Ulrich Stelzl

Key Researcher

Institute of Pharmaceutical Sciences, University of Graz, Austria

ORCID ID: http://orcid.org/0000-0003-2500-3585

SCIENTIFIC & ACADEMIC CAREER

since 04/2018 Department Head, Pharmaceutical Chemistry, University of Graz, Austria

04/20-03/22   Head, Institute of Pharmaceutical Sciences, University of Graz, Austria

since 04/2016 Faculty, BioTechMed-Graz, Austria

since 09/2015 Professor at the Institute of Pharmaceutical Sciences, Department of Pharmaceutical Chemistry, University of Graz

2007-2015   Max-Planck Research Group Leader (W2 position) at the Max-Planck Institute for Molecular Genetics (MPIMG), Berlin, Germany
            Head of the Otto Warburg Laboratory "Molecular Interaction Networks"

2002 – 2007   Postdoctoral fellow / NGFN project leader in the AG Neuroproteomics headed by Erich Wanker, Max-Delbrück Center for Molecular Medicine (MDC), Berlin-Buch, Germany

2001 – 2002   Research Fellow in the Laboratory of Dinshaw Patel at the Memorial Sloan Kettering Cancer Center (MSKCC), New York, USA

2000   Postdoctoral fellow in the AG Ribosomen, MPIMG, Berlin

1996 – 1999   Ph.D. thesis at the Max-Planck Institute Molecular Genetics, Berlin, Germany in the AG Ribosomen under the supervision of Knud Nierhaus: "In vitro selection of RNA-binding sites of proteins from random RNA fragments".
            Academic degree Dr. rer. nat., Dec. 1999, University of Vienna

1994 – 1995   Studies of Biochemistry at the ETH Zurich, Switzerland

            Diploma Thesis under the supervision of Andrea Vasella at the ETH Zurich, Laboratory for Organic Chemistry: "A new approach to Alkyne-C-Glycopyranosides"

1990 – 1996   Studies of Technical Chemistry / Biochemistry at the TU Vienna
            Graduated with honors, April 1996 at the TU Vienna

MAIN AREA OF RESEARCH

The group is focusing on the analysis of molecular interaction networks with the aim to understand the dynamics of molecular networks underlying cellular processes related to human disease. Experimental functional genomics techniques, e.g. HTP Y2H screening and mass spectrometry, are utilized in combination with biochemical, cell biological and computational methods. The current focus of our work is on the systematic analyses of the functional impact of genetic variation (population and disease variation e.g. in cancer genomes) and post-translational protein modification (phosphorylation, methylation) on protein-protein interaction, which as universal protein function underlies cellular phenotypes. Using deep scanning mutagenesis approaches, we bridge the knowledge gap between

nucleotide resolution genomics and protein resolution proteomics. Network biology offers a more comprehensive understanding of biology concomitantly improving the practice of medicine.

In the course of the MetAGE project, Ulrich Stelzl will investigate the crosstalk of lipid- and spermine metabolism to other cellular process through assessing proteome wide alterations in models of ageing. Through combined genetic (ko-strategies) and environmental / drug perturbation / aging intervention, quantitative proteomics/phospho-proteomics will help elucidating mechanistic links of aging processes in particular to autophagy, ribosome biogenesis and lipid metabolism. In collaboration with MetAGE aeras polyamines, proteostasis and the data science platform, this systems biology approach will specifically elucidate the role of kinase activities for aging processes.

ADDITIONAL RESEARCH ACTIVITIES

Peer review for more than 60 Journals incl. Nature, Science, Nat Genet, Nat Biotechnol, Nat Methods, Mol Cancer, Cell Res, Mol Cell, Nucleic Acids Res, Nat Commun, Microbiome, Genome Biol, Nat Protoc, Mol Syst Biol, Cell Syst, Genome Res, Sci Signal, elife, Drug Discov Today, Bioinformatics, Protein Sci, J Mol Biol, PLoS Comput Biol, J Proteome Res, EMBO J, PLoS Genet, Review Commons

Peer review for grant agencies / sci. societies incl. BBSRC (UK), NFRF (CA), ANEP (ES), ANR (FR), MRC (UK), GIF (IL/DE), BSF (IL), RGC (Hong Kong), NRF (South Korea), MPG (MPRGL and Minerva Center, DE), USA Universities, Slovak Academy of Sciences, Leibnitz Gemeinschaft(DE)

Associate Editor BMC Bioinformatics (05/10-02/22), Academic Editor Microbial Cell (since 07/16).

