

**SCREENING OF NEW PROTEINS POSSIBLY INVOLVED IN THE ACTIVATION OF
PLASMA MEMBRANE H⁺-ATPASE IN THE YEAST
SACCHAROMYCES CEREVISIAE.**

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The H⁺-ATPase is a protein of plasma membrane from the yeast *Saccharomyces cerevisiae* that plays an important role in the cell physiology. By proton pumping, it creates an electrochemical gradient that is essential for nutrient uptake. Nevertheless, a complete pathway involved in this regulatory process is not completely known; thus, our objective in this work was to identify other proteins involved in the activation of H⁺-ATPase. To do that, we tested the extracellular pH variation in 4,500 deleted mutants from the Euroscarf collection. First, cells were grown on 96-well plates in YPD2%, and 50µL of each culture were tested with the acid-base indicator Bromocresol blue. This indicator is yellow in acid and blue in neutral or basic media. This is a simple and fast method to identify the strains that present problems to acidify the external medium and by this way to identify those that present problems to activate the H⁺-ATPase. Our results demonstrated that 220 strains were unable to promote the decrease of pH allowing the identification the new proteins that could be involved in the sugar-induced activation of the H⁺-ATPase.

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