Article Title

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Abstract
There's nothing here yet

Contents

1. Introduction

The apicomplexan parasite *Plasmodium falciparum* is the most virulent causative agent of malaria, and responsible for over 600,000 deaths annually [1]. Along with other members of the *Plasmodium* family, *P. falciparum* has a complex lifecycle, moving between several different tissues in both mammalian and arthropod hosts. Symptomatic disease in humans occurs when *P. falciparum* undergoes rounds of asexual reproduction inside human red blood cells (RBCs) [2].

In some respects, the intracellular environment of a red blood cell is an ideal location for parasite proliferation. The cells' lack of an MHC (Major Histocompatibility Complex) system, which would otherwise be used to identify intracellular pathogens to the host immune system, renders parasites immunologically invisible [**?**], whilst the vascular system allows the parasite to travel throughout the body.

The highly specialised nature of RBCs, however, means that the intracellular environment also presents significant challenges to parasite survival, and so at least 10% of the

The Plasmodium Export Element (PEXEL) Motif
PEXEL Negative Exported Proteins (PNEPs)
1.1 Protein Structure Prediction
Disorder Prediction (metaPrDOS
Coiled Coil Prediction (Coils)
Transmembrane Prediction (TMHMM)
Combined Approaches (Phyre2 and InterPro)

2. Software Implementation

2.1 Automating Sequence Submission
2.2 Collating output formats
2.3 Visualisation

3. Limitations and Further Work

Acknowledgments

References

[1] World Health Organisation. *World Malaria Report 2013*. World Health Organization, 2013.

[2] Qijun Chen, Martha Schlichtherle, and Mats Wahlgren. Molecular Aspects of Severe Malaria. *Clinical Microbiology Reviews*, 13(3):439–450, July 2000.