

557 Supplementary Information for

558 **Endogenous structure of antimalarial target PfATP4 reveals an apicomplexan-specific P-type**
559 **ATPase modulator**

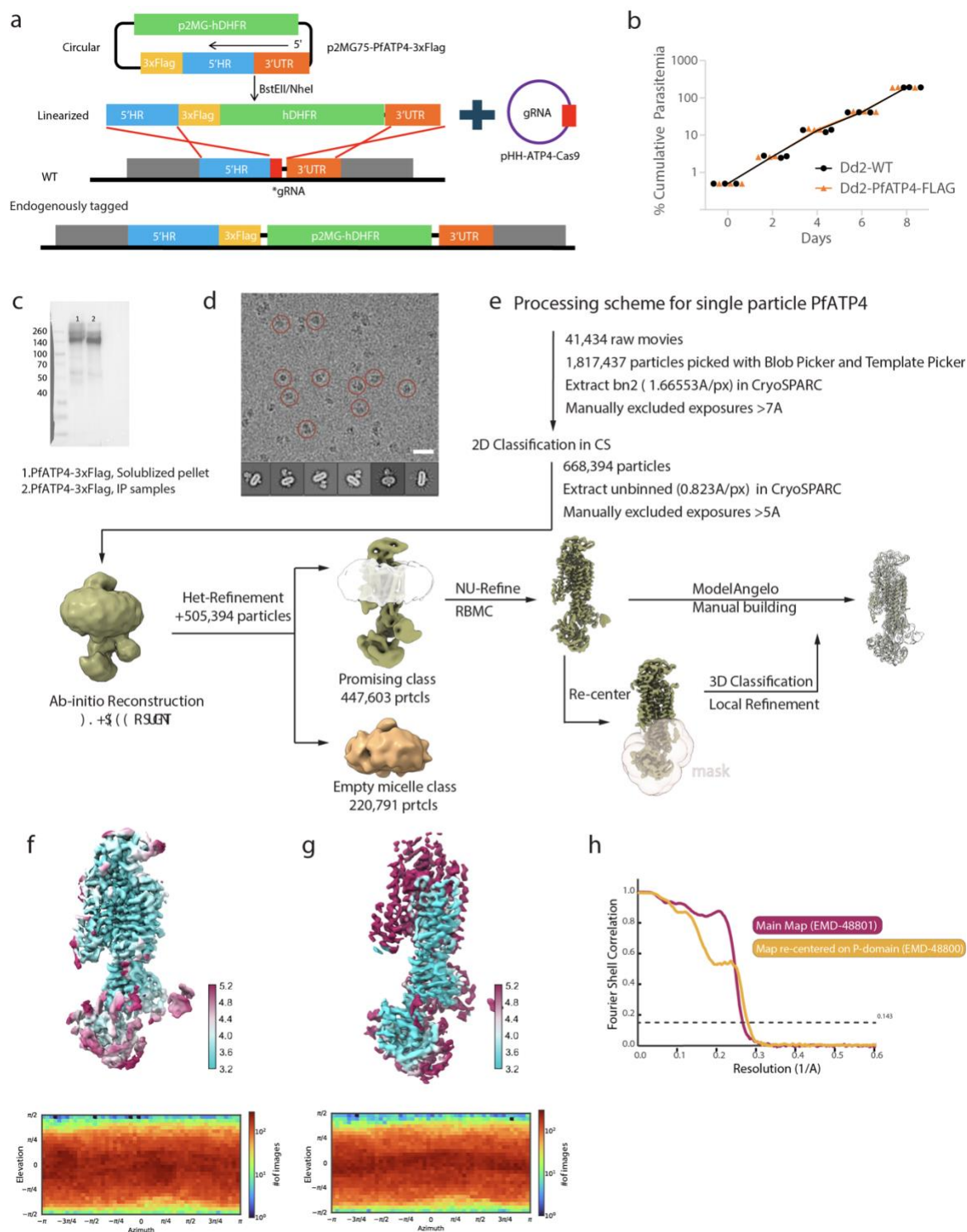
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561 **This file includes:**

