

HALO [Halle (pertaining to salt); basis for development of Central Germany's chemical industry]

[membrane] mem

Since its inception in 2006, the *Zentrum für Innovationskompetenz* (ZIK) HALOmem has served as a nucleus for biophysical analyses of reconstituted integral membrane proteins, consolidating and expanding the strong protein biochemical focus in Halle.

Membrane proteins represent almost a quarter of all proteins within living cells (the 'proteome'). They direct and regulate a wide range of essential functions, being responsible *inter alia* for communication of information between cells, transport of nutrients and generation of energy. Their vital nature is reflected by the fact that up to 70% of current drug targets are membrane proteins.

One of our major goals has been the dovetailing of membrane protein biochemistry and membrane biophysics. This was realised in 2009, with the establishment of two junior groups led by Dr. Mikio Tanabe and Jun. Prof. Dr. Kirsten Bacia.

We invite you to join us in celebrating 5 years of membrane protein research!

Prof. Dr. Milton T. Stubbs
Director, BMBF ZIK HALOmem

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Sachsen-Anhalt



Europäische Kommission
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für regionale Entwicklung
INVESTITION IN IHRE ZUKUNFT



HALOmem

membrane
protein structure
& dynamics

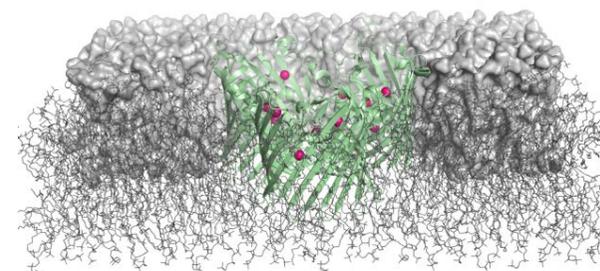
*Invitation to a celebration of 5 years
membrane protein research in*

ZIK HALOmem

DORMERO Hotel Rotes Ross
Leipziger Straße 76 · 06108 Halle

Thursday September 11th 2014

ZENTREN FÜR
INNOVATIONSKOMPETENZ
UNTERNEHMEN
Die BMBF-Innovationsinitiative
Neue Länder **REGION**



introducing ZIK HALOmem...

X-ray crystallography

The group of Dr. Stubbs possesses state-of-the-art X-ray facilities for the structural characterization of proteins and their macromolecular complexes.

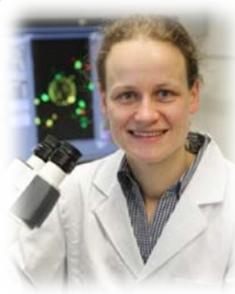
Dr. Stubbs's research interests lie in the structural biology of proteins of therapeutic relevance, with a particular focus on macromolecular conformational transitions. Target protein flexibility and its influence on ligand affinity represents a particular challenge to structure based drug design. Model systems have been established that allow dissection of the complex contributions of such conformational variability to structural, dynamic and thermodynamic properties.



Membrane biophysics

Research in the lab of Dr. Bacia is aimed at understanding the structure and function of the cellular machinery that sorts and packages proteins into membrane-enclosed vesicles for transport between intracellular compartments.

The group uses a combination of biochemical and biophysical methods for the difficult task of reconstituting and characterizing the interplay between membrane proteins and lipid bilayers outside the living cell. State-of-the art equipment introducing a fluorescence correlation spectroscopy (FCS) setup is used to study the physico-chemical properties of protein and lipid assemblies in native biological membranes and artificial membrane mimetics.



High field NMR spectroscopy

Dr. Balbach's research interests are NMR spectroscopy, structural biology of proteins, function and dynamics of proteins, biophysical methods to study protein folding. NMR

spectroscopy allows determination of the structure of proteins and protein complexes in solution at atomic resolution.

NMR relaxation provides insights into the dynamics of proteins, which are correlated with the protein function. Time-resolved NMR allows study of protein folding reactions at a residue-by-residue resolution.



Membrane protein biochemistry

Dr. Tanabe's research goal is to understand the actions of outer membrane porins and multidrug resistance transporters of pathogenic bacteria from a structural perspective. Membrane protein crystallography is especially challenging due to the difficulties of obtaining sufficient amounts of stable proteins for structural studies. The refolding of β -barrel proteins and a green-fluorescence-protein (GFP) conjugated α -helical membrane protein expression system have been established for the rapid screening of stable proteins for structural studies, supported by a multitude of protein stability assays. The group also utilizes the methods of lipidic cubic phase (LCP) and bicelle crystallization to facilitate production of suitably diffracting membrane protein crystals.

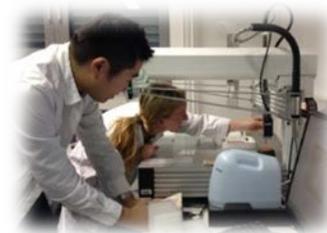


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Celebrating 5 years of membrane protein research in ZIK HALOmem

DORMERO Hotel Rotes Ross · Leipziger Straße 76 · 06108 Halle
Thursday 11th September 2014

by invitation only
R.S.V.P.

Programme

8.30 Arrival and registration

9.00 Welcoming remarks

9.15: **ZIK HALOmem: Past, present and ... future**
Milton T. Stubbs, Director ZIK HALOmem

Session I: The membrane protein challenge

9.30: **The many and varied uses of the lipid cubic phase in membrane structural and functional biology research**
Martin Caffrey, Trinity College Dublin (IE)

10.15: **Structural biology of human membrane proteins at the SGC: from ABC to ZMP**
Liz Carpenter, Structural Genomics Consortium, Oxford (UK)

11.00: Break

Session II: ZIK HALOmem, the first 5 years

11.30: **Membrane protein biochemistry**
Mikio Tanabe, ZIK HALOmem

12.30: Lunch break and poster presentations

14.30: **Membrane biophysics**
Kirsten Bacia, ZIK HALOmem

15.30: Break

Session III: Into the future?

16.00: **Structure and function of ion channels studied by native MS and ion mobility**
Frank Sobott, Universiteit Antwerpen (B)

16.45: **What X-rays cannot do: single-particle imaging, molecular tomography and the resolution revolution in cryo-EM**
Werner Kühlbrandt, Max-Planck Institut für Biophysik, Frankfurt (DE)

17.30: Poster presentations

20.00: Dinner, Round Table Discussion