Table S1. Abundant bands identified by LC-MS/MS.
For each protein details are given including the number of matching peptides, sequence coverage, the Mas

Pb number	Protein	MWt	pI	No. of peptides	Seq coverage	Mascot Score
PB001032.02.0	Chitinase	74408	5.09	71	50%	1219

PB000865.00.0	Pb28	24644	8.43	29	40%	615
PB001334.02.0	SOAP	18884	8.7	8	25%	294
PB001298.00.0	PDI	49907	5.52	52	55%	1389

PB000233.00.0	CTRP	213160	4.85	75	29%	1917

PB001177.00.0	HSP70	72130	5.15	78	54%	1733

cot score and the individual peptide sequences, including the charge state and any modification.

Peptide sequence	Charge state
K.GGTTINHPINISHTEK.Q	3
K.GGTTINHPINISHTEKQYK.S	3
K.SLSHVDALCGDSK.N	2
K.SLSHVDALCGDSKNFVCETK.Y	3
K.SLSHVDALCGDSKNFVCETK.Y	4
R.EILEEYK.K	1
R.EILEEYKK.R	2
R.KQGIIAGYYGSWNSQGASGK.Q	3
K.QGIIAGYYGSWNSQGASGK.Q	2
K.QGIIAGYYGSWNSQGASGK.Q	3
K.QMTHSNPHVSIIYIAFAR.I	3
K.QMTHSNPHVSIIYIAFAR.I Oxidation (M)	4
K.QMTHSNPHVSIIYIAFAR.I Oxidation (M)	3
R.INMNYDASKPYNGLQK.F	3
R.INMNYDASKPYNGLQK.F	2
R.INMNYDASKPYNGLQK.F Oxidation (M)	3
R.INMNYDASKPYNGLQK.F Oxidation (M)	2
K.KHGLEFETYGMMANEIK.R 2 Oxidation (M)	3
K.KHGLEFETYGMMANEIK.R 2 Oxidation (M)	4
K.HGLEFETYGMMANEIK.R 2 Oxidation (M)	3
K.HGLEFETYGMMANEIK.R 2 Oxidation (M)	2
K.HGLEFETYGMMANEIKR.I 2 Oxidation (M)	4
K.HGLEFETYGMMANEIKR.I 2 Oxidation (M)	3
K.LIDLIR.S	1
K.DEETPYNTQYLSEQMIVNPELYK.A Oxidation (M)	3
K.ASTMLSTGTFVNVFNTAK.D	2
K.ASTMLSTGTFVNVFNTAK.D Oxidation (M)	2
K.ASTMLSTGTFVNVFNTAK.D Oxidation (M)	3
K.ASTMLSTGTFVNVFNTAKDK.I Oxidation (M)	3
K.KYDITVFLGFSIEQNR.G	4
R.GGFSPDSKNLVELVSK.A	3
K.NLVELVSK.A	2
K.NLVELVSK.A	1
K.EQMPNGAYDLDGFIDNTWTHLNPGIK.S Oxidation (M)	3
K.HNDAIWVTR.S	2
R.APGIDRYEWNLVK.V	2
R.APGIDRYEWNLVK.V	3
R.YEWNLVK.V	2
K.VCYEKACNNEAAHYYNVDYPTGTK.I	4
K.ACNNEAAHYYNVDYPTGTK.I	3