562 Supplementary Figures 1-6

563 Supplementary Tables 1-5

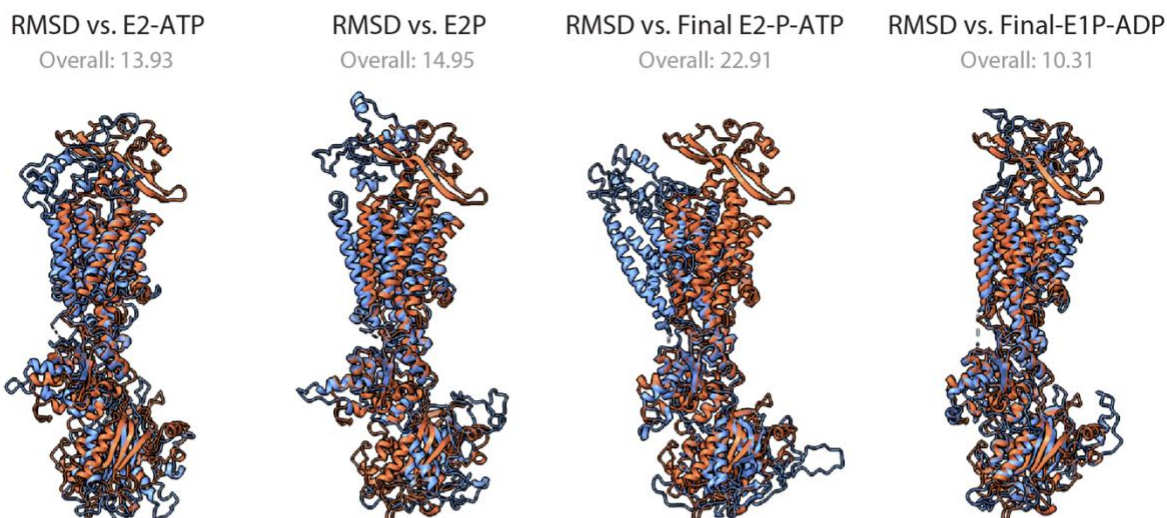
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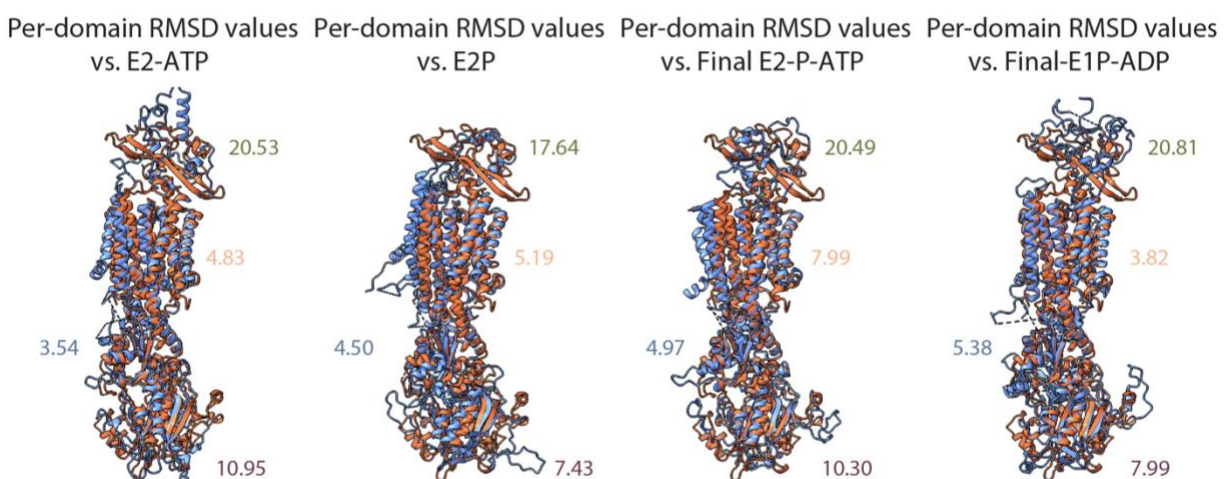
Supplementary Fig. 1: Gene editing strategy and Data Processing workflow. a, Schematic of CRISPR-Cas9 editing strategy used to tag endogenous *PfATP4* with 3xFlag epitope at the C-terminus. **b**, Growth assay of Dd2-

PfATP4-Flag parasites in comparison to Dd2-WT parasites. Triplicate samples of the parasites were fixed and stained with Sybr Green and parasitemia was calculated with Flow cytometry analysis. **c**, Western blots of solubilized and immune-purified samples probed with anti-FLAG antibody. **d**, Representative filtered cryoEM micrograph (top) and corresponding representative two-dimensional (2D) class averages of promising *Pf*ATP4 particles in multiple orientations. Scale bar = 25nm. Representative particle picks circled in red. **e**, Data processing scheme for *Pf*ATP4-*Pf*ABP with corresponding masks and steps shown. **f-g**, Final postprocessed *Pf*ATP4-*Pf*ABP maps shown colored according to local resolution (top) and angular distribution (bottom) with heat map showing number of particles for each viewing angle, as calculated in CryoSPARC. **g**, Fourier shell correlation (FSC) curves for *Pf*ATP4-*Pf*ABP to determine global resolution using the 'Gold-standard' 0.143 cut off (dotted line).

