Prof. Dr. Ursula Klingmüller



Head of Division – Systems Biology of Signal Transduction
– German Cancer Research Center (DKFZ) Heidelberg

SMART-NAFLD Coordinator

Role in LiSyM-Cancer

- Coordinator and project leader in SMART-NAFLD
- Examining signal transduction and metabolism crosstalk and its relation to plasma markers for liver cancer progression
- Project leader in C-TIP-HCC
- Emphasizing dynamic pathway modeling of TGFb signal transduction and ECM remodeling in cirrhosis context
- Interview with Ursula Klingmüller (BMFTR in german)

Expertise

- Combines quantitative analysis with mathematical modeling to understand key regulatory mechanisms in information processing and cell fate decisions.
- Focuses on signaling pathways in liver regeneration and liver cancer.
- Advances mass spectrometry-based proteomics for systems medicine, emphasizing absolute quantification of signal transduction proteins and plasma proteins quantification.

Degrees

- 2004, Venia Legendi in Cell Biology, Heidelberg University
- 2000, Habilitation and Venia Legendi in Molecular Biology and Genetics, University of Freiburg
- 1992, Graduate Studies at Heidelberg University, Doctoral Thesis in Molecular Virology
- 1988, Diploma in Molecular Biology, Cell Biology and Virology, Heidelberg University
- 1985, Bachelor of Science, University of Bayreuth

Professional Experience

- Since 2011, W3 Professor, Heidelberg University, Germany
- 2003 – 2007, Group Leader of the Theodor-Boveri-Group "Systems Biology and Signal Transduction", DKFZ, Heidelberg
- 1996 – 2003, Group Leader of an Independent Junior Group (Hans-Spemann-Laboratories), Max-Planck-Institute of Immunobiology, Freiburg, Germany
- 1993 – 1996, Postdoctoral fellow, Whitehead Institute for Biomedical Research, Cambridge, USA
- 1992 – 1993, Postdoctoral fellow, Harvard Medical School, Boston, USA

Honors and Awards (selection)

- Since 2020, Elected EMBO Member
- 2020 – 2024, Re-election as Member of the German Ethics Council
- 2016 – 2020, Election as Member of the German Ethics Council
- 2012 – 2017, Election as Member of the DFG "Hinterzartener Kreis of Cancer Research"

Publications

2026-07-07	msBayesImpute as a versatile framework for addressing missing values in biomedical mass spectrometry proteomics data *Communications Chemistry*
2026-06-10	Transient suppression of the ECM1 gatekeeper is essential for HGF/c-MET-driven liver regeneration
2025-11-01	Diclofenac and acetaminophen dim the acute-phase response but amplify expression of the iron regulator hepcidin in liver cancer cells *Cell Systems*
2025-10-02	Multicenter evaluation of label-free quantification in human plasma on a high dynamic range benchmark set *Nature Communications*
2025-08-20	SputOMICs identifies common and distinct markers in cystic fibrosis and chronic obstructive pulmonary disease
2025-06-26	Integrin beta 1 facilitates non-enveloped hepatitis E virus cell entry through the recycling endosome *Nature Communications*
2024-08-08	ProDOL: a general method to determine the degree of labeling for staining optimization and molecular counting *Nature Methods*
2024-02-21	Lysis buffer selection guidance for mass spectrometry-based global proteomics including studies on the intersection of signal transduction and metabolism (preprint) *bioRxiv*
2024-01-12	Basal MET phosphorylation is an indicator of hepatocyte dysregulation in liver disease *Molecular Systems Biology*
2023-12-01	Tumour cells can escape antiproliferative pressure by interferon-β through immunoediting of interferon receptor expression *Cancer Cell International*
2023-07-01	Tolerance of repeated toxic injuries of murine livers is associated with steatosis and inflammation *Cell Death & Disease*
2023-01-01	Repeated toxic injuries of murine liver are tolerated through minute steatosis and mild inflammation *39. Jahrestagung der Deutschen Arbeitsgemeinschaft zum Studium der Leber*
2023-01-01	Hepatocytes reprogram liver macrophages involving control of TGF-β activation, influencing liver regeneration and injury *Hepatology Communications*
2022-09-20	Erythropoietin-driven dynamic proteome adaptations during erythropoiesis prevent iron overload in the developing embryo. *Cell Rep*
2022-06-30	Deciphering signal transduction networks in the liver by mechanistic mathematical modelling *Biochemical Journal*
2022-01-01	MSPypeline: a python package for streamlined data analysis of mass spectrometry-based proteomics *Bioinformatics Advances*