K.ACNNEAAHYYNVDYPTGTK.I	2
K.IIWKGEVFSIK.Q	3
K.IIWKGEVFSIK.Q	2
K.QWHGGPPEGPYLESYEK.L	3
K.QWHGGPPEGPYLESYEK.L	2
K.LDEYSCPGLAEWNIK.H	3
K.LDEYSCPGLAEWNIK.H	2
K.HPHKPIEVEAPYEQELDG.-	2
K.HPHKPIEVEAPYEQELDG.-	3
K.HPHKPIEVEAPYEQELDG.-	4
K.ITVDTICK.G	2
K.LIQMSNHYECK.C	2
K.LIQMSNHYECK.C	3
K.LIQMSNHYECK.C Oxidation (M)	2
K.LIQMSNHYECK.C Oxidation (M)	3
K.LIQMSNHYECKCPSGYALK.T Oxidation (M)	4
K.LIQMSNHYECKCPSGYALK.T Oxidation (M)	3
K.CPSGYALK.T	2
K.CPSGYALKTENTCEPIVK.C	3
K.TENTCEPIVK.C	2
K.AFVCMCTNGYMLSQNICKPTR.C 2 Oxidation (M)	3
R.CYNYECNAGK.C	2
K.CILDSINPNNPVCSCDIGK.I	2
K.CILDSINPNNPVCSCDIGK.I	3
K.GYKYLDSNSSNPLADVK.A	3
K.YLDSNSSNPLADVK.A	2
K.YLDSNSSNPLADVKASSR.S	3
K.SATKSDNNDIDNGPVECFSSCK.S	3
R.LIPEYNEAAIMLSEK.K	2
R.LIPEYNEAAIMLSEK.K Oxidation (M)	2
R.LIPEYNEAAIMLSEKK.S Oxidation (M)	3
K.LASVDATVER.G	2
R.GLSQEYGITGYPTMILFNK.K Oxidation (M)	2
R.GLSQEYGITGYPTMILFNKK.N Oxidation (M)	3
K.FNEVGDKNR.E	2
K.TPLNDFVAIESFPLFGEINTENYR.F	2
K.TPLNDFVAIESFPLFGEINTENYR.F	3
R.NKTHFVLLNIPEYADHAK.A	4
K.ASLGINEFPGLAYQSSEGR.Y	2
R.YLLANPQQSLK.N	2
K.DIISFFK.D	2
K.DIISFFK.D	1

K.SEPIPEEDKNAAVK.V	2
K.SEPIPEEDKNAAVK.V	3
K.VVVGNSFTDVVLNSGK.D	2
K.KLEPIYEELGR.K	3
K.KLEPIYEELGR.K	2
K.KYDHIIVAK.M	2
K.MDGTLNETSLK.E	2
K.MDGTLNETSLK.E Oxidation (M)	2
K.AGSKIPLPYEGER.T	3
K.AGSKIPLPYEGER.T	2
K.GFVDFLNK.H	2
K.GFVDFLNK.H	1
K.HSTKTPITIDDVSQSYEGSSEEL.-	3
K.TPITIDDVSQSYEGSSEEL.-	2
K.SNWVEYVVPFTEQIVK.G	2
K.IGENDIHVGILLFALR.N	2
R.NRDYITFDNDIR.Y	3
R.NRDYITFDNDIR.Y	2
R.DYITFDNDIR.Y	2
K.VNDLNDDYR.A	2
R.AGGDTYILEALK.Y	2
R.AGGDTYILEALKYSLK.K	3
K.VTILFTDGNDIHASK.S	3
K.VTILFTDGNDIHASKSEFHK.M	4
K.LLVLGVSAAEESK.L	2
K.AEWETINNITNK.L	2
K.KDVIPFSEK.L	2
K.DVIPFSEK.L	2
K.LINNLNISK.D	2
K.LINNLNISKDK.V	2
R.FSKEVITDVDYSQDTR.Y	3
R.FSKEVITDVDYSQDTR.Y	2
K.EVITDVDYSQDTR.Y	2
R.YIKNDLISVVK.G	2
R.YIKNDLISVVK.G	3
K.NDLISVVK.G	2
R.TNIVDALDYSLK.N	2
K.VTILFTDGNDTSK.T	2
K.VTILFTDGNDTSKTLAEER.N	3
K.TLAEERNMGILYR.H Oxidation (M)	3
K.WNELTGITTIITDK.I	2
R.WTMEVIPFAK.D Oxidation (M)	2
K.TNYGNGHESFIVK.T	2
K.TNYGNGHESFIVK.T	3