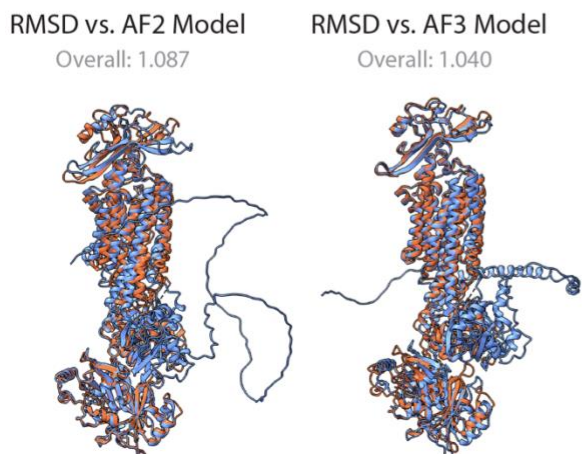
a RMSD values from comparing PfATP4 against published homology models



b Per-domain RMSD values from comparing PfATP4 against published homology models



c RMSD values from comparing PfATP4 against AF2 and AF3 models

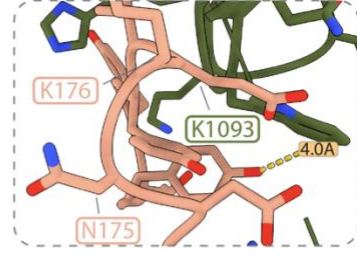
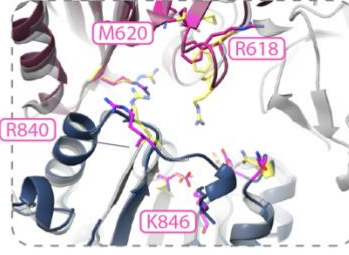
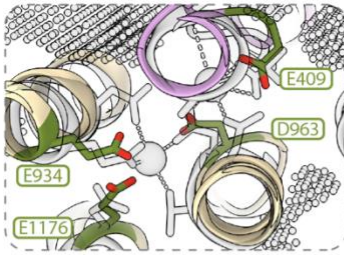


Supplementary Fig. 2: Comparison of PfATP4 against previously published homology models. a-b, Ribbon view of the *Pf*ATP4 (orange) overlayed against previously published homology models (blue) of PfATP4 in different states with overall (a) and per-domain (b) RMSD values as calculated by ChimeraX. **c,** Ribbon view of PfATP4 (orange) overlayed against AlphaFold2⁵³ (left) and AlphaFold3⁵⁴ (right) models with overall RMSD values as calculated by ChimeraX.

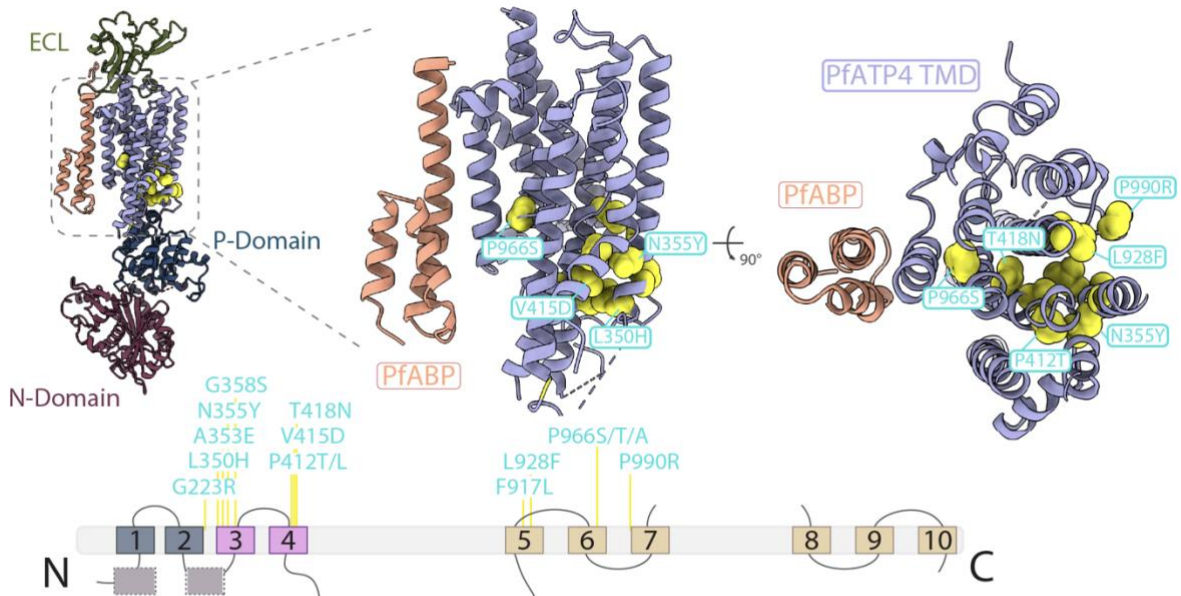
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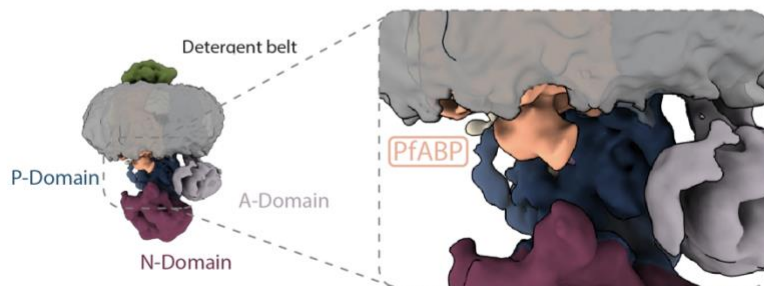
- a Na⁺ Coordination site overlayed with Ca²⁺ bound SERCA
- b ATP Binding domain overlayed against ATP-free state of SERCA
- c Pi-pi stacking between PfABP and PfATP4-ECL



