

Figure 1: Cdc42 orchestrates morphogenesis in *S. cerevisiae*. Cdc42 is activated by its GEF Cdc24 and returned to its GDP-bound state by its GAPs Rga1/2 Bem3. Cdc24 is activated by upstream bud site selection pathways and by the $\gamma\beta$ G-protein dimer released from the tripartite G-protein complex when the cognate mating pheromone interacts with the mating pheromone receptors. Acting through its immediate effectors, activated Cdc42 stimulates polarised growth, activation of the pheromone response pathway, pseudohyphal growth and cytokinesis.

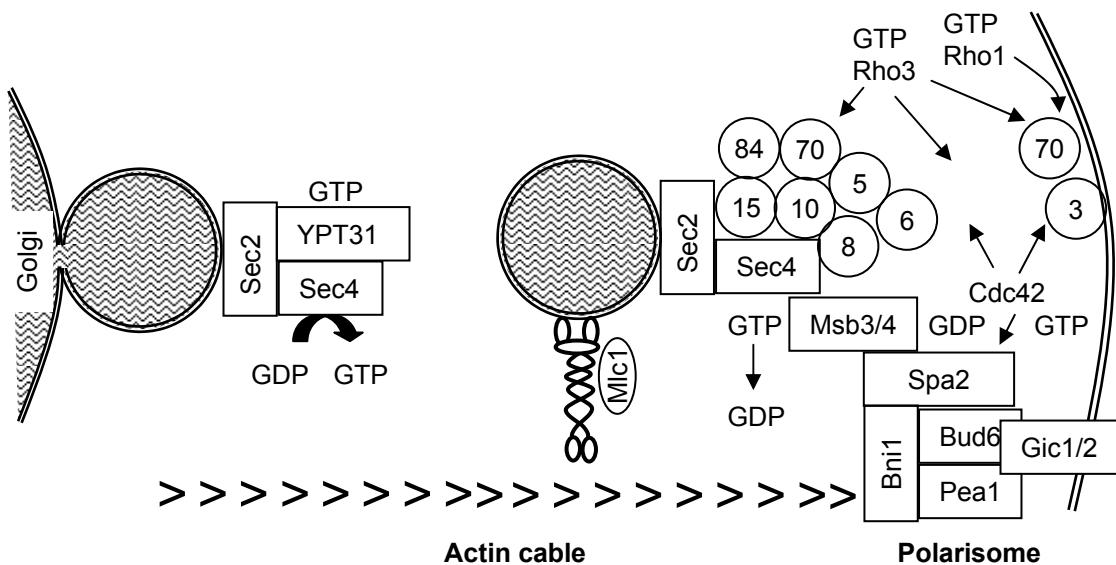


Figure 2 Polarised secretion. Secretory vesicles bleb off the late Golgi compartments and travel along actin cables, nucleated by the polarisome, to fuse with the plasma membrane at sites of polarised growth. The process is controlled by the Rab GTPase Sec4p which is activated by its GEF Sec2p. Numerals enclosed in circles refers to exocyst components encoded by Sec genes. E.g Sec15p, Sec6p etc. Encircled 70 and 84 refers to Exo70 and Exo84. For details see text.

