

Tutorial

- 3006 **An Introduction to Biological NMR Spectroscopy**
Dominique Marion
- 3026 **Tools (Viewer, Library and Validator) that Facilitate Use of the Peptide and Protein Identification Standard Format, Termed mzIdentML**
[S] ⌘ *Fawaz Ghali, Ritesh Krishna, Pieter Lukasse, Salvador Martínez-Bartolomé, Florian Reisinger, Henning Hermjakob, Juan Antonio Vizcaino, and Andrew R. Jones*

Research

- 3036 **Novel *Burkholderia mallei* Virulence Factors Linked to Specific Host-Pathogen Protein Interactions**
[S] ⌘ *Vesna Memišević, Nela Zavaljevski, Rembert Pieper, Seesandra V. Rajagopala, Keehwan Kwon, Katherine Townsend, Chenggang Yu, Xueping Yu, David DeShazer, Jaques Reifman, and Anders Wallqvist*
- 3052 **The Rhesus Macaque (*Macaca mulatta*) Sperm Proteome**
[S] *Sheri Skerget, Matthew Rosenow, Ashoka Polpitiya, Konstantinos Petritis, Steve Dorus, and Timothy L. Karr*
- 3068 **Proteomic Analysis of Eggs from *Mytilus edulis* Females Differing in Mitochondrial DNA Transmission Mode**
[S] *Angel P. Diz, Edward Dudley, Andrew Cogswell, Barry W. MacDonald, Ellen L. R. Kenchington, Eleftherios Zouros, and David O. F. Skibinski*
- 3081 **Investigations on Aberrant Glycosylation of Glycosphingolipids in Colorectal Cancer Tissues Using Liquid Chromatography and Matrix-Assisted Laser Desorption Time-of-Flight Mass Spectrometry (MALDI-TOF-MS)**
[S] ⌘ *Stephanie Holst, Kathrin Stavenhagen, Crina I. A. Balog, Carolien A. M. Koeleman, Liam M. McDonnell, Oleg A. Mayboroda, Aswin Verhoeven, Wilma E. Mesker, Rob A. E. M. Tollenaar, André M. Deelder, and Manfred Wuhrer*
- 3094 **Quantitative Phosphoproteomic Study of Pressure-Overloaded Mouse Heart Reveals Dynammin-Related Protein 1 as a Modulator of Cardiac Hypertrophy**
[S] *Yu-Wang Chang, Ya-Ting Chang, Qinchuan Wang, Jim Jung-Ching Lin, Yu-Ju Chen, and Chien-Chang Chen*
- 3108 **Molecular Responses of Mouse Macrophages to Copper and Copper Oxide Nanoparticles Inferred from Proteomic Analyses**
[S] *Sarah Triboulet, Catherine Aude-Garcia, Marie Carrière, Hélène Diemer, Fabienne Proamer, Aurélie Habert, Mireille Chevallet, Véronique Collin-Faure, Jean-Marc Strub, Daniel Hanau, Alain Van Dorsselaer, Nathalie Herlin-Boime, and Thierry Rabilloud*

On the cover: Stable-seq is a method that combines a simple genetic selection with high-throughput DNA sequencing to assess the *in vivo* stability of a large number of variants of a protein. Each variant is fused to a metabolic enzyme necessary in the selection condition, leading to a growth rate dependent on the stability of the variant. DNA sequencing of variants before and after selection enables the stability of thousands of variants to be scored simultaneously. The scores determined by Stable-seq of variants carrying single mutations are visualized in this heat map, with cell growth rates that would correspond to scores shown in the inset boxes. For more details, see the article by Ikjin Kim *et al.*, pages 3370–3378.

