

PD Dr. Ursula Klingmüller



Boveri Group “Systems Biology of Signal Transduction”

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SCIENTIFIC VITA

- 2006 Full Professor “Quantitative Systems Biology”,
Chalmers University, Gothenburg, Sweden
- 2004 *Venia Legendi* in Cell Biology, University of Heidelberg
- 2003 Group leader of the tenure-track Boveri-group
“Systems Biology of Signal Transduction”, DKFZ Heidelberg
- 2003 C3-Professorship, Technical University of Aachen (declined)
- 2000 Habilitation and *Venia Legendi* in Molecular Biology and Genetics, University of
Freiburg
- 1996 Group leader of an independent junior group (Hans-Spemann-Laboratories)
Max-Planck-Institute for Immunobiology, Freiburg
- 1993 Postdoctoral Fellow, Whitehead Institute for Biomedical Research (Cambridge,
USA) Group of Prof. Dr. Harvey F. Lodish
- 1992 Postdoctoral fellow, Harvard Medical School (Boston, USA) Group of Prof. Dr.
Lewis C. Cantley
- 1992 Graduate studies at the University of Heidelberg
Thesis Center for Molecular Biology Heidelberg (ZMBH)
- 1988 Diploma in molecular biology, cell biology and virology University of
Heidelberg Diploma thesis Center for Molecular Biology Heidelberg (ZMBH)

FIELDS OF INTEREST

Systems biology of signal transduction, dynamic pathway modeling, quantitative data generation in the hematopoietic and hepatocellular system, live cell imaging, quantitative proteomics, signal transduction through cytokine receptors

COORDINATING FUNCTIONS

- 2007-present Co-coordinator of the network “Hepatocyte Regeneration” in the 2. Funding period
of HEPATOSYS funded by the BMBF
- 2007-present Co-coordinator of the network SBCancer of the Helmholtz Association funding
initiative on systems biology
- 2006-present Board of Trustees German Cancer Research Center (DKFZ),
- 2006-present SysMo (Funding Initiative Systems Biology of Microorganisms),
- 2006-present BBSRC funding initiative on Systems Biology
- 2006 Chair of the organization committee of the international conference “Systems
Biology of Mammalian Cells (SBMC)”, 2006, Heidelberg, Germany

2005-present Roche Diagnostics scientific advisory board
2004-present Coordinator of Explorative Project "Near-infrared nanocrystal-based quantitative protein arrays", NGFN2

CURRENTLY FUNDED PROJECTS

Explorative Project "Near-infrared nanocrystal-based quantitative protein arrays", NGFN2; EU-STREP "COSBICS"; Projects B1, B5, B6 and C2 within the 2. Funding period of HEPATOSYS funded by the BMBF; Projects DKFZ.1.2 and DKFZ.2.1 in the network SBCancer of the Helmholtz Association funding initiative on systems biology; Project A.3.1 in the network VIROQUANT funded by the BMBF within ForSys,

PUBLICATIONS (10 most important publications):

U. Klingmüller, A. Bauer, S. Bohl, P. J. Nickel, K. Breitkopf, S. Dooley, S. Zellmer, C. Kern, I. Merfort, T. Sparna, J. Donauer, G. Walz, M. Geyerr, C. Kreutz, M. Hermes, F. Götschel, A. Hecht, D. Walter, L. Egger, K. Neubert, C. Borner, M. Brulport, W. Schormann, C. Sauer, F. Baumann, R. Preiss, S. MacNelly, P. Godoy, E. Wiercinska, L. Ciuclan, P. Illes, K. Zeilinger, M. Heinrich, U. M. Zanger, M. Reuss, A. Bader, R. Gebhardt, T. Maiwald, J. Timmer, F. von Weizsäcker, and J. G. Hengstler. Primary mouse hepatocytes for systems biology approaches: a standardized *in vitro* system for modeling of signal transduction pathways. IEE Proc. Systems Biology (2006), 153:444-447.

M. Schilling, T. Maiwald, S. Bohl, M. Kollmann, C. Kreutz, J. Timmer, and **U. Klingmüller**. Quantitative data generation for systems biology – the impact of randomisation, calibrators and normalisers. IEE Proc. Systems Biology (2005), 152:193-200.

M. Schilling, T. Maiwald, S. Bohl, M. Kollmann, C. Kreutz, J. Timmer, and **U. Klingmüller**. Computational processing and error reduction strategies for standardized quantitative data in biological networks. FEBS Journal (2005) 272:6400-6411.

A. C. Heinrich, R. Pelanda, and **U. Klingmüller**. A mouse model for visualization and targeted mutations in the erythroid lineage. Blood. (2004) 104(3):659-66.

I. Swameye, T. G. Müller, J. Timmer, O. Sandra, and **U. Klingmüller**. Identification of nucleocytoplasmic cycling as a remote sensor in cellular signaling by data-based dynamic modeling. PNAS (2003) 100:1028-33.

R. Ketteler, A. C. Heinrich, J. K. Offe, V. Becker, J. Cohen, D. Neumann, and **U. Klingmüller**. A functional GFP-tagged erythropoietin receptor despite separation of JAK2 binding sites and tyrosine residues. J. Biol. Chem. (2002) 277:26547-26552.

R. Ketteler, C. Moghraby, J. G. Hsiao, O. Sandra, H. F. Lodish, and **U. Klingmüller**. The cytokine-inducible SH2 domain containing protein CIS negatively regulates signaling by promoting apoptosis in erythroid progenitor cells. J. Biol. Chem. (2003) 278:2654-60.

K. F. Kubatzky, W. Ruan, R. Gurezka, J. Cohen, R. Ketteler, S. S. Watowich, D. Neumann, D. Langosch, **U. Klingmüller**. Self-assembly of the transmembrane domain promotes signal transduction through the erythropoietin receptor. Current Biology (2001) 11:110-115.

H. Wu, **U. Klingmüller**, and H. F. Lodish. Interaction of the erythropoietin and stem-cell-factor receptors. Nature (1995) 377: 242-246.

U. Klingmüller, U. Lorenz, L. C. Cantley, B. G. Neel, and H. F. Lodish. Specific recruitment of SH-PTP1 to the erythropoietin receptor causes inactivation of JAK2 and termination of proliferative signals. Cell (1995) 80:729-738.