

**Table S5. Comparison of PPlase sequences between *P. falciparum* and *P. vivax*.**

<i>P. falciparum</i>					<i>P. vivax</i>					Identity <sup>2</sup> (%)	Similarity <sup>2</sup> (%)
Name	Length (aa)	kDa	PPlase domain Region <sup>1</sup>	aa	Name	Length (aa)	kDa	PPlase domain <sup>b</sup> Region	aa		
PfCyP18.6	167	18.6	6-154	148	PvCyP18.4	167	18.4	6-154	148	88.6	98.2
PfCyP19	171	19	8-170	162	PvCyP19	170	19	7-169	162	88.9	94.7
PfCyP22 <sup>3</sup>	195	22	32-192	160	PvCyP21 <sup>3</sup>	193	21	32-192	160	79.0	89.2
PfCyP23	204	23	53-199	146	PvCyP23	203	23	52-198	146	85.3	92.6
PfCyP25	217	24.9	51-216	165	PvCyP29	262	29	96-261	165	66.8	73.6
PfCyP26	226	26	9-173	162	PvCyP26	226	26	9-173	162	87.6	94.7
PfCyP32	280	32	65-223	158	PvCyP32	276	32	65-223	158	80.0	89.6
PfCyP53	446	52.6	19-161	142	PvCyP52	456	52	19-160	141	55.4	68.7
PfCyP72	609	72.5	333-526	193	PvCyP71	616	71	322-508	186	59.0	74.1
PfCyP81	677	81	8-217	209	PvCyP65	590	65	8-194	186	37.8	54.5
PfCyP87	747	87	599-745	146	PvCyP83	737	83	589-735	146	66.4	78.3
PfFKBP-25	213	25.6	100-185	85	PvFKBP-25	215	25	102-187	85	60.0	78.2
PfFKBP-35	304	35	37-126	89	PvFKBP-34	302	34	36-125	89	79.7	90.5

<sup>1</sup> The numbers in each region indicate the starting and ending amino acid position of the PPlase domain. <sup>2</sup> The percentage of identity and similarity were obtained by comparing the amino acid sequences of *P. falciparum* PPlases with the *P. vivax* PPlases using the EMBOSS Needle tool from EMBL-EBI (<https://www.ebi.ac.uk/services>) [42]. <sup>3</sup> Proteins, PfCyP22 and PvCyP21 were considered precursors, i.e., uncleaved signal peptide. All data deposited in the table were obtained from the UniProt database [40] (<https://www.uniprot.org/>, Release 2023\_02).