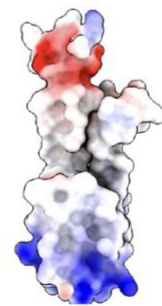
- d Mutations in PfATP4 in response to Cipargamin (KAE609)



- e PfABP extension into the parasite cytosol at low threshold



- f Cluster of charged residues at C-terminus of PfABP- TM3



Supplementary Fig. 3: Detailed views of *Pf*ATP4 and *Pf*ABP. **a**, Ribbon view of the *Pf*ATP4 Na⁺ coordination site overlayed with the ion-bound state of SERCA (PDB: [7E7S](#)), highlighting the near-identical positions of relevant side chains with cavities (indicated as patterned volumes) as calculated by pKVfinder. RMSD values for *Pf*ATP4 residues and their corresponding residue in SERCA are as follows: E1176: 1.08; E934: 1.355; D963:1.832; E409: 0.861. **b**, Detailed view of ATP-binding site of *Pf*ATP4 between the N (purple) and P (blue) domains overlayed with ATP-free state of SERCA (grey) (PDB: [7E7S](#)) comparing relevant side chains. In magenta are *Pf*ATP4 side chains and SERCA side chains are in yellow. **c**, Ribbon view highlighting Pi-pi stacking interaction between the C-terminus end of *Pf*ABP and *Pf*ATP4-ECL. Residues labelled as landmarks. **d**, Atomic model of *Pf*ATP4 highlighting mutations in response to Cipargamin (KAE609). Insets showing side (middle) and top (right) views of transmembrane domain and Na⁺ coordination site. Domain architecture of transmembrane domain of *Pf*ATP4 with all previously identified mutations noted. **e**, *Pf*ATP4-*Pf*ABP map shown at lower threshold highlighting (inset) cytosolic extension of *Pf*ABP. **f**, Molecular surface of *Pf*ATP4-TM9 and *Pf*ABP-TM3 based on electrostatic potential calculated by ChimeraX showing negatively charged region (red) at the C-terminus end of *Pf*ABP.

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a PfABP 8-day western band analysis

			% of intensity		
	aTc	no aTc		aTc	no aTc
Day 2	4393.196	157.849	Day 2	100.00	3.59
Day 4	7642.43	133.849	Day 4	100.00	1.75
Day 6	2583.447	0	Day 6	100.00	0.00
Day 8	6000.711	0	Day 8	100.00	0.00

b PfABP western band analysis

			Dd2 PfABP-HA		
			% of intensity		
	aTc	no aTc		aTc	no aTc
24 hrs	22866.04	847	24 hrs	100.00	3.70
72 hrs	14203.47	0	72 hrs	100.00	0.00

c PfATP4 western band analysis

			Dd2 PfATP4-FLAG		
			% of intensity		
	aTc	no aTc		aTc	no aTc
24 hrs	13709.31	4128.175	24 hrs	100.00	30.11
72 hrs	53808.35	0	72 hrs	100.00	0.00

Supplementary Fig. 4: Western band analysis of *PfABP* and *PfATP4*. a-c, Tables represent density of western bands measured with ImageJ software. The quantification of western bands shows complete knockdown of *PfABP* withing 24 hrs (a,b) and 70% reduction in *PfATP4* band intensity (c).

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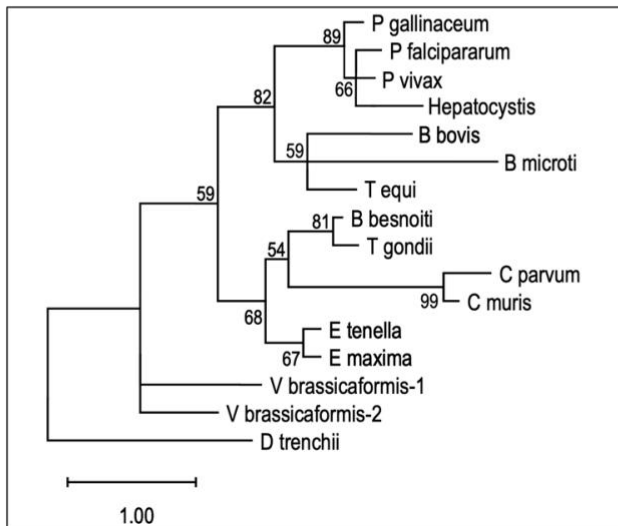
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a

