

Date: Nov 7, 2008
Location: Max-Planck Institute for Polymer Research, Staudinger Hall
<http://www.mpip-mainz.mpg.de/www/pages/kontakt>

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| 09.00 - 09.15 | Welcome |
| 09.15 - 09.45 | Thomas Fröhlich, Munich Principles of modern mass spectrometry based proteome analysis |
| 09.45 - 10.30 | Keynote Christopher M. Overall, Vancouver Metadegradomics: Quantitative N-Terminome Proteomics of the Cancer Microenvironment. |
| 10.30 - 11.00 | Break |
| 11.00 - 11.30 | Oliver Schilling, Freiburg Proteome-derived peptide libraries for high content proteomic determination of protease cleavage site specificity and subsite cooperativity. |
| 11.30 - 12.00 | Marc Zapatka, Heidelberg Sample classification using mass spectrometry data |
| 12.00 - 12.30 | Franz Grus, Mainz MS based biomarker discovery in ophthalmology |
| 12.30 - 14.00 | Lunch |
| 14.00 - 14.30 | Stefan Tenzer, Mainz Label-free quantitative analysis of CNS-Myelin from wt and PLP-KO mice by LC-MS ^E |
| 14.30 - 15.00 | Lars Kaderali, Heidelberg From Experiment to Networks: Processing of and Network Inference with High Throughput Data |
| 15.00 - 15.30 | Stefan Canzar, Saarbrücken The interval constraint coloring problem |
| 15.30 - 16.00 | Break |
| 16.00 - 16.30 | Holger Herlyn, Mainz The molecular evolution of sperm zonadhesin in the light of sexual selection |
| 16.30 - 17.00 | Ingo Röder, Leipzig Analyses of cellular genealogies |
| 17.00 - 17.30 | Peter Virnau, Mainz Protein knots |
| 17.30 - 18.00 | Business Meeting of the IAK |
| | Speakers Dinner |