Program of the GPF Symposium 2017

Integrative Omics - From Data to Biology

09:00-09:05	**Opening remarks**
	Session 1: Biological networks in health and disease
09:05-09:45	**Bernhard Küster** – Technische Universität München Chemical proteomics reveals the target landscape of clinical kinase inhibitors
09:45-10:25	**Douglas Armstrong** – The University of Edinburgh Network topology analysis reveals substructures within the synaptic proteome that have close association with complex traits
10:25-10:45	**Tim Beißbarth** – Universitätsmedizin Göttingen Integrating paired proteomics and transcriptomics data using upstream and downstream analysis
Coffee break	
	Session 2: Bioinformatic and biostatistic tools
11:15-11:55	**Martin Eisenacher** – Ruhr-Universität Bochum Bioinformatics and biostatistics for mass spectrometry-based proteomics
11:55-12:35	**Jürgen Cox** – Max-Planck-Institut für Biochemie The MaxQuant and Perseus computational platforms for comprehensive analysis of large-scale (prote)omics data
12:35-12:55	**Johannes PC Vissers** – Waters Corporation Peak detecting, de-multiplexing, and searching multidimensional data independent acquisition omics LC-MS data
Lunch break	
	Session 3: Omics approaches in metabolism
13:55-14:35	**Asaph Aharoni** – Weizmann Institute of Science Unravelling solanaceae secondary metabolism through the integration of heterogeneous and spatial data from metabolomics, genetics and informatics
14:35-14:55	**Alexander Karabatsiakis** – Universität Ulm (Agilent-invited speaker) Combined metabolite and lipid fingerprinting in women with childhood maltreatment reveals biomarkers linked to inflammation and oxidative stress
14:55-15:15	**Kirstin Feußner** – Georg-August-Universität Göttingen Metabolomics meets transcriptomics to unravel the wound response in plants
Coffee break	
	Session 4: Multi-omics data integration
15:50-16:30	**Oliver Kohlbacher** – Eberhard Karls Universität Tübingen und Max-Planck-Institut für Entwicklungsbiologie Going multi-omics – Many issues and (perhaps) a few solutions
16:30-16:50	**Philip Stegmaier** – geneXplain Multi-omics "upstream analysis"
16:50-17:10	**Jörg Dojahn** – Sciex Accelerating biological interpretation through the integration of transcriptomics and proteomics results
17:10-17:15	**Closing remarks**