<i>P. falciparum</i>	1	MGSTEDKK--EIIINLEDAYKLYNFNRDNTLSISQEN-DDCMPHSIIIDNKSNIIFNMDS	57
<i>P. vivax</i>	1	MASSSEEDK--EIIINLKDAFNLSILNRENTLLINNEN-DECFPHAILMDRKSIDLNMDS	57
<i>P. gallinaceum</i>	1	M-TGSNEEDK--GLIEFKNSYEMYNLRRENTLSIINED-DECIHHSVLNRRKNLDIFNIDS	56
<i>Hepaticocystis_sp</i>	1	MTKINIKNE--KNMYLMDTFKLYNPORENTVSIINENDYECLPHSIYVDRNRVDIFNVDV	58
<i>T. equi</i>	1	M-----	2
<i>B. bovis</i>	1	M-----	3
<i>B. microti</i>	1	M-----	1
<i>T. gondii</i>	1	MSLTANGAACAATPVESAVGSNANQ--GGVSLDLATAADSAP-----	44
<i>B. besnoiti</i>	1	MNLQTENGAVASAAAALDAVAGQHVPQEAQPAFDATAADSAP-----	45
<i>E. maxima</i>	1	M-----	1
<i>E. tenella</i>	1	MVKEGD-----	8
<i>C. muris</i>	1	M-----	1
<i>C. parvum</i>	1	M-----	1
<i>V. brassicaformis_1</i>	1	MSGGGGSGKVGSVVEVDSEAMVEVDLEE-----	32
<i>V. brassicaformis_2</i>	1	MSFEQPD-----EPMTDVGLYDIDLEE-----	24
<i>P. falciparum</i>	58	AKYQKIYKRIFNLSNRKFTD--FNFAA--SYEDVL--SDLEET--KKNE-----	106
<i>P. vivax</i>	58	TKYQKSEYKRIFNLSNRRLTDEPKFTSE--SANESK--SDLEDTQ--KKKR-----	107
<i>P. gallinaceum</i>	57	AMYQKLYKRIFNLSKSIKNEPVFASEPSISEGS--LDEDEV--KDN-----	104
<i>Hepaticocystis_sp</i>	59	AKYQKSEYKRIFNLSQVFNPKFAAPSYVEKS--SDLESV--KNES-----	107
<i>T. equi</i>	3	TSTNSTSTSLRINNSIPPLIGENDSLEPEDEKIL-----	47
<i>B. bovis</i>	4	TSARSSGSRPSYRLQSSRKVTISQTCVIPSSE--ANQHSKENEER-----	54
<i>B. microti</i>	2	MADRSSGESYKFSLKQSSLLRKE-----SSKSVNYEEKK-----	40
<i>T. gondii</i>	45	P-----HEEVGLKRRSQVHPLIKAAQED-----DVTVPVGEHSEKK-----	86
<i>B. besnoiti</i>	46	PADASVNHGSDLPTRSSQKPLLKAQKQDDESDVSLAVGGQAK-----	99
<i>E. maxima</i>	2	PQQAQSTNDTTEQMKK-----MWDAAVEEL-----DTKVFDNDTEGG-----	47
<i>E. tenella</i>	9	HGDAASATDAENPKK-----VFDGAIPEAE-----DTKVFDADTEGVD-----	53
<i>C. muris</i>	2	-----DILEE-----DINKLENKININ-----WKMKKE	24
<i>C. parvum</i>	2	-----SIFEN-----LIRKSTGLNSEKLVGSIVDEK	28
<i>V. brassicaformis_1</i>	33	VADRVIDEAT-----HAATKEEM-----EPHEIGRGPSYR-----KDDVP	71
<i>V. brassicaformis_2</i>	25	GPKAVVGEPIVGMEEAGTVVAGTVAGAPPEAR---AVPQTGVSKFFIA---AQKLD	78
<i>P. falciparum</i>	107	ITOPRINTILFFFPFICGLSYLINLK--RPSLRQYAKKALCVGSALEVIYFICGL	166
<i>P. vivax</i>	108	ILMRINTVLEFFVPFICGLSYLSLKDESSLRKVYASALCVGSALEVIYFICGL	167
<i>P. gallinaceum</i>	105	ITOPRINTILCFFPFICGLSYLINLKDESSLRKVYAKALCVGSALEVIYFICGL	164
<i>Hepaticocystis_sp</i>	108	LLVFKIYLILFFLPFICGLSYLFNLOYDASTKGRYTRALCVGSALEVIYFICGL	167
<i>T. equi</i>	48	WKLPMVFFLTITFPPLGFVNFPLNRSLNRAALYKWFNGLILGSALEVIYFICGL	107
<i>B. bovis</i>	55	ATLEIILFLVILFPIGCIIFIKRKNARKTSRDQWAYALQLOTFLEVVYFICGL	114
<i>B. microti</i>	41	PLIAGFILVLIFPIGCMTCIMKNKDNPEVYRWAFALAMGSALEVIYFICGL	100
<i>T. gondii</i>	87	ITWVVALALLAFICPPICGLAFCLNLR--EDSRITYWAVALEVGLLFVYSLVLVALL	146
<i>B. besnoiti</i>	100	IMGVVALALLFVFPFICGLAFCLSLRYPENRRYFWAVALEVGLLFVYSLVLVALL	159
<i>E. maxima</i>	48	LPYVIAFFLVVFPPLQCVAFCLSLGAPAKKAVWAEALRIGLLSFVYLLAMLL	107
<i>E. tenella</i>	54	LPYIAAFFLVVFPPLQCVAFCLSLNAPSKKAAWGEWAVRGLLFVYLLAMLL	113
<i>C. muris</i>	25	AKLPLVALILSFIFPPICGIAFLILSRAPKSPKPKVAVVYLLSALYTFIAMFL	84
<i>C. parvum</i>	29	IRLPLILFISFLFPFICGIFTLIMSRAKSPKPKIILYVYLLSALYTFIAMFL	88
<i>V. brassicaformis_1</i>	72	LTCVVAFWLSFIFPIAGCIGFCHNVTAPEETARKMMARAVLIGILSFVYLLVIA	131
<i>V. brassicaformis_2</i>	79	THAILMFFGILFPPVGCVAFGRYSTDPDNPRIKIKWALMLGSALEVIYVLYIAGV	138
<i>P. falciparum</i>	167	GQ--YIYQYDNKEIYGYTY-----	183
<i>P. vivax</i>	168	GH--YVYQYNSDFYGYTY-----	184
<i>P. gallinaceum</i>	165	GH--FLFYQYNSDRLGYTY-----	181
<i>Hepaticocystis_sp</i>	168	AR--YIYISNENHMGFTY-----	184
<i>T. equi</i>	108	HH--YVFAKTDDILGYSY-----STEIKA	130
<i>B. bovis</i>	115	HQ--YKLQSSEGLILGYSYVEIKDAVQFAS	142
<i>B. microti</i>	101	YN--IKAYSFEQDKLGFSEFM-----	118
<i>T. gondii</i>	147	SDLKLVYTGNDAAAYIGVGY-----	165
<i>B. besnoiti</i>	160	SDLKLVYTGNDKAHFGVGY-----	178
<i>E. maxima</i>	108	SE--YIYIPNSGAVLGYGF-----	124
<i>E. tenella</i>	114	SE--FYIIPNSGAVLGYGF-----	130
<i>C. muris</i>	85	LAL--VGPKYKEYVILGPAY-----	102
<i>C. parvum</i>	89	LTT--GPKRASVYHTGAAI-----	106
<i>V. brassicaformis_1</i>	132	GS--QHNNHVDNPFVNAE-----	147
<i>V. brassicaformis_2</i>	139	GSV--LCCDENPCGHN-----	153