K.YALSNYTK.G	2
K.ITMLFTDGNDSSESDIDMYNIGSLYR.T 2 Oxidation (M)	3
K.ITMLFTDGNDSSESDIDMYNIGSLYRTER.V Oxidation (M)	4
K.ITMLFTDGNDSSESDIDMYNIGSLYRTER.V 2 Oxidation (M)	3
K.LLVIGVSMASENK.L Oxidation (M)	2
K.LLVIGVSMASENKLK.Q Oxidation (M)	3
K.LLVIGVSMASENKLK.Q Oxidation (M)	2
K.QLVGCAQNLPCPFVIK.T	2
K.QVYPFTEK.F	2
K.SGGYTYIIEALNYGLANYTHHEASR.S	4
K.SGGYTYIIEALNYGLANYTHHEASR.S	3
K.VTMLFTDGNNTNPGDK.L Oxidation (M)	2
K.VTMLFTDGNNTNPGDK.L Oxidation (M)	3
K.LLSDVSLLYK.Q	2
K.LLVVGVGASTMANLR.L Oxidation (M)	2
R.LLAGCHKTDGNCPLATK.T	4
R.LLAGCHKTDGNCPLATK.T	3
K.TDGNCPLATKTEWDNLQDISK.L	3
K.TEWDNLQDISK.L	2
K.NIINMFNIGKK.N Oxidation (M)	3
K.SINRDFDDAIAYDR.T	3
K.SINRDFDDAIAYDR.T	2
R.DFDDAIAYDR.T	2
R.VLDQMDNYFSEDK.T Oxidation (M)	2
K.IALLLTDSNNDTYEK.S	2
R.GKEQWSLYR.K	2
K.IDKLQMSYSNIINLADNLK.Y Oxidation (M)	3
K.LQMSYSNIINLADNLK.Y Oxidation (M)	2
K.LIIMLVEGK.S Oxidation (M)	2
K.VSWENLLSSVEIHNK.F	2
K.VSWENLLSSVEIHNK.F	3
R.NVSPDNEMCQTFNK.T Oxidation (M)	2
K.IETEVCSVPK.C	2
K.NPKTDTSQACNDYSLFR.E	2
K.TDTSQACNDYSLFR.E	2
K.NGRVEILNNDLGNR.I	3
K.NGRVEILNNDLGNR.I	2
R.VEILNNDLGNR.I	2
R.ITPSYVSFVDGER.K	2
R.ITPSYVSFVDGERK.V	3
R.ITPSYVSFVDGERK.V	2
K.LEATLHPTQTVFDVK.R	3
K.LEATLHPTQTVFDVKR.L	3
K.LEATLHPTQTVFDVKR.L	4

