

Title: Designer parasites for improved malaria vaccination

Synopsis:

Vaccination is undoubtedly one of the most cost-effective health interventions available. Whole-organism vaccines employing *Plasmodium* sporozoites (Wsp) constitute the most promising approach to vaccination against malaria. Wsp vaccination relies on the natural ability of the immunizing parasites to productively infect the liver of a non-immune host (1). To achieve this, the parasite expresses a diverse repertoire of essential, partially redundant, or redundant genes, which moderate host-parasite interactions, not only scavenging nutrients but also evading and modulating the host's immune system to ensure survival. We hypothesize that more efficient Wsp vaccine candidates can be designed by eliminating parasite proteins that contribute to immune evasion or modulation. To develop these improved vaccine candidates, we need to better understand how the immunizing parasites present themselves to the host and which parasite molecules operate at this parasite / host interface.

In collaboration with MIMS (Sweden), we aim to use a novel genome wide, high throughput screening assay for gene function to identify Plasmodium genes that serve as decoys and hamper the mounting of a successful immune response by WOPE vaccines (2,3).

The Master's student involved in this work will acquire various technical skills, including the use of animal and cell models of *Plasmodium* infection, immunofluorescence microscopy, qRT-PCR, ELISA and flow cytometry (4).

Supervisor: António M. Mendes, Miguel Prudêncio Lab, antoniomendes@medicina.ulisboa.pt

Co-Supervisors: Diana Alves Moita, Miguel Prudêncio Lab, diana.moita@medicina.ulisboa.pt

Miguel Prudêncio, Miguel Prudêncio Lab, mprudencio@medicina.ulisboa.pt

[Webpage of the group](#)

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