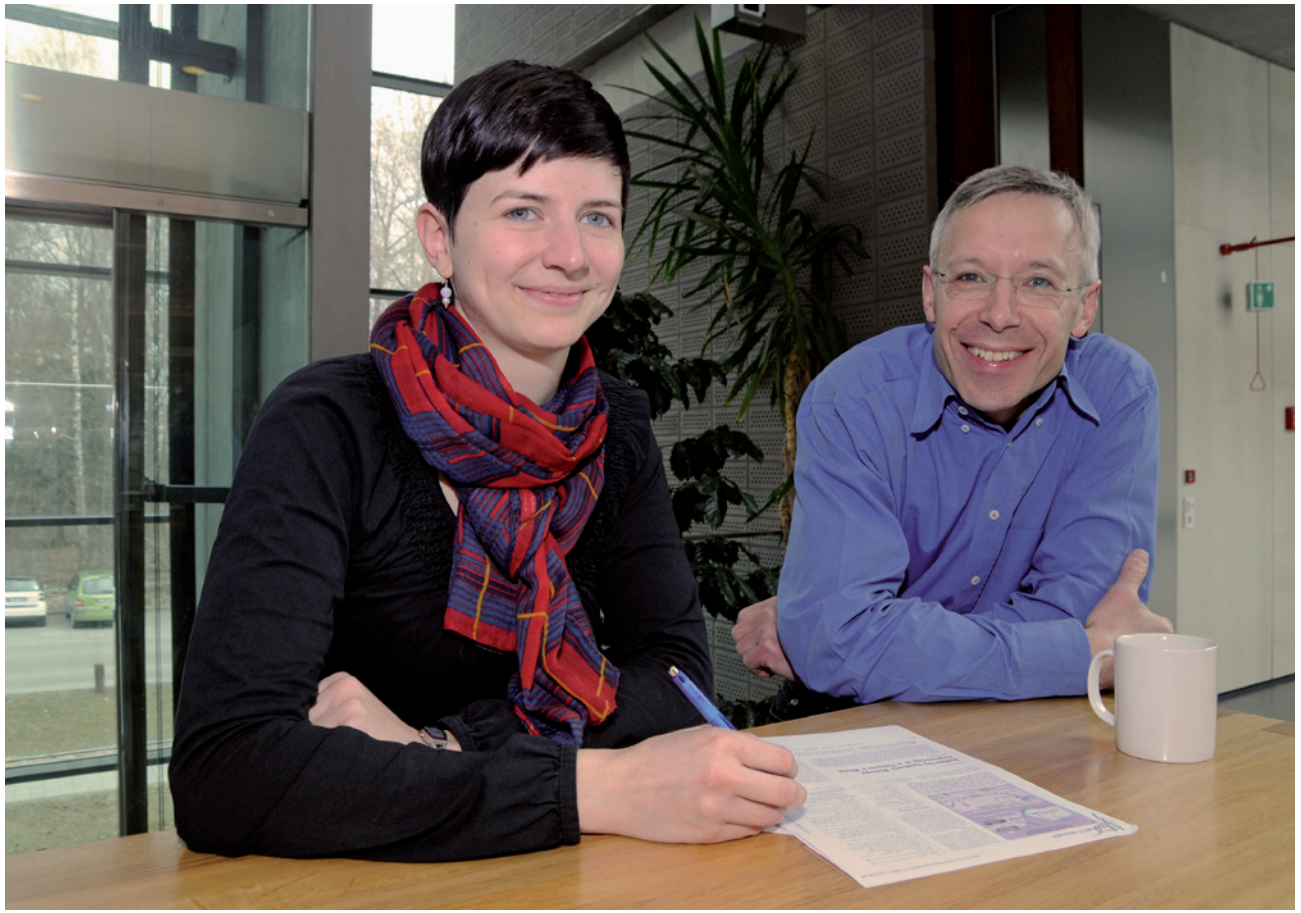

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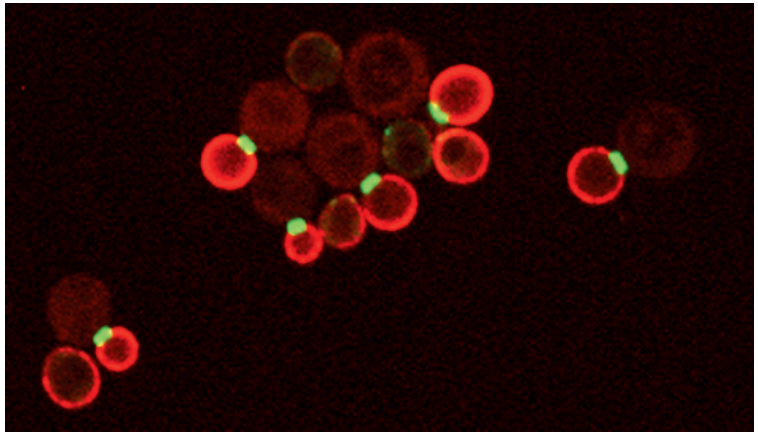
Institute of Molecular Genetics and Cell Biology

The Organization of the Polar Cortical Domain in Yeast

Head: Nils Johnsson

The small GTPase Cdc42p defines through its localized activation the polarity of a growing yeast cell. In its GTP bound state ($Cdc42_{GTP}$), $Cdc42_{GTP}$ will stimulate downstream effector proteins that organize the asymmetric formation of cellular structures and the directed transport of molecules to the site of polarization. To initiate and maintain



Co-expression of two fluorescently labelled polarity proteins in budding yeast cells. The red staining marks regions of active GTPase Cdc42p. Green staining decorates the border between mother and daughter cell and the site of future cell separation. (Photo by Julian Chollet)

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polarization, Cdc42p and its effectors are assembled at the bud tip until the polarity axis is redirected during the late G2 phase and mitosis. The organization of the proteins and lipids at the bud tip is highly dynamic and maintained through a constant exchange of its constituents. The forces that determine the structure of this so-called polar cortical domain (PCD) are interactions of the core components with $Cdc42_{GTP}$, the interactions among the proteins of the PCD, and the interactions between components of the PCD and the membrane. We are interested in two main questions