# Expression, Purification, and Hydrolase Characterization of PBLP, a Protein from the Malaria Parasite *Plasmodium yoelii*

# TBIOMD 495 TACOMA

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# Background

- In 2023 alone, globally, 597,000 malaria-related deaths and 263 million new cases of malaria were reported.<sup>2</sup>
- *Plasmodium* BEM46-like protein (PBLP) sequence orthologs are evolutionarily conserved across all *Plasmodium* parasite species. Yet, the protein's role in progressing infection has not been definitively identified.<sup>1</sup>
- PBLP shares structural and sequence homology with members of the  $\alpha/\beta$ -hydrolase superfamily.<sup>1</sup>

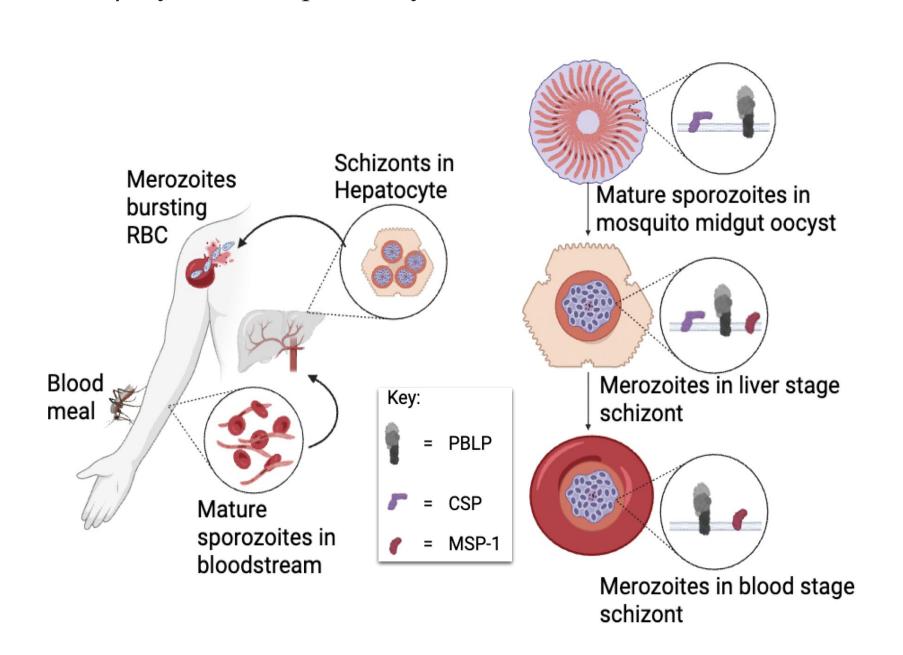
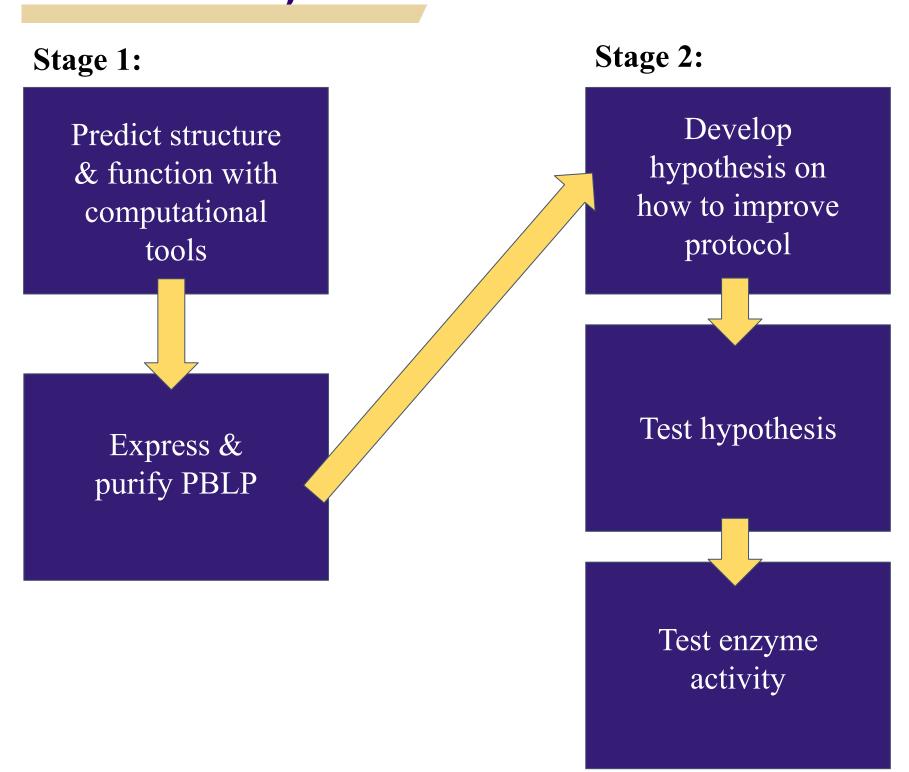