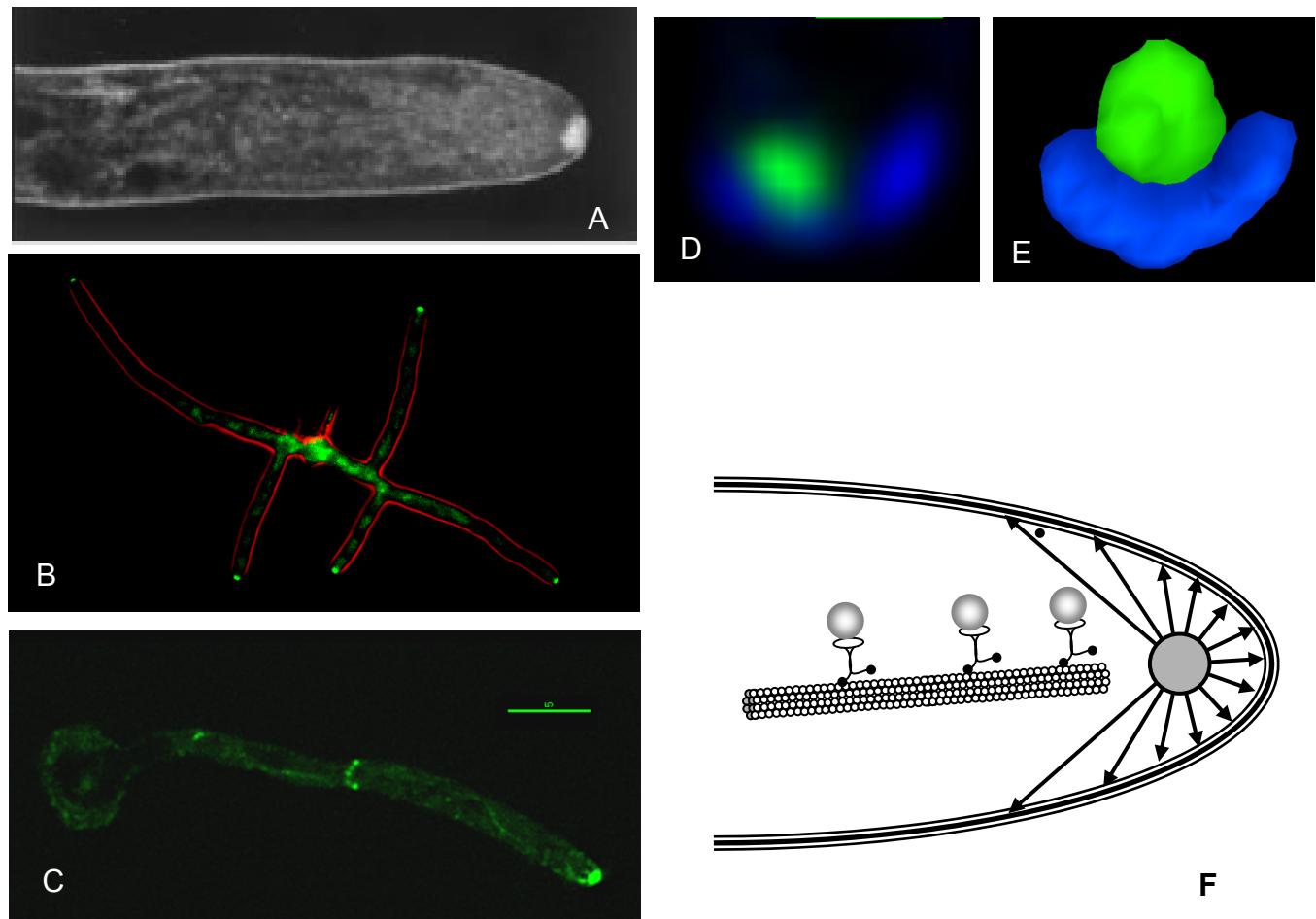


Figure 3 The Spitzenkörper. A: The *Neurospora crassa* Spitzenkörper revealed by brief FM4-64 staining which reveals secretory vesicles accumulating in a sub-apical spot (Fischer-Parton *et al.*, 2000). B: Spa 2 accumulating in the Spitzenkörper of *Ashbya gossypii* hyphae (Knechtel *et al.*, 2003). C – E Mlc1-YFP localising to the Spitzenkörper of *Candida albicans* (Crampin *et al.*, 2005). C: Mlc1-YFP in a subapical spot and the cytokinetic ring. D: Mlc1-YFP localising to the tip where the apical membrane is stained with filipin. E: Computer modelling using the information in the Z-stack from panel D, shows that Mlc1 is a 3-dimensional sphere located within the hypha rather than a two-dimensional surface crescent. F: The vesicle supply model: Secretory vesicles are delivered along microtubules by a kinesin motor protein (not to scale!). They accumulate in the Spitzenkörper before radiating in all directions. A greater concentration per unit area arrives at the tip compared to subapical areas, which drives tip growth. The shape is determined by the distance of the Spitzenkörper centre from the tip as the distance increases so also does hyphal width.

