

SUPPLEMENTARY TABLES

Supplementary Table 1. Data collection statistics for metal ion identification.

Data collection statistics	Zn²⁺ Peak	Zn²⁺ lowE	Cu²⁺ Peak	Cu²⁺ lowE
Space group	<i>P</i> 2 ₁ 2 ₁ 2 ₁	<i>P</i> 2 ₁ 2 ₁ 2 ₁	<i>P</i> 2 ₁ 2 ₁ 2 ₁	<i>P</i> 2 ₁ 2 ₁ 2 ₁
Cell dimensions				
<i>a</i> , <i>b</i> , <i>c</i> (Å)	113.5, 114.2, 149.6	113.9, 142.3, 150.4	114.2, 138.5, 151.6	114.0, 138.7, 151.4
α , β , γ (°)	90.0, 90.0, 90.0	90.0, 90.0, 90.0	90.0, 90.0, 90.0	90.0, 90.0, 90.0
Resolution (Å)	90.6-4.5 (5.0-4.5) ^a	90.8-4.5 (5.0-4.5)	91.2-4.0 (4.4-4.0)	91.1-4.5 (5.0-4.5)
Total no. observations	203091 (58522)	202269 (58194)	162680 (39482)	205189 (59218)
No. unique observations	14786 (4125)	14975 (4187)	20836 (4893)	14756 (4110)
Multiplicity	13.7 (14.2)	13.5 (13.9)	7.8 (8.1)	12.2 (6.4)
Data completeness (%)	99.9 (99.8)	99.6 (99.7)	99.7 (99.5)	99.8 (99.8)
<i>R</i> _{merge}	0.162 (0.390)	0.186 (0.577)	0.131 (0.429)	0.191 (0.440)
<i>R</i> _{r.i.m.}	0.174 (0.419)	0.191 (0.595)	0.148 (0.483)	0.203 (0.467)
<i>R</i> _{p.i.m.}	0.063 (0.152)	0.053 (0.163)	0.052 (0.168)	0.054 (0.122)
<i>I</i> / σ (<i>I</i>)	12.8 (7.2)	11.0 (4.4)	11.9 (4.8)	12.2 (6.4)

^aValues in parentheses refer to the highest resolution shell

Supplementary Table 2. Contacts at the proposed AnAPN1 dimer interface.

Domain	Molecule	Residue	Contact	Molecule	Residue
III	A	Asn529	Hydrophobic	B	Phe931
	A	Arg531	H bond, Salt bridge Hydrophobic	B	Asp653 Leu654, Arg655, Met935
	A	Ile540	Hydrophobic	B	Phe931, Leu934
	A	Ser542	Hydrophobic	B	Phe931
	A	Asp549	Hydrophobic	B	Pro553, Lys551
	A	Arg550	Hydrophobic	B	Pro553, Val552, Lys551
	A	Lys551	H bond Hydrophobic	B	Lys551 Asp549, Arg550, Val552, Pro553, Ser649, Gly650
	A	Val552	Hydrophobic	B	Pro553, Val552, Lys551
	A	Pro553	Hydrophobic	B	Lys551, Arg550, Asp549, Ser649
	A	Lys584	Hydrophobic	B	Asp926, Asn929, Gly930, Phe931, Leu934
	A	Ala585	Hydrophobic	B	Asn929, Phe931, Gly930, Leu934
	A	Arg587	Hydrophobic	B	Glu692, Leu934, Asn938
	IV	A	Glu614	Hydrophobic	B
A		Ser649	Hydrophobic	B	Lys551
A		Gly650	Hydrophobic	B	Lys551, Gly650
A		Asp653	H bond, Salt bridge	B	Arg531
A		Leu654	Hydrophobic	B	Arg531
A		Arg655	Hydrophobic	B	Arg531, Asp535
A		Arg659	Hydrophobic	B	Asp535
A		Glu692	Hydrophobic	B	Arg587
A		Asp926	Hydrophobic	B	Thr555, Ile557, Thr583, Lys584
A		Asn929	Hydrophobic	B	Thr583, Lys584, Ala585, Ala586, Arg587
A		Gly930	Hydrophobic	B	Thr583, Lys584, Ala585, Ala586, Arg587
A		Phe931	Hydrophobic	B	Ile540, Lys584, Ala585, Ala586
A		Leu934	Hydrophobic	B	Thr583, Lys584, Ala585, Ala586, Arg587
A		Met935	Hydrophobic	B	Arg531, Ser533, Ile540
A	Ser937	Hydrophobic	B	Arg587	
A	Asn938	Hydrophobic	B	Arg532, Ser533, Asp535, Asn538, Arg587	

Supplementary Table 3. Antibody Epitopes on AnAPN1. The human major histocompatibility complex II alleles present in the human population that correspond to each epitope described in this study are provided. It is important to note the numerous Class II alleles indicated in peptide 7 (P7) with several predicted binding peptides present; including alleles found in target populations in Sub-Saharan Africa, where a malaria transmission-blocking vaccine will have a tremendous impact⁸. Note that peptides 4 (P4) and 5 (P5) are part of the peptide 7 epitope recognized by monoclonal antibody 4H5B7. Peptide 1 (P1) is recognized by mAb 2A12, which does not block *P. falciparum*. The peptide 9 epitope has been described previously⁸.

Peptide	Amino acids	Sequence	MHC II Alleles
P1	60-74	DERYRLPTTSIPIHY	DR4/DR7
P4	107-121	VMHNRGLVMSSAKVS	DR1/DR3/DR4/DR7/DR8/DR11/DR13/DR15
P5	95-109	IQLQVVQATDKLVMH	DR1/DR3/ DR4/DR7/DR8/DR11/DR13/DR15
P7	98-123	QVVQATDKLVMHNRGLVMSSAKVSSL	DR1/DR3/DR4/DR7/DR8/DR11/DR13/DR15
P9	173-194	TNDDGFYVSSYVADNGERRYLA	DR3/DR4/DR8/DR11