

*IDENTIFICATION OF NOVEL
PLASMODIUM VIVAX BLOOD-STAGE
VACCINE TARGETS*



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ABSTRACT

Identification of novel Plasmodium vivax blood-stage vaccine targets

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A vaccine targeting the illness-inducing blood stage of Plasmodium vivax is hindered by major gaps in our knowledge of P. vivax biology, including critical events during merozoite invasion of erythrocytes. Only a single receptor-ligand interaction is currently known, and natural human immune responses to P. vivax during and after infection, which could provide clues for how to stimulate a protective immune response, have been the subject of only limited study. This lack of understanding of both the molecular details of invasion and the immunological responses during infection correlates with a relatively limited repertoire of potential P. vivax antigens being considered for vaccine development. A comprehensive and systematic approach is needed to advance our understanding of P. vivax invasion and to identify additional vaccine candidates.

I first addressed this knowledge gap by investigating transcription in P. vivax clinical isolates at the schizont stage, just prior to erythrocyte invasion. I purified RNA from schizont-enriched P. vivax isolates obtained directly from Cambodian patients with P. vivax malaria and sequenced the RNA using a strand-specific approach. These RNA-Seq data revealed hundreds of additional genes transcribed at this stage compared to previous microarray studies, and uncovered novel gene transcripts that enabled me to improve and annotate over 300 gene models in the reference genome. Comparisons of RNA-Seq data between clinical isolates revealed that genes related to host invasion were among the most variably-expressed genes. The data provided a basis to prioritize a list of targets consistently expressed during the late blood stages.

I next produced a library of blood-stage P. vivax proteins to use in functional and immuno-epidemiological studies. I selected candidates predicted to localize to the merozoite surface or invasive secretory organelles based on the P. vivax literature, expression during the schizont stage, and homology to P. falciparum vaccine candidates. I successfully expressed 37/39 full-length P. vivax proteins in a mammalian expression system and investigated their function using high-throughput screening methods. I screened all expressed proteins for their ability to bind reticulocytes and normocytes using a flow cytometry-based assay. I screened the complete P. vivax library against an

existing library of 40 erythrocyte surface proteins using an assay designed to detect low-affinity cell surface interactions in order to identify specific erythrocyte receptors. I also performed an intra-P. vivax library screen to identify parasite protein-protein interactions, which established that the interaction between surface proteins P12 and P41 known in P. falciparum is conserved in P. vivax, and detected several novel parasite protein-protein interactions. I then used surface plasmon resonance to biochemically confirm the intra-library interactions.

Finally, I used this protein library to characterize immune responses in P. vivax-exposed individuals. I screened the library using IgG from P. vivax-exposed individuals from Cambodia, the Solomon Islands, and Papua New Guinea (in collaboration), each with distinct transmission dynamics, in one of the first large-scale immunoepidemiological screens of a panel of full-length P. vivax merozoite proteins. Nearly all proteins were immunogenic in all 3 settings, confirming their utility in global immuno-epidemiological studies. We detected age-dependent associations for 12/34 proteins and strong correlations with clinical protection for 3 proteins, including a hypothetical protein of which little is known. Together, these data identified, characterized, and prioritized novel P. vivax vaccine targets for future pre-clinical testing in ex vivo assays.

*To Nick,
my love.*

Thank you for supporting this adventure.

Let's have some more.

*To Oscar,
my son.*

You are magical.

Keep finding the moon.

*To Elsie,
my daughter.*

You are my best surprise.

Keep dancing to your own tune.

DECLARATION

This dissertation is the result of my own work and includes nothing which is the outcome of work done in collaboration except as declared in the Acknowledgments, Appendix A, and specified in the text. I further state that no substantial part of my dissertation has already been submitted, or is being concurrently submitted for any such degree, diploma, or other qualification at the University of Cambridge or any other University of similar institution. It does not exceed the prescribed 60,000-word limit (excluding bibliography, figures and appendices) for the Biology Degree Committee.

