

**FA1-MS9-P01**

**Structural characterization of a WD-40 repeat containing Ygr223c homologue.** Karin Kühnel<sup>a</sup>, Roswitha Krick<sup>b</sup> and Michael Thumm<sup>b</sup>. <sup>a</sup>*Department of Neurobiology, Max-Planck-Institute for Biophysical Chemistry, Göttingen.* <sup>b</sup>*Department of Biochemistry II, Faculty of Medicine, University of Göttingen.*  
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Ygr223c is a membrane associated WD-40 repeat containing autophagy protein. We grew crystals of a yeast Ygr223c homologue. They belong to the cubic space group P4<sub>1</sub>32 with a=b=c=157.5 Å and  $\alpha=\beta=\gamma=90^\circ$ . We collected a 3.3 Å SAD data set from selenomethionine labelled protein and could calculate and interpretable electron density map. The native crystals diffract to 3.0 Å resolution. We are currently building the model and are trying to optimize the crystals to obtain higher resolution data.

**Keywords:** protein-structures, WD-40 repeat, autophagy

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**Structural Analysis of Nuclear Pore Proteins.** Marco Bürger, Nils Schrader, Patricia Stege, Ingrid R. Vetter. *Department of Physical Biochemistry, MPI of Molecular Physiology, Dortmund, Germany.*  
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Nuclear pore complexes (NPCs) are the sole gateways for macromolecular transport across the nuclear envelope. These complexes are 40-60 MDa in size in yeast and allow for exchange of small molecules by free diffusion whereas passage of larger proteins and RNAs is highly selective and facilitated by transporter proteins. The complex in its entirety is composed of about 30 distinct nuclear pore proteins (nucleoporins, Nups), which form the NPC with a high redundancy of these proteins.

To understand the structure and function of the NPC in detail requires information on a molecular level. Up to now, such information is very limited with only a few nucleoporins being crystallized. We like to determine the structures of selected Nups with the aid of X-ray crystallography. Since most of the Nups are very large proteins, we search for expressible fragments.

Particularly, we are currently adopting a GFP based protein folding reporter assay on them. Using this cell based screening method we try to identify soluble protein fragments in a high-throughput manner.

**Keywords:** nuclear pore complex, nucleoporin, high-throughput assay