

Special Issue: Proteomics in Europe

Guest Editorial

- 1901 **PRIME-XS, a European Infrastructure for Proteomics**
Reinout Raijmakers, Jesper V. Olsen, Ruedi Aebersold, and Albert J. R. Heck

Articles

- 1905 **qcML: An Exchange Format for Quality Control Metrics from Mass Spectrometry Experiments**
[S] ⌘ *Mathias Walzer, Lucia Espona Pernas, Sara Nasso, Wout Bittremieux, Sven Nahnsen, Pieter Kelchtermans, Peter Pichler, Henk W. P. van den Toorn, An Staes, Jonathan Vandebussche, Michael Mazanek, Thomas Taus, Richard A. Scheltema, Christian D. Kelstrup, Laurent Gatto, Bas van Breukelen, Stephan Aiche, Dirk Valkenburg, Kris Laukens, Kathryn S. Lilley, Jesper V. Olsen, Albert J. R. Heck, Karl Mechtler, Ruedi Aebersold, Kris Gevaert, Juan Antonio Vizcaino, Henning Hermjakob, Oliver Kohlbacher, and Lennart Martens*
- 1914 **Analytical Utility of Mass Spectral Binning in Proteomic Experiments by SPectral Immonium Ion Detection (SPIID)**
[S] ⌘ *Christian D. Kelstrup, Christian Frese, Albert J. R. Heck, Jesper V. Olsen, and Michael L. Nielsen*
- 1925 **Absolute Proteome and Phosphoproteome Dynamics during the Cell Cycle of *Schizosaccharomyces pombe* (Fission Yeast)**
[S] *Alejandro Carpy, Karsten Krug, Sabine Graf, André Koch, Sasa Popic, Silke Hauf, and Boris Macek*
- 1937 **A Foundation for Reliable Spatial Proteomics Data Analysis**
[S] *Laurent Gatto, Lisa M. Breckels, Thomas Burger, Daniel J. H. Nightingale, Arnoud J. Groen, Callum Campbell, Nino Nikolovski, Claire M. Mulvey, Andy Christoforou, Myriam Ferro, and Kathryn S. Lilley*
- 1953 **Chasing Phosphoarginine Proteins: Development of a Selective Enrichment Method Using a Phosphatase Trap**
[S] *Débora Broch Trentini, Jakob Fuhrmann, Karl Mechtler, and Tim Clausen*
- 1965 **Quantitative Phosphoproteome Analysis of *Bacillus subtilis* Reveals Novel Substrates of the Kinase PrkC and Phosphatase PrpC**
[S] *Vaishnavi Ravikumar, Lei Shi, Karsten Krug, Abderahmane Derouiche, Carsten Jers, Charlotte Cousin, Ahasanul Kobir, Ivan Mijakovic, and Boris Macek*
- 1979 **Convergence of Ubiquitylation and Phosphorylation Signaling in Rapamycin-treated Yeast Cells**
[S] ⌘ *Vytautas Iesmantavicius, Brian T. Weinert, and Chunaram Choudhary*
- 1993 **Global Analysis of Muscle-specific Kinase Signaling by Quantitative Phosphoproteomics**
[S] *Gerhard Dürnberger, Bahar Z. Camurdanoglu, Matthias Tomschik, Michael Schutzbier, Elisabeth Roitinger, Otto Hudecz, Karl Mechtler, and Ruth Herbst*
- 2004 **Alterations in the Cerebellar (Phospho)Proteome of a Cyclic Guanosine Monophosphate (cGMP)-dependent Protein Kinase Knockout Mouse**
[S] *Eleonora Corradini, Raghavan Vallur, Linsey M. Raaijmakers, Susanne Feil, Robert Feil, Albert J. R. Heck, and Arjen Scholten*

On the cover: This issue features research originating from the pan-European infrastructure for proteomics PRIME-XS. It is an accumulation of technology oriented projects resulting from the joint research initiatives, as well as research from users who were provided access to the infrastructure.

- 2017 **Phosphorylation Dependence and Stoichiometry of the Complex Formed by Tyrosine Hydroxylase and 14-3-3 γ**
 [S] \times *Rune Kleppe, Sara Rosati, Ana Jorge-Finnigan, Sara Alvira, Sadaf Ghorbani, Jan Haavik, José María Valpuesta, Albert J. R. Heck, and Aurora Martinez*
- 2031 **A *Saccharomyces cerevisiae* Model Reveals *In Vivo* Functional Impairment of the Ogden Syndrome N-Terminal Acetyltransferase NAA10 Ser37Pro Mutant**
 [S] *Petra Van Damme, Svein I. Støve, Nina Glomnes, Kris Gevaert, and Thomas Arnesen*
- 2042 **Daily Rhythms in the Cyanobacterium *Synechococcus elongatus* Probed by High-resolution Mass Spectrometry-based Proteomics Reveals a Small Defined Set of Cyclic Proteins**
 [S] *Ana C. L. Guerreiro, Marco Benevento, Robert Lehmann, Bas van Breukelen, Harm Post, Piero Giansanti, A. F. Maarten Altelaar, Ilka M. Axmann, and Albert J. R. Heck*
- 2056 **Conserved Peptide Fragmentation as a Benchmarking Tool for Mass Spectrometers and a Discriminating Feature for Targeted Proteomics**
 [S] \times *Umut H. Toprak, Ludovic C. Gillet, Alessio Maiolica, Pedro Navarro, Alexander Leitner, and Ruedi Aebersold*
- 2072 **Proteomic Analysis of Arginine Methylation Sites in Human Cells Reveals Dynamic Regulation During Transcriptional Arrest**
 [S] *Kathrine B. Sylvestersen, Heiko Horn, Stephanie Jungmichel, Lars J. Jensen, and Michael L. Nielsen*
- 2089 **Phosphoproteome Dynamics in Onset and Maintenance of Oncogene-induced Senescence**
 [S] *Erik L. de Graaf, Joanna Kaplon, Houjiang Zhou, Albert J. R. Heck, Daniel S. Peeper, and A. F. Maarten Altelaar*
- 2101 **Profiling the Secretome and Extracellular Proteome of the Potato Late Blight Pathogen *Phytophthora infestans***
 [S] *Harold J. G. Meijer, Francesco M. Mancuso, Guadalupe Espadas, Michael F. Seidl, Cristina Chiva, Francine Govers, and Eduard Sabidó*
- 2114 **Early Targets of miR-34a in Neuroblastoma**
 [S] *Pasqualino De Antonellis, Marianeve Carotenuto, Jonathan Vandenbussche, Gennaro De Vita, Veronica Ferrucci, Chiara Medaglia, Iolanda Boffa, Alessandra Galiero, Sarah Di Somma, Daniela Magliulo, Nadia Aiese, Alessandro Alonzi, Daniela Spano, Lucia Liguori, Cristina Chiarolla, Antonio Verrico, Johannes H. Schulte, Pieter Mestdagh, Jo Vandesomepele, Kris Gevaert, and Massimo Zollo*
- 2132 **Proteomic Analysis of the Multimeric Nuclear Egress Complex of Human Cytomegalovirus**
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- 2147 **Deciphering Thylakoid Sub-compartments using a Mass Spectrometry-based Approach**
 [S] *Martino Tomizioli, Cosmin Lazar, Sabine Brugière, Thomas Burger, Daniel Salvi, Laurent Gatto, Lucas Moyet, Lisa M. Breckels, Anne-Marie Hesse, Kathryn S. Lilley, Daphné Seigneurin-Berny, Giovanni Finazzi, Norbert Rolland, and Myriam Ferro*

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