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TABLE OF CONTENTS

1 INTRODUCTION.....	1
1.1 <i>PLASMODIUM VIVAX</i> : A MAJOR AND NEGLECTED HUMAN PATHOGEN	1
1.1.1 <i>Global burden of malaria historically</i>	1
1.1.2 <i>P. vivax epidemiology</i>	3
1.1.3 <i>Plasmodium life cycle</i>	5
1.1.4 <i>P. vivax pathology</i>	9
1.1.5 <i>Current P. vivax treatment and control measures</i>	10
1.2 <i>P. FALCIPARUM AND P. VIVAX GENOMICS</i>	12
1.2.1 <i>P. falciparum and P. vivax whole genome sequencing</i>	12
1.2.2 <i>P. falciparum and P. vivax transcriptome studies</i>	15
1.3 ERYTHROCYTE INVASION	22
1.3.1 <i>Overview of invasion</i>	22
1.3.2 <i>P. falciparum erythrocyte invasion ligands</i>	26
1.3.3 <i>P. vivax reticulocyte invasion</i>	30
1.4 NATURAL IMMUNITY TO <i>PLASMODIUM</i> INFECTIONS.....	32
1.4.1 <i>Immunity development to P. falciparum</i>	33
1.4.2 <i>Immunity development to P. vivax</i>	35
1.5 APPROACHES TO A <i>PLASMODIUM</i> VACCINE DEVELOPMENT	37
1.5.1 <i>Vaccine targets at different stages of the life cycle</i>	37
1.5.2 <i>P. falciparum vaccine development</i>	38
1.5.3 <i>P. vivax blood-stage vaccine candidate: Duffy binding protein</i>	39
1.5.4 <i>Other blood-stage candidates</i>	40
1.5.5 <i>Future P. vivax vaccine development</i>	42
1.6 CHARACTERIZATION OF <i>PLASMODIUM</i> VACCINE ANTIGENS	42
1.6.1 <i>Producing Plasmodium vaccine antigens</i>	42
1.6.2 <i>High-throughput screening of vaccine antigens</i>	44
1.7 SPECIFIC AIMS	46
2 GENERAL METHODS	48
2.1 <i>P. VIVAX SCHIZONT TRANSCRIPTOME SEQUENCING</i>	48
2.1.1 <i>Schizont enrichment of P. falciparum samples for testing</i>	48
2.1.2 <i>Comparison of RNA extraction methods</i>	49

2.1.3 Field isolate collection and enrichment for schizonts	49
2.1.4 RNA extraction of field isolates	50
2.1.5 cDNA synthesis and PCR.....	51
2.1.6 Strand-specific RNA library production	51
2.2 <i>P. vivax</i> RNA SEQUENCE ANALYSIS	54
2.2.1 Sequence mapping and quality control.....	54
2.2.2 RNA-Seq expression analysis.....	56
2.2.3 Expression variability between isolates.....	57
2.3 PRODUCTION OF RECOMBINANT <i>P. vivax</i> ECTODOMAIN LIBRARY	58
2.3.1 <i>P. vivax</i> candidate selection.....	58
2.3.2 Subcloning <i>P. vivax</i> recombinant library	59
2.3.3 <i>P. vivax</i> library expression in the HEK293E system	61
2.4 CONFIRMATION AND ASSESSMENT OF PROTEIN EXPRESSION	62
2.4.1 Confirmation of protein expression by ELISA	62
2.4.2 Normalisation of β -lactamase tagged membrane protein ectodomains	63
2.4.3 SDS-PAGE, Western blotting and NativePAGE.....	63
2.5 HIGH-THROUGHPUT FUNCTIONAL SCREENS	63
2.5.1 Erythrocyte/reticulocyte binding experiments by flow cytometry.....	63
2.5.2 Protein screens using AVEXIS.....	65
2.6 BIOPHYSICAL ANALYSIS OF PROTEIN INTERACTIONS	65
2.6.1 Purification of 6-His-tagged membrane protein ectodomains	65
2.6.2 Surface plasmon resonance (SPR).....	66
2.7 <i>P. vivax</i> SEROEPIDEMIOLOGY	66
2.7.1 Seroepidemiology of recombinant <i>P. vivax</i> proteins in Cambodian patients...66	
2.7.2 Seroepidemiology of recombinant <i>P. vivax</i> proteins in Solomon Islander patients.....	70
2.7.3 Seroepidemiology of recombinant <i>P. vivax</i> proteins in Papua New Guinea patients.....	72
2.8 COMMONLY USED BUFFERS AND SOLUTIONS	75
3 TRANSCRIPTOME PROFILING BEFORE INVASION.....	76
3.1 INTRODUCTION.....	76
3.1.1 Benefits of this study	80
3.1.2 Objectives.....	80