b



Supplementary Fig. 5: Multiple sequence alignment and phylogenetic analysis of *Pf*ABP and likely orthologues. **a**, Alignment of selected orthologues highlighted with ClustalX background coloring (as implemented in Jalview)⁵⁴. NCBI BLAST searches with both BLOSUM62 and BLOSUM50 matrices were used to identify prospective orthologues, and reciprocity of the matches was checked for the orthologues in the alignment, which are listed in Supplementary Table 4. The alignment was generated using MAFFT (L-INS-i)^{55,56}. **b**, Maximum likelihood tree calculated by phyML⁵⁷ with initial conditions determined by SMS⁵⁸. The filtered alignment submitted to phyML was constructed with the aid of TCS analysis⁵⁹, and a more distant match from the dinoflagellate *Durussinium trenchii* was added to the alignment to serve as an outgroup before running the analysis. Support values are shown from 500 bootstrap repetitions, with branches having less than 50% support condensed.

1	112
PfABP-Full	MGSFTEDKKEIINLEDAKLYNFNRNTLSISQENDDCMPHSIIIDNKSLNIFNMDSAKYQKIEYKRIFNLNSRKFTDEPNFASAI SYEDVLSDEETKKNEEENDITQPRI
Pep2	-----EIIINLEDAK-----
Pep1	-----DNTLSISQENDDCMPHSIIIDNK-----
Pep3	-----
Pep4	-GSFTEDKK-----
Pep5	-----IFNLNSR-----
Pep6	-----KNEEENDITQPR-----
Pep7	-----NEEENDITQPR-----
Pep8	-----SLNIFNMDSAK-----
Pep9	-----
.....	
113	183
PfABP-Full	HTILSFFFPFGCLSYLINLKYPEPSLRQYAKKALCVGSALSVIYSFILCSLLGQYIYQYDNKEIYGTY
Pep2	-----
Pep1	-----
Pep3	-----EIIYGTY-----
Pep4	-----
Pep5	-----
Pep6	-----
Pep7	-----
Pep8	-----
Pep9	-----YPEPSLR-----
.....	

Supplementary Fig. 6: Multiple sequence alignment of mass spectrometry detected fragments of *Pf*ABP. Peptides detected in tryptic digest liquid chromatography–tandem mass spectrometry (LC–MS/MS) analysis of the purified protein corresponding to *Pf*ABP.

