Repeat proteins are, next to antibodies, the most widely used class of specific binding proteins in nature. By analyzing their architecture, consensus structures have been built where only the potentially interacting residues are randomized (1,2). Designed Ankyrin Repeat Proteins (DARPins) have been selected and evolved by ribosome display and phage display to bind to a wide variety of targets with picomolar affinity, and a number of structures of such complexes have been determined. DARPins are very highly expressed, and full consensus proteins are extraordinarily stable (3). We have used such DARPins for applications in cell biology, tumor targeting (4) and crystallography (2,5). More recently, Armadillo Repeat Proteins have been designed for binding to peptides or extended regions from proteins, with a view of generating a completely modular set of building blocks for peptide sequence recognition (6). Finally, methods of directed evolution can also be used to help uncover the structures and mechanisms of membrane proteins (7). Progress in the evolution of GPCRs for high stability will be discussed, with a view on uncovering the rules.
References


Universitätshauptgebäude, Hörsaal 3, Donnerstag, den 3. Februar 2011 um 17 Uhr c.t

gez. Prof. Dr. Thomas Koop, Prof. Dr. Jochen Mattay, Prof. Norbert Sewald