3.2 RESULTS	81
3.2.1 High-quality RNA extracted from <i>P. vivax</i> clinical isolates.....	81
3.2.2 Library and mapping statistics	83
3.2.3 Assessing DNA contamination.....	85
3.2.4 Assessing asexual stage time point	89
3.2.5 Assessing gametocyte contamination.....	92
3.2.6 Using RNA-Seq data to improve the <i>P. vivax</i> reference genome.....	93
3.2.7 Comparing mapping to <i>P. vivax</i> Sal 1 and <i>P. vivax</i> P01 reference genomes...	93
3.2.8 Comparing expression data between clinical isolates at genome scale	95
3.2.9 Comparing expression between 4 clinical isolates at the individual gene level	97
3.2.10 Assessing the impact of diversity and mapping on expression data	101
3.3 DISCUSSION.....	102
3.3.1 Limitations and future work.....	106
3.4 CONCLUSION.....	107
4 P. VIVAX RECOMBINANT PROTEIN LIBRARY	108
4.1 INTRODUCTION.....	108
4.1.1 Benefits of these studies	115
4.1.2 Objectives.....	115
4.2 RESULTS	116
4.2.1 <i>P. vivax</i> merozoite library candidate selection.....	116
4.2.2 <i>P. vivax</i> merozoite protein library expression in HEK293E cells	121
4.2.3 Erythrocyte binding experiments by flow cytometry.....	124
4.2.4 High-throughput protein interaction screens	127
4.2.5 Biophysical analysis with SPR.....	135
4.3 DISCUSSION.....	141
4.3.1 Limitations and future work.....	144
4.4 CONCLUSION.....	145
5 IMMUNOEPIDEMIOLOGY OF <i>P. VIVAX</i> PROTEIN LIBRARY	147
5.1 INTRODUCTION.....	147
5.1.1 Benefits of these studies	152
5.1.2 Objectives.....	153
5.2 RESULTS	153

<i>5.2.1 Antibody responses to <i>P. vivax</i> recombinant proteins in Cambodia</i>	<i>153</i>
<i>5.2.2 Antibody responses to <i>P. vivax</i> recombinant proteins in Solomon Islands and Papua New Guinea</i>	<i>163</i>
5.3 DISCUSSION.....	175
<i>5.3.1 Key findings in Cambodian plasma screens</i>	<i>175</i>
<i>5.3.2 Key findings in SI and PNG populations</i>	<i>177</i>
<i>5.3.3 Limitations and future work.....</i>	<i>179</i>
5.4 CONCLUSION.....	180
6 DISCUSSION	181
6.1 KEY REMAINING CHALLENGES IN <i>P. VIVAX</i> RESEARCH FIELD	181
<i>6.1.1 In vitro culture</i>	<i>181</i>
<i>6.1.2 Hypnozoites.....</i>	<i>182</i>
<i>6.1.3 <i>P. vivax</i> invasion</i>	<i>183</i>
<i>6.1.4 <i>P. vivax</i> infections of Duffy-negative individuals</i>	<i>185</i>
<i>6.1.5 <i>P. vivax</i> vaccine development</i>	<i>186</i>
6.2 <i>P. VIVAX</i> RESEARCH SUMMARY	189
6.3 CONCLUSION.....	192
BIBLIOGRAPHY	194
APPENDIX A: LIST OF CONTRIBUTORS.....	224
APPENDIX B: SUPPLEMENTARY TABLES	227