concerning the structure and function of the PCD. Can we understand the dynamic structure of the PCD through the self-assembly and self-organization of critical protein-protein and protein-membrane interactions? How do certain protein members of the PCD perform their role as hinges between the GTPase Cdc42p and its effectors?

Selected Publications:

- *Moreno D, Neller J, Kestler HA, Kraus J, Dünkler A and Johnsson N (2013): A fluorescent reporter for measuring cellular protein-protein interactions in time and space. Mol Syst Biol. 9, 647.*
- *Gronemeyer T, Wiese S, Ofman R, Bunse C, Pawlas M, Hayen H, Eisenacher M, Stephan C, Meyer HE, Waterham HR, Erdmann E, Wanders RJ, Warscheid B (2013): The proteome of human liver peroxisomes: Identification of five new peroxisomal constituents by a label-free quantitative proteomics survey. PLoS-ONE 8; e57395*
- *Labedzka K, Tian C, Nussbaumer U, Timmermann S, Walther P, Müller J, Johnsson N (2012): Sho1p connects the plasma membrane with proteins of the cytokinesis network via multiple isomeric interaction states. J Cell Sci. 25, 4103-4113.*
- *Dünkler A, Müller J and Johnsson N (2012): Detecting protein protein interactions with the Split-Ubiquitin sensor. Methods Mol. Biol. 786, 115-130.*
- *Hruby A, Zapatka M, Heucke S, Rieger L, Wu Y, Nussbaumer U, Timmermann S, Dünkler A, Johnsson N (2011): A constraint network of interactions: Protein Protein-protein interaction analysis of the yeast type II phosphatase Ptc1p and its adaptor protein Nbp2p. J Cell Sci. 124, 35-46.*