Fig 1. The *Plasmodium* parasite completes its asexual life cycle in mammalian hosts, and PBLP co-localizes with a selection of parasitic plasma membrane (PPM) proteins at various life stages of *P. yoelii*.

# Research Objectives

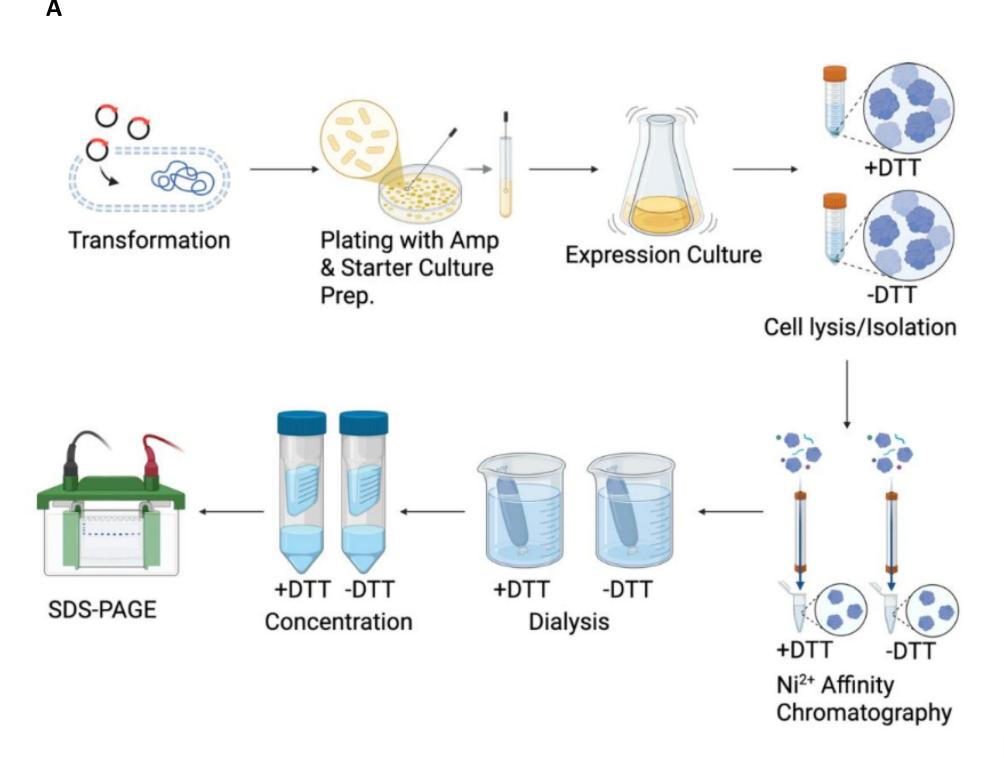


### **Hypothesis** (two-fold):

- 1. PBLP functions as a lipid esterase that hydrolyzes ester bonds of PPM lipids.
- 2. Adding dithiothreitol (DTT) as a reducing agent to isolation, column, and dialysis buffers will result in a greater yield of soluble PBLP.

