ERICH E. WANKER

Max Delbrueck Center for Molecular Medicine in the Helmholtz Association (MDC), Department of Neuroproteomics.

Positions and Employment

1991 Visiting Researcher, Department of Microbiology, TNO Medical Biological Laboratory, Rijswijk, The Netherlands

1993-1995 Postdoctoral Fellow at Department of Biochemistry, University of California, Los Angeles, USA

1995-1999 Group Leader, Max-Planck-Institute for Molecular Genetics, Berlin, Germany

1999-2001 Independent Group Leader (C3) at Max-Planck-Institute for Molecular Genetics, Berlin, Germany

2001-present Full Professorship of Molecular Medicine at Charité Berlin (C4) and Head of the Group Proteomics and Molecular Mechanisms of Neurodegenerative Diseases at the Max Delbrück Center for Molecular Medicine in the Helmholtz Association, Berlin, Germany

Other Experience and Professional Memberships

1998-2011 Investigator, Huntington's Disease Society of America (HDSA)

2001-2004 Coordinator, Core Area Platform Protein Interactions, National Genome Research Network (NGFN-1)

2001-2006 Coordinator, Research Unit SCA3, German Research Foundation (DFG)

2001-2009 Board Member, Collaborative Research Centre 577

2004 Member, Review Panel German Research Foundation

2004-2008 Coordinator, Systematic Methodological Platform Protein, National Genome Research Network (NGFN-2)

2004-2008 Project Committee Member, National Genome Research Network (NGFN-2)

2006 Head Conference Organizing Committee, "Neurodegenerative Diseases: Molecular Mechanisms in a Functional Genomics Framework", Berlin, Germany

2008-2011 Coordinator, Consortium NeuroNet, National Genome Research Network (NGFN-Plus)

2007-2012 Coordinator, MDC Systems Biology Network & Technology Platform, Helmholtz Alliance on Systems Biology

2008-2012 Deputy Coordinator, Helmholtz Alliances on Systems Biology

2010 Member Scientific Advisory Board SYSCILIA, “A systems biology approach to dissect cilia function and its disruption in human genetic disease”, EU Consortium, FP 7

2010 International Evaluation Committee Member Japanese Ministry of Education, Culture, Sports, Science and Technology

2010 Head Organizing Committee, “PPI Berlin: Current Trends in Network Biology”

2015 Vice-Chair Gordon Research Conference on CAG Triplet Disorders

Editorial boards: Amyloid, Journal of Neurodegenerative Diseases, Prion, Journal of Biological Chemistry

Honors

1993 Erwin Schrödinger Fellowship, Austrian Science Fund, Austria

1998 BioFuture-Research Award, German Ministry of Education and Research (BMBF), Germany

2000 James Heinemann-Research Award, Minna-James-Heineman-Foundation, Germany

2006 GoBio Research Award, German Ministry of Education and Research (BMBF), Germany

2008 Erwin-Schrödinger Award, Helmholtz Association (HGF), Germany 2

B. Selected Peer-reviewed publications

Stroedicke, M., Bounab, Y., Strempel, N., Klockmeier, K., Yigit, S., Friedrich, R.P., Chaurasia, G., Li, S., Hesse, F., Riechers, S.-P.,Russ, J., Nicoletti, C., Boeddrich, A., Wiglenda, T., Haenig, C., Schnoegl, S., Bates, G., Priller, J., Andrade-Navarro, M., Futschik, M.,Wanker, E.E. (2015). Systematic interaction network filtering identifies CRMP1 as a novel suppressor of huntingtin misfolding and neurotoxicity. Genome Research 25(5):701-713.

Weimann, M., Grossmann, A., Woodsmith, J., Özkan, Z., Birth, P., Meierhofer, D., Benlasfer, N., Valovka, T., Timmermann, B.,Wanker, E.E., Sauer, S. and Stelzl, U. (2013). A Y2H-seq approach to define the human protein methyltransferase interactome. Nat Methods 10(4):339-342.

Petrakis, S., Rasko, T., Russ, J., Friedrich, R.P., Stroedicke, M., Riechers, S.P., Muehlenberg, K., Moeller, A., Reinhardt, A.,Vinayagam, A., Schaefer, M.H., Boutros, M., Tricoire, H., Andrade-Navarro, M.A., Wanker, E.E. (2012). Identification of human proteins that modify misfolding and proteotoxicity of pathogenic ataxin-1. PLoS Genetics 8(8):e1002897.