Supplementary Table 1: List of Oligonucleotides used for inserting epitope tag onto PATP4 and editing PfABP

Primer	Sequence
Guide RNA	CTTAGATGAAATAGTACCAA
3' UTR-F (XhoI)	TGTACATGTGGTAAAAATTTTGCTTG (612 bp)
3' UTR-R (BstEII/NheI)	TTAAATCACCCTACAACCATCTTGGTAACC
PfATP 5'HR Synthetic gene	GACGCGAGGAAAATTAGCATGCATC <u>GCTAGC</u> tata att <u>GTTACCA</u> AAGATGGTTGTAGTGGTGATTTAAC ACTTGATGAAAATGGATGGTGTAGGCCAAAGG ATAATAAAACGTCTGATGGATACAATGATGAAC TTGAGGGAATATTAAAAAAGGTTTTGAAGATG TCACGGCAAAGGTTCAAAACGTGGTAGAACA ATGGCATTATATCAGCTGTTTGGTGTGAAATG CTTAGAGCTTATACAGTAAGAAGTTGGGAACCT TTCTATAAAGTATTTAATAGAAACATGTGGATG CATTTAGCATGTAGTATATCTGCAACTTTAACA TTTCTTTCAACATGTATACCTGGTATTACTTCTA TTTTGAATACAACATGTTTGTTATGGTGGCAAT ATTTATTAGCTATATTTTGGGCTCTTTTAAATTT ATTTCTTGACGAGATTGTTCTTAAAGTaATtTATc GtAGgAAgTAcATGACaATaAAaAA <u>ccctagg</u> AATGG AGACTACAAGGACGATGACGATAAAggtGATTA TAAAGACGATGACGATAAAggaGATTATAAGA TGACGATGACAAATAA <u>cgtacg</u> tcgagttatataatattatg
PfABP Guide RNA1	TGTACATGTGGTAAAAATTTTGCTTG (612 bp)
PfABP Guide RNA1	TTAAATCACCCTACAACCATCTTGGTAACC
PfABP Synthetic gene	Ggccccttccggcgcgcttaagccgtaggatattatattatataattatat ggaatttgtaaagataatacaccataaatatataaaaagatctatctatcta tatttatattattattattttaattattctatttttttttaaaaaatttc atatttaattgcctatttttagtaaatcatatcataatttaaaatttttaatagaa ttcatttttaaacatatacatatatatatatatattattattttattta tttattttatttattgcttatcaggacattttaatttttttaagaatttgcata tttatatatatatattttttcttcttaatatatgtgttatatatattttatg tcaataaattattattgatttttttttttttttaagtaacaactatatattat aaaaaCCGCGGgatatatataaagtgtttataatattttagtaatatata actatggtatataaaaaatatatatatatatatatatatatatatattta

	tttattgtgatatgtatatttatattttttaccttttagGATTCTGAAGAAA CTAAAAAGAATGAAGAAGAGAATGATATAACTCAGCCACG TATACACACAATTCTAAGTTTTTTTTTTCCTTTTATAGgtatga aaaaaatatgataccttacatgtatatatatatatataacctgtata atatatatttgcacacctttctcttgatagGCTGCCTTCTTATTTAAT AAATTTAAAATACCCTGAACCATCTTTAAGACGCCAATACG CAAAGAAGGCATTGTGCGTTGGGAGTGCTTTAAGTGTTAT TTATTCTTTCATTCTTTGTTCCTTGTTAGGACAGTATATTTAT CAATATGATAATAAGGAAATTTATGGATATACATATcatCA GGTTACCCCCGGTTTG
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Supplementary Table 2: Cryo-EM data collection, refinement and validation statistics

	PfATP4-PfABP (EMDB-48801) (PDB 9N10)	PfATP4-PfABP recentered on the P-domain (EMDB-48800)
Data collection and processing		
Magnification	x105,000	x105,000
Voltage (kV)	300	300
Electron exposure (e-/Å²)	58	58
Defocus range (µm)	-1.5 to -2.5	-1.5 to -2.5
Pixel size (Å)	0.823	0.823
Symmetry imposed	C1	C1
Initial particle images (no.)	1,817,437	1,817,437
Final particle images (no.)	447,603	447,603
Map resolution (Å)	3.7	3.8
FSC threshold		
Map resolution range (Å)	3.1 – 6.0	3.1 – 6.3
Refinement		
Initial model used (PDB code)	De novo	
Model resolution (Å)	3.7	
FSC threshold	0.5	
Model resolution range (Å)		
Map sharpening <i>B</i> factor (Å²)	-200	
Model composition		
Non-hydrogen atoms	8,361	
Protein residues	1,064	
Ligands	0	
<i>B</i> factors (Å²)		
Protein	52	
Ligand	N/A	
R.m.s. deviations		
Bond lengths (Å)	0.003	
Bond angles (°)	0.659	
Validation		
MolProbity score	1.48	
Clashscore	5.99	
Poor rotamers (%)	0.75	
Ramachandran plot		
Favored (%)	97.16	
Allowed (%)	2.84	
Disallowed (%)	0	

Supplementary Table 3: Top twenty proteins detected with tryptic digest mass spectrometry of affinity purified *Pf*ATP4