**Rationale:** PBLP's inferred membrane-associated involvement in *Plasmodium* life cycle advancement and evolutionary conservation makes it a high-priority protein to functionally investigate, as it may be a beneficial target to incorporate in combination therapies.

# Wet Lab Methods



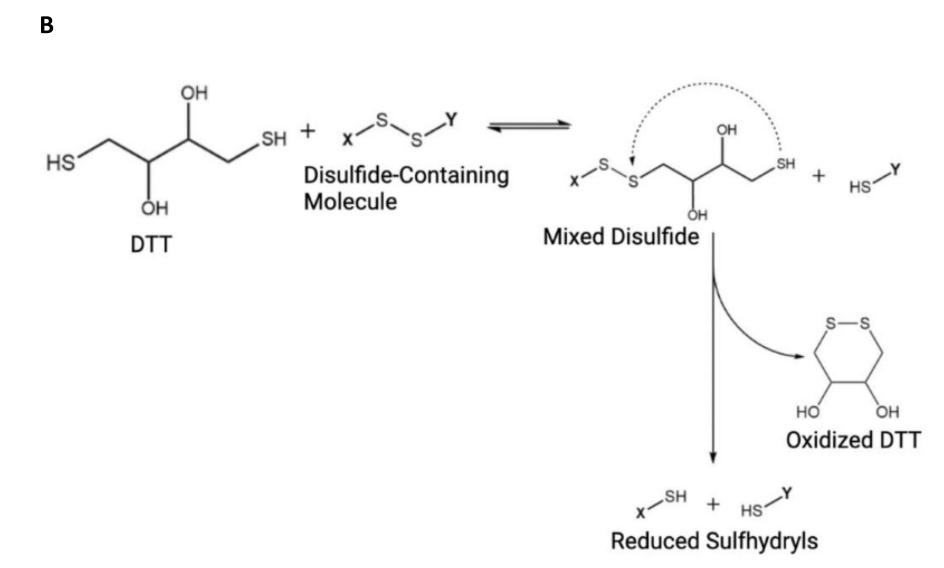
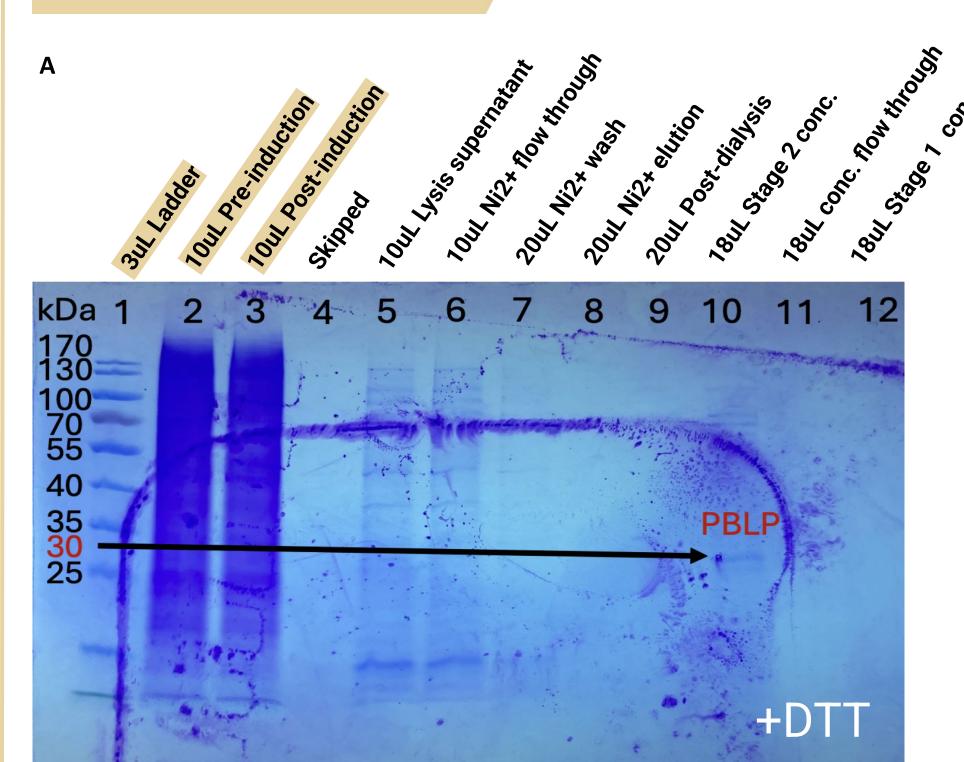


