Study of potential therapeutic targets for *Candida glabrata* infections: biochemical and structural characterizations

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Infections caused by diverse *Candida* species have dramatically increased in this past few years resulting in local or systemic disorders. These infections cause high morbidity and mortality, notably in hospital and intensive care units, and particularly for immunocompromised patients.

Like *Candida albicans*, *Candida glabrata* is one of the pathogenic fungi with the highest human prevalence [1]. Nowadays, only a few antifungal compounds are available, such as azoles and echinocandins targeting the fungal cell wall. Despite a good understanding of resistance mechanisms at the molecular level, no new treatments have been developed in recent years.

Within this context, we are studying a protease of interest of the yeast *Candida glabrata*. Although the mechanism of these proteases is still little known today, they have been identified as actors of programmed cell death in yeasts and other unicellular organisms. This study would allow a better comprehension in the structure-function relationships of theses proteases and the discovery of new therapeutic strategies. Here we present the preliminary results obtained, the three-dimensional structure of the protease as well as new information on the functionality and activity of the enzyme.

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