Special Section Organizer/Chair at ISMB 2013, program committee member of ISMB 2015, ISMB 2016 and ISMB2017

Session organizer and chair of the 16th ÖGMBT Annual Meeting, Sept 17-19, 2024, Graz, AT

Selected Presentations from >90

Research seminar at Department of Chemistry - Biochemistry and Molecular Biology; May 6, 2024; University of Hamburg, DE

CMBI lecture Series; 15th Jan 2024; Center for Molecular Biosciences, Innsbruck

Research seminar at Dep. of Chemistry - BMC, Biochemistry, Uppsala University; Sept 21, 2023, SE

15th Annual Meeting of the Austrian Association of Molecular Life Sciences and Biotechnology (OeGMBT); September 19-21, 2023; Faculty of Natural Sciences, University of Salzburg

NetSci23, International School and Conference on Network Science; 10-14 July 2023; Vienna, Austria

CSH Network Biology 2023; Mar 14 - Mar 18 2023; Cold Spring Harbor Laboratory, New York, USA;

Honors & Awards

2008   Erwin Schrödinger Preis of the HGF (50 TEuro price money, shared)
                 http://www.helmholtz.de/ueber_uns/forschungspreise/erwin_schroedinger_preis/

10 MOST IMPORTANT PUBLICATIONS

Kohlmayr JM, Grabner GF, Nusser A, Höll A, Manojlović V, Halwachs B, Masser S, Jany-Luig E, Engelke E, Zimmermann R, **Stelzl U** (2024); Mutational scanning pinpoints distinct binding sites of key ATGL regulators in lipolysis; *Nat Commun 15*, 2516; doi: 10.1038/s41467-024-46937-x [OA]

Moesslacher CS, Auernig E, Woodsmith J, Feichtner A, Jany-Luig E, Jehle S, Worseck JM, Heine CL, Stefan E, **Stelzl U** (2023); Missense variant interaction scanning reveals a critical role of the FERM domain for tumor suppressor protein NF2 conformation and function; *Life Sci Alliance 6*: 202302043; doi: 10.26508/lsa.202302043 [OA]

Jehle S, Kunowska N, Benlasfer N, Woodsmith J, Weber G, Wahl MC, **Stelzl U** (2022); A human kinase yeast array for the identification of kinases modulating phosphorylation-dependent protein-protein interactions; *Mol Syst Biol 18*, e10820; doi: 10.15252/msb.202110820 [OA]

Woodsmith J, Casado-Medrano V, Benlasfer N, Eccles RL, Hutten S, Heine CL, Thormann V, Abou-Ajram C, Rocks O, Dormann D, **Stelzl U** (2018). Interaction modulation through arrays of clustered methyl-arginine protein modifications. *Life Sci Alliance 1*, e201800178; doi: 10.26508/lsa.201800178 [OA]

Woodsmith J, Apelt L, Casado-Medrano V, Özkan Z, Timmermann B, **Stelzl U** (2017). Protein interaction perturbation profiling at amino acid resolution. *Nat Methods 14*, 1548-7091; doi: 10.1038/nmeth.4464 [free at pure.mpg.de]

Corwin T, Woodsmith J, Apelt F, Fontaine JF, Meierhofer D, Helmuth J, Grossmann A, Andrade-Navarro MA, Ballif BA, **Stelzl U** (2017). Defining Human Tyrosine Kinase Phosphorylation Networks Using Yeast as an In Vivo Model Substrate. *Cell Syst 5*, 128-139; doi: 10.1016/j.cels.2017.08.001 [Free via Cell Press]

Grossmann A, Benlasfer N, Birth P, Hegele A, Wachsmuth F, Apelt L, **Stelzl U** (2015). Phospho-tyrosine dependent protein-protein interaction network. *Mol Syst Biol 11*, 794; doi: 10.15252/msb.20145968 [OA]

Weimann M, Grossmann A, Woodsmith J, Özkan Z, Birth P, Meierhofer D, Benlasfer N, Valovka T, Timmermann B, Wanker EE, Sauer S, **Stelzl U** (2013). A Y2H-seq approach defines the human protein methyltransferase interactome, *Nat Methods 10*, 339-342; doi: 10.1038/nmeth.2397 [free at pure.mpg.de]

Hegele A, Kamburov A, Grossmann A, Sourlis C, Wowro S, Weimann M, Will CL, Pena V, Lührmann R, **Stelzl U** (2012). Dynamic protein-protein interaction wiring of the human spliceosome, *Mol Cell 45*, 567-580; doi: 10.1016/j.molcel.2011.12.034 [Free via Cell Press]

Stelzl U, Worm U, Lalowski M, Haenig C, Brembeck FH, Goehler H, Stroedicke M, Zenkner M, Schoenherr A, Koeppen S, Timm J, Mintzlaff S, Abraham C, Bock N, Kietzmann S, Goedde A, Toksöz E, Droege A, Krobitsch S, Korn B, Birchmeier W, Lehrach H, Wanker EE (2005). A Human Protein-Protein Interaction Network: A Resource for Annotating the Proteome. *Cell 122*, 957-968; doi: 10.1016/j.cell.2005.08.029 [Free via Cell Press]