- 3123 **Multi-dimensional Co-separation Analysis Reveals Protein–Protein Interactions Defining Plasma Lipoprotein Subspecies**
 [S] *Scott M. Gordon, Jingyuan Deng, Alex B. Tomann, Amy S. Shah, L. Jason Lu, and W. Sean Davidson*
- 3135 **Cell Cycle Regulation of Microtubule Interactomes: Multi-layered Regulation Is Critical for the Interphase/Mitosis Transition**
 [S] * *Heather M. Syred, Julie Welburn, Juri Rappsilber, and Hiroyuki Ohkura*
- 3148 **A Label-free Selected Reaction Monitoring Workflow Identifies a Subset of Pregnancy Specific Glycoproteins as Potential Predictive Markers of Early-onset Pre-eclampsia**
 [S] *Richard T. Blankley, Christal Fisher, Melissa Westwood, Robyn North, Philip N. Baker, Michael J. Walker, Andrew Williamson, Anthony D. Whetton, Wanchang Lin, Lesley McCowan, Claire T. Roberts, Garth J. S. Cooper, Richard D. Unwin, and Jenny E. Myers*
- 3160 **Exploring the N-glycosylation Pathway in *Chlamydomonas reinhardtii* Unravels Novel Complex Structures**
 [S] *Elodie Mathieu-Rivet, Martin Scholz, Carolina Arias, Flavien Dardelle, Stefan Schulze, François Le Mauff, Gavin Teo, Ana Karina Hochmal, Amaya Blanco-Rivero, Corinne Loutelier-Bourhis, Marie-Christine Kiefer-Meyer, Christian Fufezan, Carole Burel, Patrice Lerouge, Flor Martinez, Muriel Bardor, and Michael Hippler*
- 3184 **Interactions Affected by Arginine Methylation in the Yeast Protein–Protein Interaction Network**
 [S] *Melissa A. Erce, Dhanushi Abeygunawardena, Jason K. K. Low, Gene Hart-Smith, and Marc R. Wilkins*
- 3199 **Interactome Analysis Reveals that C1QBP (complement component 1, q subcomponent binding protein) Is Associated with Cancer Cell Chemotaxis and Metastasis**
 [S] *Xiaofang Zhang, Fei Zhang, Lin Guo, Yanping Wang, Peng Zhang, Ruirui Wang, Ning Zhang, and Ruibing Chen*
- 3210 **Identification and Quantification of AKT Isoforms and Phosphoforms in Breast Cancer Using a Novel Nanofluidic Immunoassay**
 [S] *Demetris C. Iacovides, Aimee B. Johnson, Nick Wang, Shanta Boddapati, Jim Korkola, and Joe W. Gray*
- 3221 **Linking Spermatid Ribonucleic Acid (RNA) Binding Protein and Retrogene Diversity to Reproductive Success**
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- 3237 **A Proteomic Perspective of Inbuilt Viral Protein Regulation: pUL46 Tegument Protein is Targeted for Degradation by ICP0 during Herpes Simplex Virus Type 1 Infection**
 [S] *Aaron E. Lin, Todd M. Greco, Katinka Döhner, Beate Sodeik, and Ileana M. Cristea*
- 3253 **Regulation of Stress-Inducible Phosphoprotein 1 Nuclear Retention by Protein Inhibitor of Activated STAT PIAS1**
Iaci N. Soares, Fabiana A. Caetano, Jordan Pinder, Bruna Roz Rodrigues, Flavio H. Beraldo, Valeriy G. Ostapchenko, Chantal Durette, Grace Schenatto Pereira, Marilene H. Lopes, Nicolle Queiroz-Hazarbassanov, Isabela W. Cunha, Paulo I. Sanematsu, Sergio Suzuki, Luiz F. Bleggi-Torres, Caroline Schild-Poulter, Pierre Thibault, Graham Dellaire, Vilma R. Martins, Vania F. Prado, and Marco A. M. Prado
- 3271 **Plasma Membrane Proteomics of Tumor Spheres Identify CD166 as a Novel Marker for Cancer Stem-like Cells in Head and Neck Squamous Cell Carcinoma**
 [S] *Ming Yan, Xihu Yang, Lizhen Wang, David Clark, Hui Zuo, Dongxia Ye, Wantao Chen, and Ping Zhang*
- 3285 **Selective Targeting of the Cysteine Proteome by Thioredoxin and Glutathione Redox Systems**
Young-Mi Go, James R. Roede, Douglas I. Walker, Duc M. Duong, Nicholas T. Seyfried, Michael Orr, Yongliang Liang, Kurt D. Pennell, and Dean P. Jones
- 3297 **Comparative Phosphoproteomics Reveals Components of Host Cell Invasion and Post-transcriptional Regulation During *Francisella* Infection**
 [S] *Ernesto S. Nakayasu, Rebecca Tempel, Xiaolu A. Cambronne, Vladislav A. Petyuk, Marcus B. Jones, Marina A. Gritsenko, Matthew E. Monroe, Feng Yang, Richard D. Smith, Joshua N. Adkins, and Fred Heffron*

