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Candida albicans (*C. albicans*), a microscopic fungus living in humans, has the potential to cause a range of diseases. The pathogenicity of *C. albicans* to an elongated form known as a hypha that invades tissues, spreads to cells, evades host immune cells and can eventually lead to disease.

C. albicans were selected for ASH1 alignment. Results showed that there were little to no similarities in ASH1 mRNA among species with or without She2p suggesting that there is limited functional or structural conservation of ASH1. From the alignment, I selected the segment of ASH1 mRNA that DOLJQV ZLWK EDNHU and predicted the structure of that segment for *C. albicans*. Confirming the alignment results, the E3 structure was not similar between *C. albicans*

lab next summer or in my senior year.

Through literature search, computer alignment experiments, and weekly meetings with the McBride lab, I have built important skills such as presenting on literature sources, keeping laboratory notebooks, designing experiments and communicating with members of the McBride lab.

Faculty Mentor: Anne McBride
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References