizwan, I. Miller, F. Tasneem, J. Bohm, M. Gemeiner, and E. Razzazi-Fazeli

Y106 *Preserving the Yeast Proteome from Sample Degradation*
Julia Grassl, Jules A Westbrook, Aisling Robinson, Mats Borén, Michael J Dunn and Rosemary K Clyne