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Table S1. The main ligand-receptor interactions taking place during merozoite invasion of RBCs or reticulocytes.

Ligand	Receptor	Ligand Mrz location	Kd	Enzyme treatment			Invasion process involved	Interface interaction	Receptor-ligand structure	Ref
				T	C	N				
***Pf*MSP-1$_{83}$**	**GPA**	**Surface**	**ND**	**S**	**R**	**S**	IC	MSP1 N-terminus	ND	[1]
***Pf*MSP-1$_{42}$**	Heparin	Surface	ND	-	-	-	IC	ND	ND	[2]
***Pf*MSP-1$_{19}$**	Band3	Surface	ND	R	S	R	IC	MSP1$_{19}$ C-terminal binds to Band3 720–761aa	ND	[3]
***Pf*Rh1**	Y	Rhoptries	ND	R	R	S	AR	Rh1 RII-3 500-833aa	ND	[4,5]
***Pf*Rh2b**	Z	Rhoptries	ND	R	S	R	AR	ND	ND	[6,7]
***Pf*Rh4**	CR1	Rhoptries	2.9 ± 0.2 μM	S	S	R	AR	Rh4 ^{328}N–^{588}D aa binds to CR1^{18}D-^{20}F aa	ND	[8–12]
***Pf*Rh5**	BSG	Rhoptries	1.12 ± 0.09 μM	R	R	S / R	AR	Detailed in Figure 5	X-ray crystallography PDB: 4U0Q	[13]
***Pf*CyRPA**	Ternary complex with Rh5 and Ripr	Microneme	ND	-	-	-	AR	Cyrpa ^{393}L, ^{397}L, ^{494}F and ^{498}I aa form a Rh5 groove in contact with ^{185}Y, ^{187}F and ^{226}F presented by CyRPA loops β4 and β 4–β 5	Cryo-EM PDB: 6MPV	[14,15]
***Pf*Ripr**	Ternary complex with Rh5 and CyRPA	Microneme	ND	-	-	-	AR	Ripr 196-211 aa binds to CyRPA blade 6	Cryo-EM PDB: 6MPV	[14]
***Pf*EBA-175**	GPA	Microneme	~0.26 μM	S	R	S	AR	Detailed in Figure 6	X-ray crystallography PDB: 1ZRL and 1ZRO	[16]

***Pf*EBA-140**	GPC	Microneme	ND	S	R	S	AR	Both EBA-140 DBL domains	ND	[17,18]
***Pf*EBA-181/**	Sialic residues - Band 4.1	Microneme	745 nM	R	S	S	AR	EBA-181 binds to Band 4.1 (10 kDa domain 404-471aa)	ND	[19]
***Pf*EBL-1**	GPB	Microneme	ND	R	S	S	AR	EBL-1 region 2	ND	[20]
***Pf*AMA-1**	Kx	Microneme	ND	R	S	S	TJF	AMA1 domain III	ND	[21]
***Pf*TRAMP**	SEMA7A/ Aldolase	Microneme	1.18 ± 0.40 μM	-	-	-	AR and TJF	The two TSR domains ligand / entire SEMA7A ectodomain	ND	[22]
***Pv*MSP-1$_{19}$**	GPA-Band 3?	Surface	ND	S	R	S	IC	*Pv*MSP1$_{19}$ (C-terminal region) EGF-like motifs 1 and 2 bind to RBC	ND	[23,24]
***Pv*MSP-9**	Band3?	Surface	ND	R	S	R	IC	ND	ND	[25]
***Pv*TRAg36**	Band3	Surface	ND	R	S	R	IC	ND	ND	
***Pv*TRAg38**	Band3 BSG	Surface	Band 3 and the M-*Pv*TRAg38 fragment 7.39 ± 1.24 x 10^8M BSG and the *Pv*TRAg 38 3.0 ± 0.68 10^{6} M	R R	S R	R S	IC	*Pv*TRAg38 (^{197}KWVQWKNDKIRSWLSSEW^{214}) / Band 3 *Pv*TRAg38 (161TQWGNWIKTEGRKILEAQ178) / Basigin	ND	[26,27]
***Pv*AMA1**	GPB?	Surface	1.9 ± 0.34 μM	R	S	S	TJF	*Pv*AMA-DI-II (^{81}EVENAKYRIPAGRCPVFGKG^{100}) binding to young reticulocytes (CD71^{+}CD45^{-})	ND	[28]
***Pv*RBP2b**	TfR	Rhoptries		S	S	R	AR	Ternary complex TfR1-Tf-*Pv*RBP2b TfR1TfR1 (residues 120–760) binding to two iron-	Cryo-EM PDB: 6D03, 6D04 and 6D05	[29,30]

								loaded Tf molecules (residues 1–679) with two *Pv*RBP2b molecules (residues 168–633) bound on either side.		
DBP1	DARC	Microneme	8.7 nM	R	S	S	TJF	Detailed in Figures 2 and 3	NMR, X-ray crystallography PDB: 3RRC, 4NUU, 4NUV, 5F3J, 6OAN, 6OAO 6R2S	[31–33]

ND: not determined**; Kd:** dissociation constant; **T**: trypsin; **C**: chymotrypsin; **N**: neuraminidase; **IC:** initial contact; **AR:** apical reorientation; **TJF:** tight-junction formation. GPC (Glycophorin C); TfR (Transferrin Receptor).

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