

## Research

- 3540 **Quantitative Protein Profiling of *Chlamydia trachomatis* Growth Forms Reveals Defense Strategies Against Tryptophan Starvation**  
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*Ole Østergaard, Frank Follmann, Anja W. Olsen, Niels H. Heegaard, Peter Andersen, and Ida Rosenkrands*
- 3551 **Time-resolved Analysis of Proteome Dynamics by Tandem Mass Tags and Stable Isotope Labeling in Cell Culture (TMT-SILAC) Hyperplexing**  
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*Kevin A. Welle, Tian Zhang, Jennifer R. Hryhorenko, Shichen Shen, Jun Qu, and Sina Ghaemmaghami*
- 3564 **Immunoseroproteomic Profiling in African American Men with Prostate Cancer: Evidence for an Autoantibody Response to Glycolysis and Plasminogen-Associated Proteins**  
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*Tino W. Sanchez, Guangyu Zhang, Jitian Li, Liping Dai, Saied Mirshahidi, Nathan R. Wall, Clayton Yates, Colwick Wilson, Susanne Montgomery, Jian-Ying Zhang, and Carlos A. Casiano*
- 3581 **Identification of 2-oxohistidine Interacting Proteins Using *E. coli* Proteome Chips**  
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- 3594 **The Salivary Protein Repertoire of the Polyphagous Spider Mite *Tetranychus urticae*: A Quest for Effectors**  
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- 3614 **Multi-omics Evidence for Inheritance of Energy Pathways in Red Blood Cells**  
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- 3624 **Proteome-scale Binary Interactomics in Human Cells**  
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*Sam Lievens, José Van der Heyden, Delphine Masschaele, Leentje De Ceuninck, Ioanna Petta, Surya Gupta, Veronic De Puyseleir, Virginie Vauthier, Irma Lemmens, Dries J. H. De Clercq, Dieter Defever, Nele Vanderroost, Anne-Sophie De Smet, Sven Eyckerman, Serge Van Calenbergh, Lennart Martens, Karolien De Bosscher, Claude Libert, David E. Hill, Marc Vidal, and Jan Tavernier*
- 3640 **Robust Label-free, Quantitative Profiling of Circulating Plasma Microparticle (MP) Associated Proteins**  
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- 3653 **Salmonella Typhimurium Enzymatically Landscapes the Host Intestinal Epithelial Cell (IEC) Surface Glycome to Increase Invasion**  
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*Dayoung Park, Narine Arabyan, Cynthia C. Williams, Ting Song, Anupam Mitra, Bart C. Weimer, Emanuel Maverakis, and Carlito B. Lebrilla*

On the cover: A simultaneous discovery and targeted monitoring (DTM) approach utilizing liquid chromatography, ion mobility spectrometry and mass spectrometry. In DTM, heavy labeled peptides are spiked into tryptic digests and analyzed. The heavy peptides and light counterparts co-drift through the ion mobility drift cell, allowing absolute quantitation for the light targets and high proteomic coverage as all peptides are retained and detected. For details, see the article by Kristin E. Burnum-Johnson, et al., pages 3694–3705.

3665 **Instant Integrated Ultradeep Quantitative-structural Membrane Proteomics Discovered Post-translational Modification Signatures for Human Cys-loop Receptor Subunit Bias**  
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3685 **Deficiency in Outer Dense Fiber 1 Is a Marker and Potential Driver of Idiopathic Male Infertility**  
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## **Technological Innovation and Resources**

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