INDEX OF FIGURES

FIGURE 1.1: <i>P. VIVAX</i> ENDEMICITY IN 2010	5
FIGURE 1.2: <i>P. VIVAX</i> LIFE CYCLE	7
FIGURE 1.3: INTRAERYTHROCYTIC DEVELOPMENT CYCLE (IDC) OVERVIEW FOR <i>P. FALCIPARUM</i>	18
FIGURE 1.4: <i>PLASMODIUM</i> MEROZOITE STRUCTURE.....	23
FIGURE 1.5: OVERVIEW OF <i>P. FALCIPARUM</i> INVASION OF ERYTHROCYTES	25
FIGURE 1.6: AVIDITY-BASED EXTRACELLULAR INTERACTION SCREEN (AVEXIS).....	46
FIGURE 3.1: SHORT TERM <i>EX VIVO</i> CULTURE OF <i>P. VIVAX</i> CLINICAL ISOLATES	78
FIGURE 3.2: RNA-SEQ ILLUMINA LIBRARY CONSTRUCTION	79
FIGURE 3.3: MINOR DNA CONTAMINATION AND/OR INCOMPLETELY SPLICED TRANSCRIPTS IN <i>P. VIVAX</i> RNA EXTRACTIONS	83
FIGURE 3.4: ILLUMINA READ ALIGNMENTS AGAINST THE <i>P. VIVAX</i> , <i>P. FALCIPARUM</i> , AND HUMAN REFERENCE GENOMES	85
FIGURE 3.5: SEQUENCE BREADTH DISTRIBUTIONS ACROSS THE <i>P. VIVAX</i> P01 REFERENCE GENOME IN EXONS, INTRONS, AND OTHER REGIONS	86
FIGURE 3.6: SEQUENCE DEPTH DISTRIBUTIONS ACROSS THE <i>P. VIVAX</i> P01 REFERENCE GENOME IN EXONS, INTRONS, AND OTHER REGIONS	86
FIGURE 3.7: GENE EXPRESSION IN <i>P. VIVAX</i> CLINICAL ISOLATES IS MOST SIMILAR TO THE SCHIZONT STAGE IN <i>P. FALCIPARUM</i>	90
FIGURE 3.8: <i>P. VIVAX</i> CLINICAL ISOLATES CORRELATE WITH THE EARLY SCHIZONT TIME POINT FROM <i>P. VIVAX</i> MICROARRAY DATA.....	91
FIGURE 3.9: <i>P. VIVAX</i> AND <i>P. BERGHEI</i> SCHIZONT RNA-SEQ DATA ARE HIGHLY CORRELATED	92
FIGURE 3.10: EXPRESSION IN <i>P. VIVAX</i> CLINICAL ISOLATES IS HIGHLY CORRELATED	94
FIGURE 3.11: FPKM DISTRIBUTIONS ARE SIMILAR BETWEEN <i>P. VIVAX</i> CLINICAL ISOLATES	96
FIGURE 3.12: THREE METHODS FOR RANKING EXPRESSION VARIABILITY IN <i>P. VIVAX</i> CLINICAL ISOLATES	99
FIGURE 3.13: VARIABLE EXPRESSION IN <i>P. VIVAX</i> CLINICAL ISOLATES	101
FIGURE 4.1: GPI-ANCHORED <i>P. VIVAX</i> PROTEINS	110
FIGURE 4.2: BAIT AND PREY PROTEIN CONSTRUCTS	112
FIGURE 4.3: HIGH-THROUGHPUT BEAD-BASED INTERACTION SCREENING METHOD	113
FIGURE 4.4: OVERVIEW OF AVEXIS	114
FIGURE 4.5: <i>P. VIVAX</i> RECOMBINANT PROTEIN EXPRESSION DETECTED BY ELISA	122

