

# Mathematical Modeling of the cAMP/PKA pathway in *S. Cerevisiae*

Christian Waltermann<sup>1,\*</sup>, Edda Klipp<sup>1,2</sup>

1. Computational Systems Biology Group, Max Planck Institute for Molecular Genetics
  2. Group of Theoretical Biophysics, Humboldt University of Berlin, Berlin, Germany
- \*E-mail: christian.waltermann@molgen.mpg.de

## Abstract

The cAMP/PKA pathway plays a crucial role in responses of yeast cells to complex environmental changes. For instance, an increase in the concentration of extracellular glucose triggers the cAMP/PKA pathway through the activation of the Ras2 and Gpa2 proteins by extracellular glucose sensors and eventually leads to changes in the transcriptome which allow for an optimal cell proliferation rate [4]. Limitation for nitrogen but sufficient supply with glucose, for instance, is thought to alter the mode of operation of the cAMP/PKA pathway via crosstalk from the TOR pathway and causes diploid budding yeast cells to switch to a pseudohyphal growth pattern [2]. Ras2 is able to activate the filamentation MAPK cascade and the synthesis of cAMP in parallel and both the filamentous growth pathway and the cAMP/PKA pathway converge on the FLO11 gene [3], which is required for pseudohyphal growth and diploid invasive growth [1]. However, little is yet known about how the additional information due to nitrogen deprivation alters the response of the cAMP/PKA pathway and how that in turn affects the pseudohyphal growth program. Here we present a mathematical model of the cAMP/PKA pathway which generates new hypotheses about how the interplay of the cAMP/PKA pathway with upstream activators and downstream targets is organized, and which predicts how robust its components versus perturbations are.

## Structural model

Please see next page.

## References

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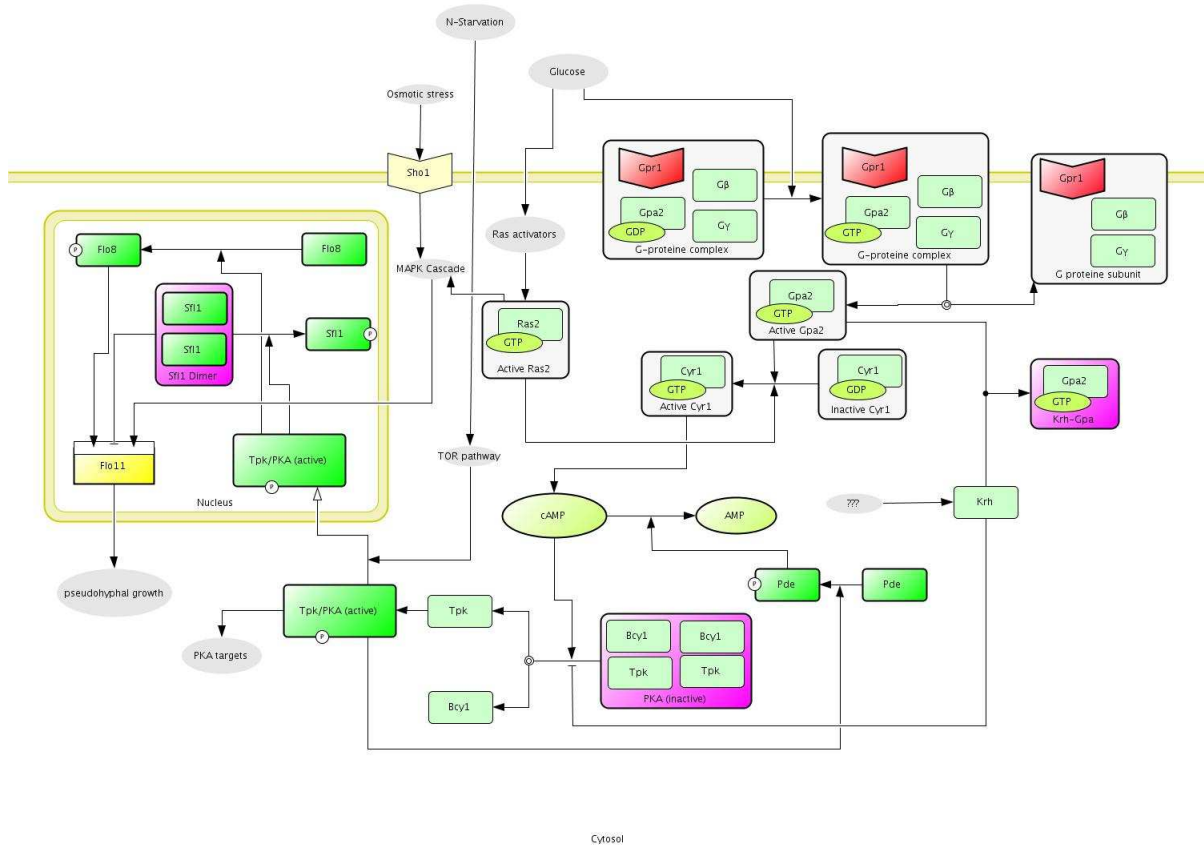


Figure 1: Structural model of the biochemical interactions in the cAMP/PKA pathway in budding yeast including stress inputs and its interfaces to neighboring signaling cascades.