

## Research

- 1705 **Global Proteome and Ubiquitinome Changes in the Soluble and Insoluble Fractions of Q175 Huntington Mice Brains**  
[S] *Karen A. Sap, Arzu Tugce Guler, Karel Bezstarosti, Aleksandra E. Bury, Katrin Juenemann, Jeroen A. A. Demmers, and Eric A. Reits*
- 1721 **Posttranslational Modifications Drive Protein Stability to Control the Dynamic Beer Brewing Proteome**  
[S] *Edward D. Kerr, Christopher H. Caboche, and Benjamin L. Schulz*
- 1732 **Cross-linking Proteomics Indicates Effects of Simvastatin on the TLR2 Interactome and Reveals ACTR1A as a Novel Regulator of the TLR2 Signal Cascade**  
[S] *Abu Hena Mostafa Kamal, Jim J. Aloor, Michael B. Fessler, and Saiful M. Chowdhury*
- 1745 **Proteomics Analysis of Extracellular Matrix Remodeling During Zebrafish Heart Regeneration**  
[S] ✎ *Anna Garcia-Puig, Jose Luis Mosquera, Senda Jiménez-Delgado, Cristina García-Pastor, Ignasi Jorba, Daniel Navajas, Francesc Canals, and Angel Raya*
- 1756 **Systems-level Analysis Reveals Multiple Modulators of Epithelial-mesenchymal Transition and Identifies DNAJB4 and CD81 as Novel Metastasis Inducers in Breast Cancer**  
[S] *Zeynep Cansu Uretmen Kagiali, Erdem Sanal, Özge Karayel, Ayse Nur Polat, Özge Saatci, Pelin Gülizar Ersan, Kathrin Trappe, Bernhard Y. Renard, Tamer T. Önder, Nurcan Tuncbag, Özgür Şahin, and Nurhan Ozlu*
- 1772 **Targeted and Interactome Proteomics Revealed the Role of PHD2 in Regulating BRD4 Proline Hydroxylation**  
[S] *Luke Erber, Ang Luo, and Yue Chen*
- 1782 **NOTCH Activation Promotes Valve Formation by Regulating the Endocardial Secretome**  
[S] *Rebeca Torregrosa-Carrión, Luis Luna-Zurita, Fernando García-Marqués, Gaetano D'Amato, Rebeca Piñeiro-Sabarís, Elena Bonzón-Kulichenko, Jesús Vázquez, and José Luis de la Pompa*
- 1796 **Identification of Salivary Biomarkers for Oral Cancer Detection with Untargeted and Targeted Quantitative Proteomics Approaches**  
[S] *Hao-Wei Chu, Kai-Ping Chang, Chia-Wei Hsu, Ian Yi-Feng Chang, Hao-Ping Liu, Yi-Ting Chen, and Chih-Ching Wu*
- 1807 **Multi-omics Biomarker Pipeline Reveals Elevated Levels of Protein-glutamine Gamma-glutamyltransferase 4 in Seminal Plasma of Prostate Cancer Patients**  
[S] *Andrei P. Drabovich, Punit Saraon, Mikalai Drabovich, Theano D. Karakosta, Apostolos Dimitromanolakis, M. Eric Hyndman, Keith Jarvi, and Eleftherios P. Diamandis*
- 1824 **Canine Bone Marrow-derived Mesenchymal Stem Cells: Genomics, Proteomics and Functional Analyses of Paracrine Factors**  
[S] *Filip Humenik, Dasa Cizkova, Stefan Cikos, Lenka Luptakova, Aladar Madari, Dagmar Mudronova, Maria Kuricova, Jana Farbakova, Alexandra Spirkova, Eva Petrovova, Martin Cente, Zuzana Mojzisova, Soulaïmane Aboulouard, Adriana-Natalia Murgoci, Isabelle Fournier, and Michel Salzet*

Differences in proneness to diet-induced obesity correlate with differences in the fecal microbiota proteome. Understanding how the microbiota proteome influences metabolism may yield novel strategies to combat the obesity epidemic. For details, see the article by Tran *et al.*, pages 1864–1879.

- 1836 **A Targeted Mass Spectrometry Strategy for Developing Proteomic Biomarkers: A Case Study of Epithelial Ovarian Cancer**  
[S] *Ruth Hüttenhain, Meena Choi, Laura Martin de la Fuente, Kathrin Oehl, Ching-Yun (Veavi) Chang, Anne-Kathrin Zimmermann, Susanne Malander, Håkan Olsson, Silvia Surinova, Timothy Clough, Viola Heinzlmann-Schwarz, Peter J. Wild, Daniela M. Dinulescu, Emma Niméus, Olga Vitek, and Ruedi Aebersold*
- 1851 **Identification of Serum Biomarkers for Systemic Lupus Erythematosus Using a Library of Phage Displayed Random Peptides and Deep Sequencing**  
[S] *Fan-Lin Wu, Dan-Yun Lai, Hui-Hua Ding, Yuan-Jia Tang, Zhao-Wei Xu, Ming-Liang Ma, Shu-Juan Guo, Jing-Fang Wang, Nan Shen, Xiao-Dong Zhao, Huan Qi, Hua Li, and Sheng-Ce Tao*
- 1864 **Associations of the Fecal Microbial Proteome Composition and Proneness to Diet-induced Obesity**  
[S] ✎ *Hao Q. Tran, Robert H. Mills, Nicole V. Peters, Mary K. Holder, Geert J. de Vries, Rob Knight, Benoit Chassaing, David J. Gonzalez, and Andrew T. Gewirtz*

## Technological Innovation and Resources

- 1880 **MS-Empire Utilizes Peptide-level Noise Distributions for Ultra-sensitive Detection of Differentially Expressed Proteins**  
[S] *Constantin Ammar, Markus Gruber, Gergely Csaba, and Ralf Zimmer*
- 1893 **Integration and Analysis of CPTAC Proteomics Data in the Context of Cancer Genomics in the cBioPortal**  
[S] *Pamela Wu, Zachary J. Heins, James T. Muller, Lizabeth Katsnelson, Ino de Bruijn, Adam A. Abeshouse, Nikolaus Schultz, David Fenyö, and Jianjiong Gao*
- 1899 **Small-protein Enrichment Assay Enables the Rapid, Unbiased Analysis of Over 100 Low Abundance Factors from Human Plasma**  
[S] *Dylan J. Harney, Amy T. Hutchison, Zhiduan Su, Luke Hatchwell, Leonie K. Heilbronn, Samantha Hocking, David E. James, and Mark Larance*

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