FIGURE 4.6: WESTERN BLOTT ANALYSIS CONFIRMS EXPRESSION OF 34/37 <i>P. VIVAX</i> RECOMBINANT PROTEINS	123
FIGURE 4.7: <i>P. VIVAX</i> RECOMBINANT LIBRARY EXPRESSION AND BEAD SATURATION ASSAY BY ELISA	125
FIGURE 4.8: ERYTHROCYTE AND RETICULOCYTE BINDING TO <i>P. VIVAX</i> RECOMBINANT PROTEINS	126
FIGURE 4.9: ERYTHROCYTE PREY NORMALIZATION ASSAY	129
FIGURE 4.10: AVEXIS BETWEEN <i>P. VIVAX</i> RECOMBINANT PROTEINS AND ERYTHROCYTE RECEPTOR LIBRARY.....	130
FIGURE 4.11: <i>P. VIVAX</i> RECOMBINANT PREY NORMALIZATION.....	132
FIGURE 4.12: AVEXIS REVEALS NOVEL INTERACTIONS INVOLVING <i>P. VIVAX</i> RECOMBINANT PROTEINS	133
FIGURE 4.13: REPLICATED INTRA-LIBRARY INTERACTIONS WITH AVEXIS	134
FIGURE 4.14: SEC FOR <i>P. VIVAX</i> P12 AND P41 AND MSP7.1.....	136
FIGURE 4.15: P12, P41, AND MSP7.1 MAY EXIST AS HOMODIMERS OR OLIGOMERS.....	137
FIGURE 4.16: QUANTIFICATION OF THE <i>P. VIVAX</i> P12-P41 INTERACTION AFFINITY BY SURFACE PLASMON RESONANCE	138
FIGURE 4.17: <i>P. VIVAX</i> P12 AND <i>P. VIVAX</i> P41 SHOW NO SELF-BINDING BY SURFACE PLASMON RESONANCE.....	139
FIGURE 4.18: SURFACE PLASMON RESONANCE CONFIRMS THE <i>P. VIVAX</i> MSP3.10-MSP7.1 INTERACTION	140
FIGURE 4.19: SURFACE PLASMON RESONANCE SUPPORTS A WEAK INTERACTION BETWEEN <i>P. VIVAX</i> P12 AND <i>P. VIVAX</i> PVX_110945	140
FIGURE 5.1: IMMUNOEPIDEMIOLOGICAL STUDY SITES.....	148
FIGURE 5.2: <i>PLASMODIUM</i> MALARIA CASES IN CAMBODIA FROM 2004 TO 2014.....	149
FIGURE 5.3: MALARIA INCIDENCE IN THE SOLOMON ISLANDS FROM 1969 TO 2011.....	151
FIGURE 5.4: TESTING CAMBODIAN PATIENT PLASMA AGAINST <i>P. VIVAX</i> RECOMBINANT PROTEINS	154
FIGURE 5.5: CAMBODIAN PATIENT PLASMA IgG REACTIVITY TO FULL-LENGTH <i>P. VIVAX</i> RECOMBINANT PROTEIN ECTODOMAINS	155
FIGURE 5.6: MULTIPLE <i>P. VIVAX</i> RECOMBINANT PROTEINS ARE IMMUNOREACTIVE AND CONTAIN CONFORMATIONAL EPITOPIES	157
FIGURE 5.7: REACTIVITY IN INDIVIDUAL CAMBODIAN PLASMA SAMPLES	159
FIGURE 5.8: SEROPREVALENCE IN “ACUTE” CAMBODIAN PLASMA SAMPLES	160
FIGURE 5.9: IgG RESPONSES IN ACUTE AND CONVALESCENT CAMBODIAN PATIENT PLASMA SAMPLES (UNPAIRED).....	161

