The giant muscle protein titin extends over one half of the muscle sarcomere. In its largest isoform titin comprises more than 38,000 residues and about 300 domains. Its structural complexity does not allow the application of classical structural biology methods to determine its overall architecture. Therefore, we have decided to chop the protein into smaller fragments and determine the high resolution structures of representative parts. Within this endeavor, we have also become interested to consider known ligands involved in the titin interactome for structural-functional analysis. Over the last decade, we determined structures of the N-terminal assembly complex (Zou et al., 2006), from the I-band (Mayans et al., 2001; Vega et al., unpublished) and from the A-band including the kinase domain and down-stream signaling complexes (Mayans et al., 1998; Muller et al., 2006; Muller et al., 2007; Muller et al., unpublished; Chen et al., unpublished). The available data allow modeling a large part of the titin proteome and to interpret available low resolution data of the entire titin filament. Combined with complementary functional data, our findings reveal key structural/functional relationships of titin and its interactions partners. Structural biology results from a related sarcomeric filament protein, myomesin (also known as mini-titin) will be presented in a separate contribution. Some of the data have been published recently (Pinotsis et al., 2008).

References:

Keywords: muscle proteins, protein/protein interactions, kinase structure

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**The assembly process of the double-layered capsids of phytoreoviruses**

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Viruses in the family *Reoviridae* have an inner core with a large interior cavity that contains the 10 to 12 segmented double-stranded RNA as a genome, and a transcriptional complex that includes proteins with RNA polymerase, helicase, guanylyltransferase and transmethylase activities and an RNA-binding protein. The core particle is surrounded by one or two layers of outer capsid proteins. During X-ray crystallographic and Cryo-electromicroscopic studies of the structural organization of *Rice dwarf virus*, a member of the genus *Phytoreovirus* in the family *Reoviridae*, we have identified possible structural mechanisms that allow creation of a large cavity inside a double-layered spherical particle that consists of heterologous proteins with different lattices. The viral particle seems to be created in a genetically economical manner, with the sealing of joints between inner-layer proteins by a second layer of proteins, suggesting the organization of a rigid protein layer that separate from and, probably, protects the interior of the virus from the cytoplasmic environment within infected cells. Procedure of the virus assembly was analyzed combined with molecular cytopathological data in virus infected cells.

Keywords: virus assembly, viral structure and function, virus host interactions