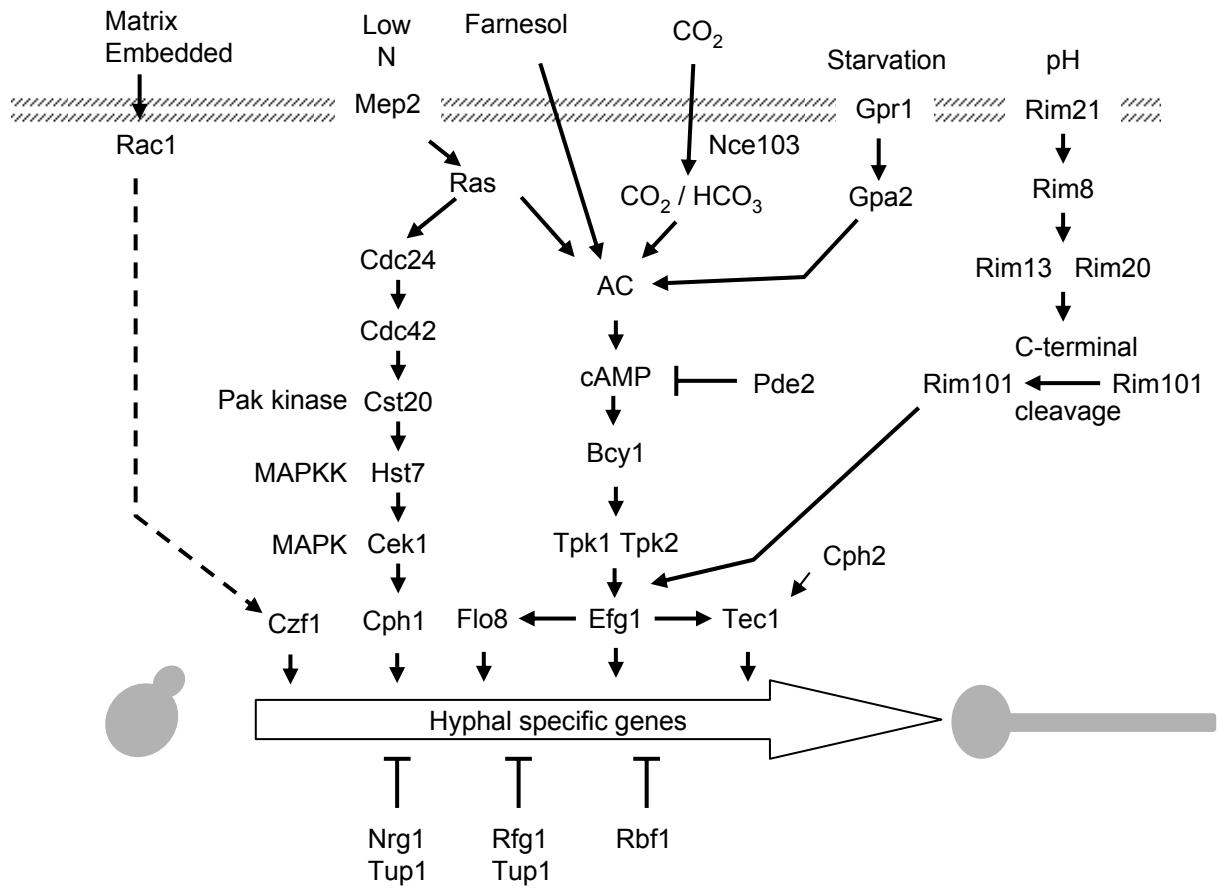


Figure 3 Signal transduction pathways regulated hyphal development in *Candida albicans*. External environmental cues stimulate multiple pathways that target downstream transcription factors. Note the central role played by AC (adenylyl cyclase) and the transcription factor Efg1p. Cst1, Hst1, Cek1 and Cph1 are the homologues of *S. cerevisiae* proteins Ste20, Ste7, Fus3/Kss1 and Ste12 respectively that form the MAPK module mediates the pheromone response and promotes pseudohyphal growth.