- 3310 **Host-centric Proteomics of Stool: A Novel Strategy Focused on intestinal Responses to the Gut Microbiota**
 [S] *Joshua S. Lichtman, Angela Marcobal, Justin L. Sonnenburg, and Joshua E. Elias*
- 3319 **A Specific PTPRC/CD45 Phosphorylation Event Governed by Stem Cell Chemokine CXCL12 Regulates Primitive Hematopoietic Cell Motility**
 [S] *Andrew J. K. Williamson, Andrew Pierce, Ewa Jaworska, Cong Zhou, Mark Aspinall-O’Dea, Lee Lancashire, Richard D. Unwin, Sheela A. Abraham, Michael J. Walker, Sara Cadecco, Elaine Spooncer, Tessa L. Holyoake, and Anthony D. Whetton*

Technological Innovation and Resources

- 3330 **Rapid and Deep Human Proteome Analysis by Single-dimension Shotgun Proteomics**
Mohammad Pirmoradian, Harshavardhan Budamgunta, Konstantin Chingin, Bo Zhang, Juan Astorga-Wells, and Roman A. Zubarev
- 3339 **Development of a 5-plex SILAC Method Tuned for the Quantitation of Tyrosine Phosphorylation Dynamics**
 [S] *Manuel Tzouros, Sabrina Golling, David Avila, Jens Lamerz, Marco Berrera, Martin Ebeling, Hanno Langen, and Angélique Augustin*
- 3350 **Interrogating cAMP-dependent Kinase Signaling in Jurkat T Cells via a Protein Kinase A Targeted Immune-precipitation Phosphoproteomics Approach**
 [S] *Piero Giansanti, Matthew P. Stokes, Jeffrey C. Silva, Arjen Scholten, and Albert J. R. Heck*
- 3360 **Amine-reactive Neutron-encoded Labels for Highly Plexed Proteomic Quantitation**
 [S] *Alexander S. Hebert, Anna E. Merrill, Jonathan A. Stefely, Derek J. Bailey, Craig D. Wenger, Michael S. Westphall, David J. Pagliarini, and Joshua J. Coon*
- 3370 **High-throughput Analysis of *in vivo* Protein Stability**
 [S] *Ikjin Kim, Christina R. Miller, David L. Young, and Stanley Fields*
- 3379 **ProteoMirExpress: Inferring MicroRNA and Protein-centered Regulatory Networks from High-throughput Proteomic and mRNA Expression Data**
 [S] *Jing Qin, Mulin Jun Li, Panwen Wang, Nai Sum Wong, Maria P. Wong, Zhengyuan Xia, George S. W. Tsao, Michael Q. Zhang, and Junwen Wang*
- 3388 **Proteogenomic Analysis of *Bradyrhizobium japonicum* USDA110 Using Genosuite, an Automated Multi-algorithmic Pipeline**
 [S] *Dhirendra Kumar, Amit Kumar Yadav, Puneet Kumar Kadimi, Shivashankar H. Nagaraj, Sean M. Grimmond, and Debasis Dash*
- 3398 **Network-based Analysis of Genome Wide Association Data Provides Novel Candidate Genes for Lipid and Lipoprotein Traits**
 [S] *Amitabh Sharma, Natali Gulbahce, Samuel J. Pevzner, Jörg Menche, Claes Ladenvall, Lasse Folkersen, Per Eriksson, Marju Orho-Melander, and Albert-László Barabási*
- 3409 **LuciPHOR: Algorithm for Phosphorylation Site Localization with False Localization Rate Estimation Using Modified Target-Decoy Approach**
 [S] *Damian Fermin, Scott J. Walmsley, Anne-Claude Gingras, Hyungwon Choi, and Alexey I. Nesvizhskii*
- 3420 **Deep Coverage of the *Escherichia coli* Proteome Enables the Assessment of False Discovery Rates in Simple Proteogenomic Experiments**
 [S] *Karsten Krug, Alejandro Carpy, Gesa Behrends, Katarina Matic, Nelson C. Soares, and Boris Macek*
- 3431 **Application of an Improved Proteomics Method for Abundant Protein Cleanup: Molecular and Genomic Mechanisms Study in Plant Defense**
 [S] *Yixiang Zhang, Peng Gao, Zhuo Xing, Shumei Jin, Zhide Chen, Lantao Liu, Nasie Constantino, Xinwang Wang, Weibing Shi, Joshua S. Yuan, and Susie Y. Dai*

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