Fig 2. PBLP expression, isolation, and purification. A. Stepwise Stage 2 laboratory experiment with alterations to the original protocol: the addition of DTT to isolation, column, and dialysis buffers. Schematic created using BioRender illustration software. B. Mechanism of DTT acting as a reducing agent, adapted from Iris Biotech (2020).

# **Experimental Results**



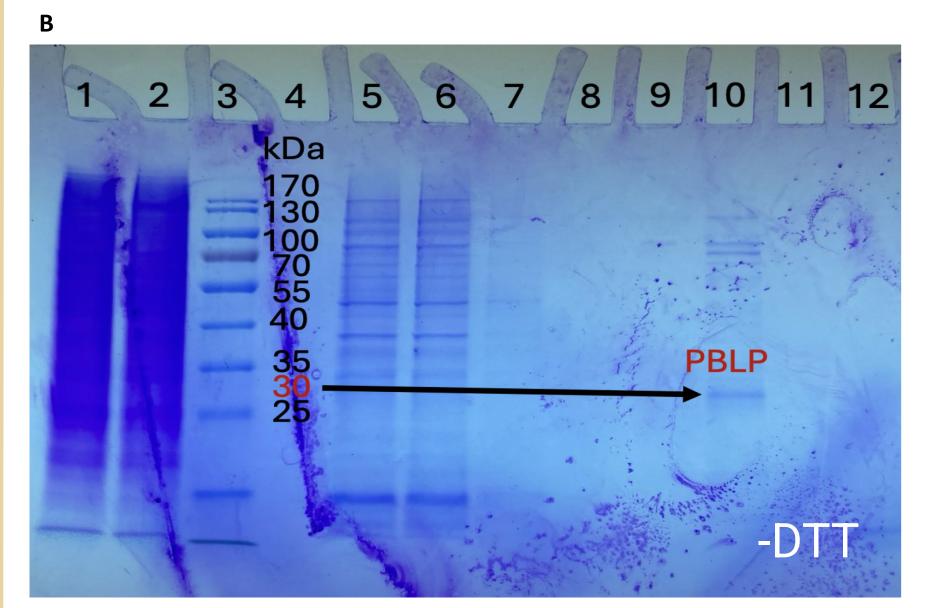


Fig 3. SDS-PAGE gel results reveal purified PBLP protein present in the Stage 2 concentrate samples for both -DTT control (B) and +DTT experimental (A) conditions. The presence of other bands not a 30 kDa in lanes 10 indicates only a partial purification of PBLP, and the absence of bands in lanes 8 and 9 indicates that protein concentrations were too low for detection prior to sample concentration.

