Stefan Wiemann

PhD at the University of Kaiserslautern (1990)
Postdoctoral work at the DKFZ and EMBL (1990-1995)
Group Leader at DKFZ (1995-2008)
Habilitation Faculty of Biosciences University Heidelberg (2003)
Head of the Division of Molecular Genome Analysis at the DKFZ (since 2008)
Head of the Genomics and Proteomics Core Facility at the DKFZ (since 2011)

Current Research

The central objective of our division is to understand the complex molecular mechanisms that have evolved in the regulation of signaling networks and how these impact on cancer development, metastasis, and drug resistance. To this end, we generate and maintain resources for large-scale experimentation, apply high-throughput functional genomics and proteomics technologies, and analyze candidate genes using *in vitro* as well as *in vivo* systems. Effects of perturbations (gene gain- and loss-of-function, miRNA, drugs) imposed on the signaling processes are experimentally tested and then computationally modeled. This generates mechanistic knowledge that is exploited to identify new diagnostic and prognostic markers as well as to develop novel strategies for therapeutic intervention. Along these lines our major focus is on breast cancer, where we investigate protein and non-protein factors that are involved in the progression of different subtypes via their activities in interrelated signaling networks

Future Projects and Goals

We have already seen from our current data that signaling is not regulated in isolated pathways but rather in complex networks. Therefore, in the future we will investigate the impact individual perturbations have in a variety of cellular pathways and at different levels (DNA, RNA, protein, metabolite, …, phenotype). This should provide us with a better understanding of the connectivity in multi-layer interaction systems.

Such information will be inevitable, for example, to identify strategies that should help to overcome drug resistance

While much of our current knowledge is based on in vitro experiments we need to validate findings in vivo in order to prove their relevance. To this end, we will generate and test animal models and challenge our hypotheses with patient samples. Collaborations to this end have been established.

Selected Publications

Uhlmann S, Mannsperger H, Zhang JD, Horvat E-A, Schmidt C, Küblbeck M, Henjes F, Ward A, Tschulena U, Zweig K, Korf U, Wiemann S, Sahin O (2012) Global microRNA level regulation of EGFR-driven cell cycle protein network in breast cancer. *Mol Syst Biol* 8: 570.

Keklikoglou I*, Koerner C, Schmidt C, Zhang JD, Heckmann D, Shavinskaya A, Allgayer H, Guckel B, Fehm T, Schneeweiss A, Sahin O, Wiemann S*, Tschulena U (2011) MicroRNA-520/373 family functions as a tumor suppressor in estrogen receptor negative breast cancer by targeting NF-kappaB and TGF-beta signaling pathways. *Oncogene*. epub

Temple G, Gerhard DS, Rasooly R, Feingold EA, Good PJ, Robinson C, Mandich A, Derge JG, Lewis J, Shoaf D et al (2009) The Completion of the Mammalian Gene Collection (MGC). *Genome Res* 19:2324-2333.

Sahin O, Löbke C, Korf U, Appelhans H, Sultmann H, Poustka A, Wiemann S, Arlt D (2007) Combinatorial RNAi strategy: The next generation of quantitative protein network analysis. *Proc Natl Acad Sci USA* 104(16):6579-6584.

Simpson JC, Wellenreuther R, Poustka A, Pepperkok R, Wiemann S (2000) Systematic subcellular localization of novel proteins identified by large scale cDNA sequencing. *EMBO Rep* 1: 287-292.

Contact

PD Dr. Stefan Wiemann
Division of Molecular Genome Analysis
Genomics and Proteomics Core Facility
Im Neuenheimer Feld 580
69120 Heidelberg
Germany

Tel: +49 - 6221 - 42 47 02 / 47 00
Fax: +49 - 6221 - 42 34 54
email: s.wiemann@dkfz.de

home page Molecular Genome Analysis:
http://www.dkfz.de/en/mga/