

LUDWIG-MAXIMILIANS-UNIVERSITÄT MÜNCHEN



Computational Biochemistry

Symposium

Thursday, 17 September 2015 Gene Center Munich

13:00	Dr. Ville Mustonen, Sanger Institute, Cambridge (UK)	Using time-resolved genetic data to monitor evolving populations
13:45	Dr. Stefan Legewie, Institute of Molecular Biology, Mainz	Robustness in biochemical reaction networks
	coffee break	
14:45	Dr. Richard Neher, MPI for Developmental Biology, Tübingen	Quantifying and predicting the evolution of RNA viruses
15:30	Prof. Dr. Philip M. Kim, University of Toronto	Integration of structural modeling, machine learning and high-throughput screening
	coffee break	
16:30	Prof. Dr. Rob Russell, University of Heidelberg	The interface between proteomics and genetics: how disease variants can illuminate biological mechanism and vice versa
17:15	Prof. Dr. Thomas Höfer, German Cancer Research Center, Heidelberg	Learning from data with mathematical models: From gene regulation to stem cell dynamics