Protein Group	Protein Names	Peptides	Intensity
A0A075B6S2;	KV229 HUMAN; KVD26 HUMAN; KVD29 HUMAN	2	353644000
PF3D7_1211900.1-p1	non-SERCA-type Ca ²⁺ -transporting P-ATPase	83	181981000
PF3D7_1315500.1-p1	conserved protein, unknown function	9	35395200
PF3D7_1436900.1-p1	histidine triad protein, putative	8	20104900
PF3D7_1456800.1-p1	V-type H (+)-translocating pyrophosphatase, putative	19	17879000
PF3D7_0722200.1-p1	rhoptry-associated leucine zipper-like protein 1	41	13848600
PF3D7_1309300.1-p1	U4/U6 small nuclear ribonucleoprotein PRP3, putative	8	8760720
PF3D7_1343900.1-p1	U4/U6 small nuclear ribonucleoprotein PRP4, putative	32	8373780
PF3D7_1468900.1-p1	zinc finger protein, putative	48	7930770
P81605	DCD HUMAN	3	7871470
PF3D7_0804800.1-p1	peptidyl-prolyl cis-trans isomerase	7	7405420
PF3D7_0818900.1-p1	heat shock protein 70	22	7167370
PF3D7_1347200.1-p1	nucleoside transporter 1	4	6074750
PF3D7_0517000.1-p1	60S ribosomal protein L12, putative	7	5942120
P68871	HBB HUMAN	9	5786940
PF3D7_1462800.1-p1	glyceraldehyde-3-phosphate dehydrogenase	17	5740020
PF3D7_1415400.1-p1	Btz domain-containing protein, putative	30	5714070
PF3D7_0818200.1-p1	14-3-3 protein	10	5617530
P11142	HSP7C HUMAN	7	5582920
PF3D7_1237700.1-p1	conserved protein, unknown function	6	5406680

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Supplementary Table 4: Non-abbreviated Versions of *Pf*ABP homologs used for Phylogenetic Analysis with corresponding accession IDs

Species	Gene locus	Uniprot ID
<i>Plasmodium falciparum</i>	PF3D7_1315500	Q8IEF9
<i>P. vivax</i>	PVP01_1416400	A0A1G4H4J0
<i>P. gallinaceum</i>	PGAL8A_00511800	A0A1J1GZ83
<i>Hepatocystis sp. ex Piliocolobus</i>	HEP_00232400	A0A653H359
<i>Theileria equi</i>	BEWA_018410	L0AVF5
<i>Babesia bovis</i>	BBOV_III010310	A7APV3
<i>B. microti</i>	BMR1_01G02745	A0A1N6LX20
<i>Toxoplasma gondii</i>	TGME49_255410	A0A125YKX2
<i>Besnoitia besnoiti</i>	BESB_083850	A0A2A9MB78
<i>Eimeria maxima</i>	EMWEY_00019600	U6MBK4
<i>E. tenella</i>	ETH2_1113800	(C-term of U6L4Y9)
<i>Cryptosporidium muris</i>	CMU_014170	B6AEX4
<i>C. parvum</i>	cgd7_4040	Q5CY19
<i>Vitrella brassicaformis</i> (1)	Vbra_8004	A0A0G4EP91
<i>V. brassicaformis</i> (2)	Vbra_4845	A0A0G4EE69
<i>Durusdinium trenchii</i>	CCMP2556_LOCUS32409	(CAK9066014.1)*

*no Uniprot entry; NCBI ID shown

Supplementary Table 5: Top twenty proteins detected with tryptic digest mass spectrometry pulled down with *Pf*ABP-HA

Protein Group	Protein Names	Peptides	Intensity
PF3D7_1211900	non-SERCA-type Ca ²⁺ -transporting P-ATPase	82	3.64E+11
PF3D7_0507100	60S ribosomal protein L4	28	2.76E+11
PF3D7_0322900	40S ribosomal protein S3A, putative	27	2.31E+11
PF3D7_1105400	40S ribosomal protein S4, putative	18	1.99E+11
PF3D7_0307200	60S ribosomal protein L7, putative	19	1.99E+11
PF3D7_1447000	40S ribosomal protein S5	20	1.88E+11
PF3D7_0818900	heat shock protein 70	40	1.7E+11
PF3D7_1424400	60S ribosomal protein L7-3, putative	18	1.7E+11
PF3D7_1424100	60S ribosomal protein L5, putative	20	1.61E+11
PF3D7_1027800	60S ribosomal protein L3	25	1.61E+11
PF3D7_1465900	40S ribosomal protein S3	16	1.54E+11
PF3D7_1341200	60S ribosomal protein L18, putative	12	1.5E+11
PF3D7_0930300	merozoite surface protein 1	98;2;1	1.49E+11
PF3D7_1338200	60S ribosomal protein L6, putative	12	1.46E+11
PF3D7_0317600	40S ribosomal protein S11, putative	17	1.44E+11
PF3D7_1130200	60S ribosomal protein P0	22	1.42E+11
PF3D7_0814000	60S ribosomal protein L13-2, putative	21	1.39E+11
PF3D7_0516900	60S ribosomal protein L2	10	1.37E+11
PF3D7_1462800	glyceraldehyde-3-phosphate dehydrogenase	26	1.36E+11
PF3D7_1408600	40S ribosomal protein S8e, putative	16	1.36E+11

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