

# Modular Organization and Dynamics of the Budding Yeast Polarity Protein Network

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Polarity establishment in budding yeast must be precisely controlled in order to ensure that bud formation is coordinated with other cell cycle events. More than 110 proteins which physically localize to the bud tip have been identified to play a role in polarity establishment. It is interesting to divide these proteins into groups and study the dynamics of these proteins.

A functional module is a discrete entity whose function is separable from those of other modules <sup>[1]</sup>. Based on the physical interaction data from *Saccharomyces* Genome Database (SGD), we used a simulated annealing algorithm for modulization <sup>[2,3]</sup> to define 5 functional modules (Signaling module, Transport module, endocytic module, Mitotic exit module and Exocytosis module) in the interaction network formed by these 110 proteins.

Every protein is assigned by this algorithm a universal role according to its pattern of intra- and inter-module connections. For example, most proteins in the network are either ultra-peripheral nodes or peripheral nodes. Cdc42p in the Signaling module is a Connector Hub for the network, which means that it is not only a hub inside its own module, it also connects some other modules as a connector. This is consistent with Cdc42p's key role in polarity establishment.

An unanswered question about polarity maintenance is whether polarity is maintained on stable scaffolds or as a dynamic steady state with constant flux. We characterized the dynamics of 26 GFP-tagged proteins in Signaling module and Transport module in a systematic way, using iFRAP (inverse Fluorescence Recovery After Photobleaching) and calibrated confocal microscopy. With Metamorph and house-made programs, we quantified the iFRAP images systematically and obtained parameter T-Half which measures the time for the exchange of half of the mobile fraction between bleached and unbleached regions.

The dynamic behavior of proteins might correlate with molecular function or modular organization. On average, the proteins in the Signaling module are more dynamic than the proteins in Transport module. T-tests under both equal and unequal variance assumption show that T-Half values for these two modules are significantly different. We also found that several proteins have significantly longer T-half values than other proteins, suggesting that they might play a scaffolding role in the maintenance of cell polarity.

## Reference:

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