# PBLP's Enzyme Activity on PNP-Based Substrates

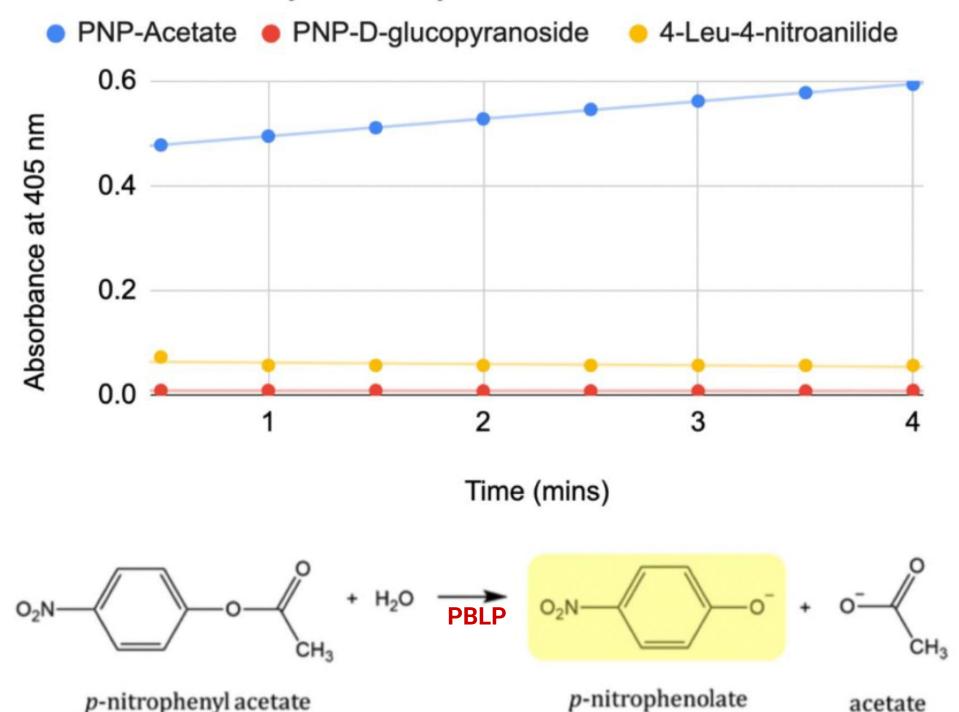


Fig 5. PBLP hydrolyzes the ester bond of PNP-Acetate to produce PNP and acetate products. Absorbance at 405 nm measured the amount of chromogenic product (PNP) produced by the enzymatic hydrolysis of each substrate.

anion (yellow)

# Discussion/Conclusions

#### Did DTT improve the yield of soluble PBLP?

- PBLP was successfully expressed, isolated, and partially purified from the *E. coli* cells under both +DTT and -DTT conditions.
- The concentrate bands were similar intensities for both the +/-DTT conditions, however the -DTT prep was more concentrated. Therefore, we know that the addition of DTT facilitated a greater recovery of soluble and natively folded PBLP.
- → +DTT: 15.8-fold
- → -DTT: 45-fold
- → Stage 1: 2.8-fold

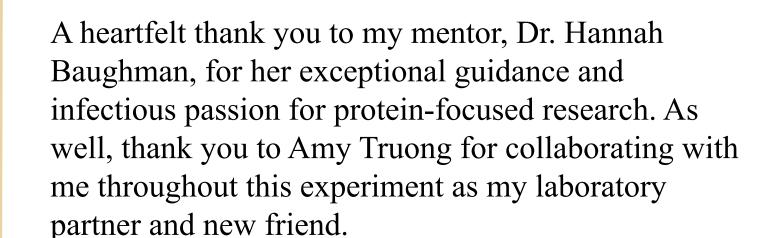
#### What do we know about PBLP activity now?

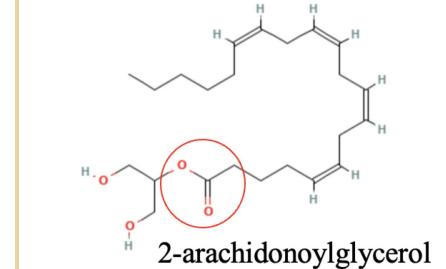
- We have experimentally confirmed that PBLP has hydrolase activity.
- Given the structure of PNP Acetate, we know that PBLP cleaved an ester bond to produce PNP product.

## Next Steps

- Additional assays with PPM-associated substrates in *Plasmodium* would help determine PBLP's significance to the parasite.
- Consideration of pharmaceutical development involving PBLP as an antimalarial target. Continue PBLP gene knockout investigations. <sup>1</sup>

# Acknowledgements & References





Computational Results

Fig 4. Putative membrane-associated ligands of PBLP display favorable conformations at the active site that position ester carbonyl groups proximal to the serine nucleophile of the Ser-His-Asp catalytic triad. A. 2-arachidonoylglycerol as the substrate. B. chlorogenic acid as the substrate. Images are PyMOL-generated visualizations using the AlphaFold3 prediction of the full-length structure of PBLP. Positions of 2-AG and chlorogenic acid were predicted using SwissDock protein docking.