Bieschke, J., Herbst, M., Wiglenda, T., Friedrich, R.P., Boeddrich, A., Schiele, F., Kleckers, D., Lopez del Amo, J.M., Gruning, B.A.,Wang, Q., Schmidt, M.R., Lurz, R., Anwyl, R., Schnoegl, S., Fändrich, M., Frank, R.F., Reif, B., Günther, S., Walsh, D.M., Wanker, E.E. (2011). Small-molecule conversion of toxic oligomers to nontoxic beta-sheet-rich amyloid fibrils. Nat Chem Biol 8:93-101.

Goehler, H., Droege, A., Lurz, R., Schnoegl, S., Chernoff, Y. and Wanker, E. E. (2010). Pathogenic polyglutamine tracts are potent inducers of spontaneous Sup35 and Rnq1 amyloidogeneses. PLoS ONE 5(3):e9642.

Venkatesan, K., Rual, .J.-F. Vazquez, A., Stelzl, U., Lemmens, I., Hirozane-Kishikawa, T., Hao, T., Zenkner, M., Xin, X., Goh, K.-I.,Yildirim, M.A., Simonis, N., Heinzmann, K., Gebreab, F., Sahalie, J.M., Cevik, S., Simon, C., de Smet, A.-S., Dann, E., Smolyar, A.,Vinayagam, A., Yu, H., Szeto, D., Borick. H., Dricot, A., Klitgord, N.,Murray, R.R., Lin, C., Lalowski, M., Timm, J., Rau, K., Boone, C.,Braun, P., Cusick, M.E., Roth, F.P., Hill, D.E., Tavernier, J., Wanker, E.E., Barabási, A.-L., Vidal, M. (2009). An empirical framework for binary interactome mapping. Nat Methods 6(1):83-90.

Ehrnhoefer, D.E., Bieschke, J., Boeddrich, A., Herbst, M., Masino, L., Lurz, R., Engemann, S., Pastore, A., Wanker, E.E. (2008).EGCC redirects amyloidogenic polypeptides into unstructured, off-pathway oligomers. Nat Struct Mol Biol 15 (6):558-66.

Boeddrich, A., Gaumer, S., Haacke, A., Tzvetkov, N., Albrecht, M., Evert, B.O., Müller, E.C., Lurz, R., Breuer, P., Schugardt, N., Plaßmann, S., Xu, K., Warrick, J.M., Suopanki, J., Wüllner, U., Frank, R., Hartl, U.F., Bonini, N.M., and Wanker, E.E. (2006). An arginine/lysine-rich motif is crucial for VCP/p97-mediated modulation of ataxin-3 fibrillogenesis. EMBO J. 25(7):1547-1558.

Stelzl, U., Worm, U., Lalowski, M., Haenig, C., Brembeck, F.H., 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., and Wanker, E.E. (2005). A human protein-protein interaction network: a resource for annotating the proteome. Cell 122:957-968.

Goehler, H., Lalowski, M., Stelzl, U., Waelter, S., Stroedicke, M., Worm, U., Droege, A., Lindenberg, K.S., Knoblich, M., Haenig, C.,Herbst, M., Suopanki, J., Scherzinger, E., Abraham, C., Bauer, B., Hasenbank, R., Fritzsche, A., Ludewig, A.H., Bussow, K.,Coleman, S.H., Gutekunst, C.A., Landwehrmeyer, B.G., Lehrach, H., Wanker, E.E. (2004). A protein interaction network links GIT1, an enhancer of huntingtin aggregation, to Huntington's disease. Mol Cell 15:853-865.

C. Research Support (Active)

2012-2015 BMBF, GERAMY, German Consortium for Systemic Light Chain Amyloidosis.

2013-2016 ERA-Net NEURON, ABETA ID - „Preparation of amyloid-beta aggregate species from patient-derived material to define disease-causing mechanisms“

2014-2015 HDSA, „Development of a novel Htt aggregation assay as diagnostic tool for Huntington’s disease“

2014-2016 BMBF, eMed – IntegraMent: “Integrated, systems-based approach for pathway analysis in psychiatric disease”, sub project: “Networks of protein-protein interactions and cell malfunctioning in schizophrenia”

2014-2018 BIH Collaborating Research Grant: “Elucidating the proteostasis network to control Alzheimer’s disease“

2015-2016 Helmholtz-Israel Program: „Network based identification of personalized targets for Huntington’s disease“

2015-2018 DFG, Collaborative Research Centre 740, B01: „Functional and Structural Characterization of Heterotetrameric p97/ASPL complexes”