FIGURE 5.10: IgG RESPONSES IN ACUTE AND CONVALESCENT CAMBODIAN PATIENT PLASMA SAMPLES (PAIRED)	162
FIGURE 5.11: <i>P. vivax</i> RECOMBINANT PROTEINS ARE IMMUNOREACTIVE IN SI PATIENT PLASMA SAMPLES.....	166
FIGURE 5.12: SEROREACTIVITY IN SI.....	167
FIGURE 5.13: BREADTH OF ANTIGENS RECOGNIZED IN SI	170
FIGURE 5.14: AGE- AND INFECTION-ASSOCIATED INCREASES IN IgG IN SI	171
FIGURE 5.15: HIGH IgG RESPONSES TO PVX_081550, P12, AND P41 ARE ASSOCIATED WITH REDUCED INCIDENCE OF CLINICAL DISEASE	174
FIGURE 6.1: OVERVIEW OF EACH EXPERIMENTAL CHAPTER, WITH SUMMARIZED AIMS, APPROACHES, AND RESULTS.....	190

INDEX OF TABLES

TABLE 1.1: PRECLINICAL AND CLINICAL <i>PLASMODIUM</i> VACCINE CANDIDATES*	41
TABLE 2.1: EXPRESSION PLASMID BACKBONES	59
TABLE 2.2: PRIMERS	60
TABLE 2.3: PLASMA SAMPLES FROM CAMBODIAN PATIENTS WITH ACUTE VIVAX MALARIA	68
TABLE 2.4: BUFFERS, MEDIA AND SOLUTIONS	75
TABLE 3.1: PATIENT AND SAMPLE PROFILES FOR <i>P. VIVAX</i> CLINICAL ISOLATES	81
TABLE 3.2: RNA EXTRACTION RESULTS	82
TABLE 3.3: RNA EXTRACTION RESULTS AFTER DNA DIGESTION	82
TABLE 3.4: RNA-SEQ MAPPING STATISTICS TO THE <i>P. VIVAX</i> P01 GENOME	84
TABLE 3.5: EXON-TO-INTRON COVERAGE COMPARISON FOR 50 (~1% OF THE GENOME) LOWEST, MIDDLE AND HIGHEST COVERAGE GENES	88
TABLE 3.6: READS MAPPING TO <i>P. VIVAX</i> SAL 1 VS. <i>P. VIVAX</i> P01	93
TABLE 3.7: HOST AND INVASION GENES ENRICHED IN TOP 130 VARIABLY-EXPRESSED GENES FROM <i>P. VIVAX</i> SCHIZONT-STAGE CLINICAL ISOLATES	100
TABLE 4.1: <i>P. VIVAX</i> RECOMBINANT MEROZOITE PROTEINS	116
TABLE 5.1: PILOT CAMBODIAN SEROPOSITIVITY SUMMARY	156
TABLE 5.2: <i>P. VIVAX</i> RECOMBINANT PROTEINS USED IN SI AND PNG SCREENS	164
TABLE 5.3: SEROREACTIVITY IN SI COMPREHENSIVE SCREEN	168
TABLE 5.4: SEROREACTIVITY IN SI AND CAMBODIAN PARASITEMIC PLASMA SAMPLES	168
TABLE 5.5: <i>P</i> VALUES FROM ANOVA FOR SI COMPREHENSIVE SCREEN	172
TABLE 5.6: ASSOCIATION BETWEEN LEVELS OF IGG TO <i>P. VIVAX</i> MEROZOITE PROTEINS AND PROTECTION AGAINST CLINICAL MALARIA IN PNG CHILDREN*	174
SUPPLEMENTARY TABLE A: <i>P. VIVAX</i> SAL 1 REFERENCE ANNOTATION CHANGES BASED ON RNA-SEQ DATA	227
SUPPLEMENTARY TABLE B: VARIABLY-EXPRESSED GENES IN <i>P. VIVAX</i> CLINICAL ISOLATES	236
SUPPLEMENTARY TABLE C: TOP-EXPRESSED GENES UNIQUE TO RNA-SEQ DATA	242
SUPPLEMENTARY TABLE D: <i>P. VIVAX</i> RECOMBINANT PROTEIN ECTODOMAINS	246

