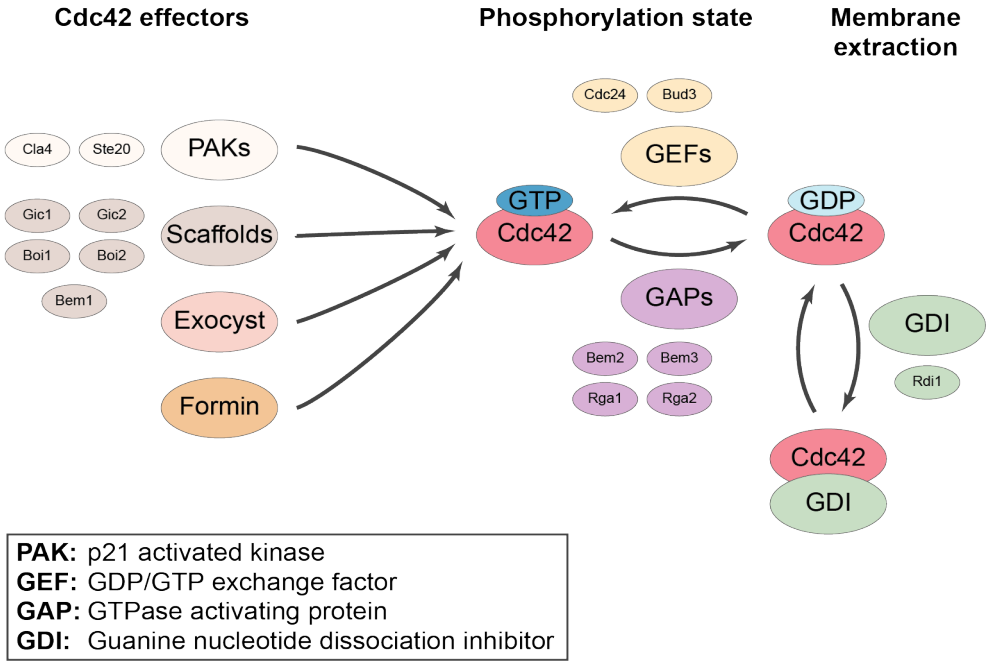
Exploring how polarity proteins shake hands – with whom, when, how fast, and how long?

Saccharomyces cerevisiae proliferates through budding; a daughter cell grows by budding off on one side of the mother. The first step towards budding is the establishment of a Cdc42-based protein pattern on the cell membrane marking the site of bud-emergence. This pattern arises from local activation and accumulation of the GTPase Cdc42. Cdc42 is highly regulated through several proteins that constitute the polarity protein network (Fig. 1).
Our group works on reconstituting Cdc42 accumulation in an *in vitro* system. To make such a system work, knowing how the proteins in that system interact on a **qualitative** and **quantitative** level is indispensable.
We are using qualitative and quantitative biochemical and single-molecule assays, in combination with kinetic **modelling**, to investigate the protein – protein interactions in the yeast polarity network.

Such methods include:

- Protein pull-down assays
- GTPase activity assay
- GTP/GDP exchange assay using fluorescent spectroscopic methods
- …

Figure 1: The yeast polarity protein network. Figure based on [1].



[1] Chiou et al. Ann. Rev. Cell Dev. Biol. 2017.

We are looking for students interested to combine precise experiments with modelling to gain **qualitative** and **quantitative** insights into protein-protein interactions.
If you are interested in being part of this project, send an e-mail to s.tschirpke[at]tudelft.nl.