

SYMPOSIUM: Associate Professorship for Computational Biology

Monday, April 18, 2011

**Max Delbrück Communications Center, Axon 2
Robert-Rössle-Str. 10, 13125 Berlin**

- 09:00 Introduction by Nikolaus Rajewsky
- 09:10 Gunnar Rätsch, Friedrich Miescher Laboratory, Tübingen
Computational challenges in RNA-seq-based transcriptome reconstruction
- 09:40 Nils Blüthgen, Charité - Universitätsmedizin Berlin, Berlin
Systems biology approaches to signal transduction and gene regulation
- 10:10 Coffee break
- 10:30 Uwe Ohler, Duke University, Durham
Computational approaches to decode eukaryotic transcription control
- 11:00 Jana Wolf, Max Delbrück Center for Molecular Medicine, Berlin
Mathematical modelling of cellular systems, from metabolism and signalling to gene regulation
- 11:30 Andreas Beyer, Technische Universität, Dresden
Understanding genetic networks controlling complex traits
- 12:00 Lunch break
- 13:00 Wolfgang Huber, European Molecular Biology Laboratory, Heidelberg
Statistical methods for transcriptomics and genetics
- 13:30 Christoph Bock, Broad Institute and Harvard University, Cambridge
Computational epigenetics: Methods, systems, diagnostics