

## Special Issue: Prospects in Space and Time

- O112.017731 **Advancing Cell Biology Through Proteomics in Space and Time (PROSPECTS)**  
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*Angus I. Lamond, Mathias Uhlen, Stevan Horning, Alexander Makarov, Carol V. Robinson, Luis Serrano, F. Ulrich Hartl, Wolfgang Baumeister, Anne Katrin Werenskiold, Jens S. Andersen, Ole Vorm, Michal Linial, Ruedi Aebersold, and Matthias Mann*
- O111.013698 **Ultra High Resolution Linear Ion Trap Orbitrap Mass Spectrometer (Orbitrap Elite) Facilitates Top Down LC MS/MS and Versatile Peptide Fragmentation Modes**  
[S] ✂  
*Annette Michalski, Eugen Damoc, Oliver Lange, Eduard Denisov, Dirk Nolting, Mathias Müller, Rosa Viner, Jae Schwartz, Philip Remes, Michael Belford, Jean-Jacques Dunyach, Juergen Cox, Stevan Horning, Matthias Mann, and Alexander Makarov*
- M111.013722 **System-wide Perturbation Analysis with Nearly Complete Coverage of the Yeast Proteome by Single-shot Ultra HPLC Runs on a Bench Top Orbitrap**  
[S] ✂  
*Nagarjuna Nagaraj, Nils Alexander Kulak, Juergen Cox, Nadin Neuhauser, Korbinian Mayr, Ole Hoerning, Ole Vorm, and Matthias Mann*
- M111.013185 **A Framework for Intelligent Data Acquisition and Real-Time Database Searching for Shotgun Proteomics**  
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*Johannes Graumann, Richard A. Scheltema, Yong Zhang, Jürgen Cox, and Matthias Mann*
- M111.013987 **Estimation of Absolute Protein Quantities of Unlabeled Samples by Selected Reaction Monitoring Mass Spectrometry**  
[S] ✂  
*Christina Ludwig, Manfred Claassen, Alexander Schmidt, and Ruedi Aebersold*
- O111.009613 **A Protein Epitope Signature Tag (PrEST) Library Allows SILAC-based Absolute Quantification and Multiplexed Determination of Protein Copy Numbers in Cell Lines**  
[S] ✂  
*Marlis Zeiler, Werner L. Straube, Emma Lundberg, Mathias Uhlen, and Matthias Mann*
- M111.014126 **Expanding the Chemical Cross-Linking Toolbox by the Use of Multiple Proteases and Enrichment by Size Exclusion Chromatography**  
[S] ✂  
*Alexander Leitner, Roland Reischl, Thomas Walzthoeni, Franz Herzog, Stefan Bohn, Friedrich Förster, and Ruedi Aebersold*
- R111.014027 **Joining Forces: Integrating Proteomics and Cross-linking with the Mass Spectrometry of Intact Complexes**  
✂  
*Florian Stengel, Ruedi Aebersold, and Carol V. Robinson*
- M111.014050 **Comparative Proteomic Analysis of Eleven Common Cell Lines Reveals Ubiquitous but Varying Expression of Most Proteins**  
[S] ✂  
*Tamar Geiger, Anja Wehner, Christoph Schaab, Juergen Cox, and Matthias Mann*

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On the cover: The EU-funded PROSPECTS project (PROteomics SPECification in Time and Space) brings together leading European research groups spanning from instrumentation to biomedicine in an initiative to develop novel technology and applications for the functional analysis of proteins. The wide range of approaches taken in this collaboration is illustrated in this composition of experimental results. For details see the articles in this issue.

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- M111.014068 **Analysis of High Accuracy, Quantitative Proteomics Data in the MaxQB Database**  
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*Christoph Schaab, Tamar Geiger, Gabriele Stoehr, Juergen Cox, and Matthias Mann*
- M111.013458 **Antibody-based Protein Profiling of the Human Chromosome 21**  
[S] ☞  
*Mathias Uhlén, Per Oksvold, Cajsa Ålgenäs, Carl Hamsten, Linn Fagerberg, Daniel Klevebring, Emma Lundberg, Jacob Odeberg, Fredrik Pontén, Tadashi Kondo, and Åsa Sivertsson*
- M111.014035 **Identification of Autophagosome-associated Proteins and Regulators by Quantitative Proteomic Analysis and Genetic Screens**  
[S] ☞  
*Jörn Dengjel, Maria Høyer-Hansen, Maria O. Nielsen, Tobias Eisenberg, Lea M. Harder, Søren Schandorff, Thomas Farkas, Thomas Kirkegaard, Andrea C. Becker, Sabrina Schroeder, Katja Vanselow, Emma Lundberg, Mogens M. Nielsen, Anders R. Kristensen, Vyacheslav Akimov, Jakob Bunkenborg, Frank Madeo, Marja Jäättelä, and Jens S. Andersen*
- M111.011429 **A Quantitative Spatial Proteomics Analysis of Proteome Turnover in Human Cells**  
[S] ☞  
*François-Michel Boisvert, Yasmeen Ahmad, Marek Gierliński, Fabien Charrière, Douglas Lamont, Michelle Scott, Geoff Barton, and Angus I. Lamond*
- M111.013680 **Systematic Analysis of Protein Pools, Isoforms, and Modifications Affecting Turnover and Subcellular Localization**  
[S] ☞  
*Yasmeen Ahmad, Francois-Michel Boisvert, Emma Lundberg, Mathias Uhlen, and Angus I. Lamond*
- M111.014654 **Quantitative Proteomics Reveals That Hsp90 Inhibition Preferentially Targets Kinases and the DNA Damage Response**  
[S] ☞  
*Kirti Sharma, R. Martin Vabulas, Boris Macek, Stefan Pinkert, Jürgen Cox, Matthias Mann, and F. Ulrich Hartl*
- M111.014407 **Characterization of MRFAP1 Turnover and Interactions Downstream of the NEDD8 Pathway**  
[S] ☞  
*Mark Larance, Kathryn J. Kirkwood, Dimitris P. Xirodimas, Emma Lundberg, Mathias Uhlen, and Angus I. Lamond*
- M111.013730 **Kinetics in Signal Transduction Pathways Involving Promiscuous Oligomerizing Receptors Can Be Determined by Receptor Specificity: Apoptosis Induction by TRAIL**  
[S] ☞  
*Eva Szegezdi, Almer M. van der Sloot, Devalingam Mahalingam, Lynda O'Leary, Robbert H. Cool, Inés G. Muñoz, Guillermo Montoya, Wim J. Quax, Steven de Jong, Afshin Samali, and Luis Serrano*