

On our home page you probably already read that we work on a complex system that leads to complicated questions. Don't fear though, as there is a way to make them simpler! In this project, we work on a minimal *in vitro* system of yeast cell polarity, which means we try to build a simplified, isolated version of the polarity mechanism. With this approach, we characterize the proteins of interest and try to uncover the ways in which they contribute to the establishment of the yeast cell polarity spot.

The minimal *in vitro* cell polarity system consists of an artificial membrane with purified protein. We focus on three core proteins. The polarity spot in budding yeast is defined by an accumulation of Cdc42, a GTPase. Cdc42 cell polarity is highly regulated within the cell, but also shows high adaptability (Laan et al., 2015). An essential protein in this regulatory network is Cdc24, this protein activates Cdc42. To bind to the membrane, Cdc24 needs scaffold protein Bem1. With just these four components, we find exiting, unexpected protein properties that are not directly observable in the living cell. These so-called hidden protein functions do not only teach us more about the individual proteins, but also help us understand how cells can be both robust and adaptive. These hidden properties could both help the cell to rescue functions of failing machinery and help the cell to adapt quickly in changing environments (Schwille & Frohn, 2022).

By investigating less trivial protein properties, we aim to dissect the mechanisms behind this fascinating, complex system.

Interested in joining this project for a BEP or MEP? Contact me! [n.m.hettema@tudelft.nl](mailto:n.m.hettema@tudelft.nl)

Projects might include:

- The role of membrane composition on oligomerization
- Adding complexity: the role of membrane dissociation factor Rdi1 on Cdc42 cycling
- Computational simulations of the emergence of the polarity spot
- Studying of (mutant) protein domains and their effects on protein dynamics

Laan, L., Koschwanetz, J. H., & Murray, A. W. (2015). Evolutionary adaptation after crippling cell polarization follows reproducible trajectories. *ELife*, 4, e09638.

<https://doi.org/10.7554/eLife.09638>

Schwille, P., & Frohn, B. P. (2022). Hidden protein functions and what they may teach us. *Trends in Cell Biology*, 32(2), 102–109. <https://doi.org/10.1016/j.tcb.2021.09.006>