

Malaria is caused by the Plasmodium genus of parasites which, depending on the species of Plasmodium, infect different mammalian species. The parasite is evolving at rates that overcome the effectiveness of currently available antimalarials. Knocking out the Plasmodium BEM-46 Like Protein (PBLP) has been shown to greatly reduce parasitemia within rodent models. This shows its potential as a new drug target to combat antimalarial resistance. PBLP is a part of the BEM46 protein family, which appears to be involved in cell growth and polarity. The BEM46 protein family has not been studied in vitro and therefore has uncharacterized purification procedures from E. coli and unknown substrates.. Here we used various computational tools to predict the superfamily, enzymatic function, 3D structure, and interactions with substrates. We developed a novel purification scheme of PBLP from E. coli using a harsh osmotic shock procedure that liberates PBLP from the periplasmic space. This scheme provides a significantly higher protein yield than prior attempts as visualized through SDS-PAGE. We have demonstrated the previously predicted hydrolase activity of PBLP through a p-nitrophenol-based enzyme assay and developed a protocol for future PBLP substrate assays. Further testing of enzymatic activity can allow for potential identification of its natural substrate to identify its specific function in cell growth and inform the development of a new antimalarial drug.