LIST OF ABBREVIATIONS

6-cys	Six-cysteine
ACT	Artemisinin combination therapy
AMA1	Apical membrane antigen 1
Amp	Ampicillin
AVEXIS	Avidity-based extracellular interaction screening
BSG	Basigin
BLAST	Basic local alignment search tool
BSA	Bovine serum albumin
Ca2+	Calcium
COMP	Cartilage oligomeric matrix protein
CV	Column volume
DARC	Duffy antigen receptor for chemokines
DBL	Duffy binding-like
DBP	Duffy-binding protein
DMSO	Dimethyl sulfoxide
DNA	Deoxyribonucleic acid
DRM	Detergent-resistant membrane
DTT	Dithiothreitol
<i>E. coli</i>	<i>Escherichia coli</i>
EBA	Erythrocyte-binding antigen
EBL	Erythrocyte binding-like
EDTA	Ethylenediaminetetraacetic acid
EGF	Epithelial growth factor
ELISA	Enzyme-linked immunosorbent assay
FBS	Fetal bovine serum
G6PD	Glucose-6-phosphate dehydrogenase
GMEP	Global Malaria Eradication Programme
GPI	Glycosylphosphatidylinositol
HBS	HEPES-buffered saline
HEK293	Human embryonic kidney 293
6-His	Hexa-histidine
HI-FBS	Heat-inactivated fetal bovine serum
HRP	Horseradish peroxidase
IDC	Intraerythrocytic development cycle
IgG	Immunoglobulin G
IRS	Indoor residual spraying
LB	Lysogeny broth/Luria broth
LLIN	Long-lasting insecticide-treated net
LM	Light microscopy

LMVR	Laboratory of Malaria and Vector Research
Mg2+	Magnesium
MolFOB	Molecular force of blood-stage exposure
MSP	Merozoite surface protein
MTRAP	Merozoite thrombospondin-related anonymous protein
MW	Molecular weight
NAI	Naturally-acquired immunity
NCBI	National Center for Biotechnology Information
NEB	New England Biolabs
NHS	National Health Service
PBS	Phosphate-buffered saline
PCR	Polymerase chain reaction
PEI	Polyethylenimine
Pf	<i>Plasmodium falciparum</i>
Pv	<i>Plasmodium vivax</i>
PV	Parasitophorous vacuole
RBL	Reticulocyte binding-like
RCF	Relative centrifugal force
RDT	Rapid diagnostic test
RH	Reticulocyte-binding protein homologue
RNA	Ribonucleic acid
RON	Rhoptry neck protein
RPM	Revolution per minute
RPMI media	Roswell Park Memorial Institute media
RT	Room temperature
RU	Response units
SDS-PAGE	Sodium dodecyl sulphate polyacrylamide gel electrophoresis
SNP	single-nucleotide polymorphism
SOC	super optimal broth with catabolite repression
SPR	Surface plasmon resonance
TBE	Tris-borate-EDTA
V	Volts
WHO	World Health Organization
WTSI	Wellcome Trust Sanger Institute

One letter code for amino acids

A	Alanine
C	Cysteine
D	Aspartate
E	Glutamate
F	Phenylalanine

G	Glycine
H	Histidine
I	Isoleucine
K	Lysine
L	Leucine
M	Methionine
N	Asparagine
P	Proline
Q	Glutamine
R	Arginine
S	Serine
T	Threonine
V	Valine
W	Tryptophan
Y	Tyrosine