R.TLLPYEIVNNEGKPNIR.V	3
R.VQIKDKPTTFAPEQISAMVLEK.M Oxidation (M)	4
R.VQIKDKPTTFAPEQISAMVLEK.M Oxidation (M)	3
K.DKPTTFAPEQISAMVLEK.M Oxidation (M)	3
K.DKPTTFAPEQISAMVLEK.M Oxidation (M)	2
K.DKPTTFAPEQISAMVLEKMK.E 2 Oxidation (M)	4
K.MKEIAQSFLGKPVK.N Oxidation (M)	2
K.MKEIAQSFLGKPVK.N Oxidation (M)	3
K.EIAQSFLGKPVK.N	3
K.EIAQSFLGKPVK.N	2
K.NAVVTVPAYFNDAQR.Q	3
K.NAVVTVPAYFNDAQR.Q	2
R.QATKDAGAIAGLNIVR.I	3
R.QATKDAGAIAGLNIVR.I	2
K.DAGAIAGLNIVR.I	2
R.IINEPTAAALAYGLDK.K	2
R.IINEPTAAALAYGLDK.K	3
R.IINEPTAAALAYGLDKK.E	3
R.IINEPTAAALAYGLDKK.E	2
R.VMDYFIK.M	2
R.VMDYFIK.M Oxidation (M)	2
K.FEELNDDLFR.E	2
K.VLDDAKYEK.S	2
K.SKIDEIVLVGGSTR.I	3
K.SKIDEIVLVGGSTR.I	2
K.IDEIVLVGGSTR.I	2
K.IDEIVLVGGSTRIPK.I	3
K.DFFNGKEPNR.G	3
K.DFFNGKEPNR.G	2
K.SQTFSTYQDNQPAVLIQVFEGER.A	3
R.ALTKDNHLLGK.F	3
K.FELSGIPPAQR.G	2
K.NGILHVEAEDKGTGK.S	3
K.MINDAEKFADEDK.N Oxidation (M)	3
K.VESKNNLDNYIQSMK.A Oxidation (M)	3
K.NNLDNYIQSMK.A	2
K.NNLDNYIQSMK.A Oxidation (M)	2
K.EDKDTILNTIK.E	3
K.EDKDTILNTIK.E	2
K.EAEDWLNNNSNADSEALK.Q	2
K.EAEDWLNNNSNADSEALKQK.L	3
K.LKEVEAICQPIIVK.L	3
K.LKEVEAICQPIIVK.L	2
K.EVEAICQPIIVK.L	2
K.LYGQPGANTPPPGDEDVDSDEL.-	2

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Table S2 Proteins detected in the microneme enriched fraction by MudPIT shotgun proteomics

The Plasmodium berghei (Pb) number identifier of the protein detected is indicated with the Plasmodiun assigned a MIPs functional classification and the associated number of peptides, spectra and sequence co proteins are shown: Sec (secretory pathway), Api (apicoplast), ER (ER resident), Mito (mitochondrial), N predictions are also shown.

Pb number	Pf number	Description
PB001032.02.0	PFL2510w	chitinase
PB001334.02.0	PF14_0040	SOAP
PB000233.00.0	PFC0640w	CTRP
PB000247.02.0	PFL0800c	CelTOS
PB000020.03.0	PF08_0136b	WARP
PB000843.02.0	MAL13P1.56	m1-family aminopeptidase
PB001298.00.0	MAL8P1.17	protein disulfide isomerase
PB000100.01.0	PF08_0050	PPLP4
PB000676.00.0	PF14_0553	Falcipain-1*
PB000757.02.0	PF14_0425	Fructose-bisphosphate aldolase
PB000865.00.0	PF10_0302	P28
PB000266.01.0	PF10_0303	P25
PB000977.02.0	PF14_0067	LAP1
PB001526.02.0	PF13_0248	pf47*
PB000400.01.0	PFE0395c	Pf38*
PB000800.03.0	MAL7P1.12	erythrocyte membrane-associated antigen
PB105376.00.0		integral membrane protein
PB001411.02.0	PFL0620c	choline transporter*
PB000079.01.0	MAL13P1.63	Asparagine-rich protein
PB001178.00.0	PFI0880c	acid phosphatase
PB000652.01.0	PF14_0723	LAP2
PB000504.02.0	PF14_0532	LAP4
PB106570.00.0	PF10_0323	etramp10.2*
PB001124.02.0	PFC0975c	cyclophilin
PB001172.01.0	PFA0445w	LAP3
PB001116.03.0	PFL1880w	long-chain-fatty-acid--CoA ligase
PB001011.01.0	PFL1530w	asparagine-rich protein*
PB001146.01.0	PF10_0075	Asparagine-rich antigen
PB001166.02.0	PFF1035w	Pfs77 protein*
PB001108.00.0	PF10_0361	Pfemp3-like protein*
PB000924.03.0	PF10_0115	QF122 antigen
PB000861.02.0	PF13_0119	Rab11a
PB300822.00.0	PFI0155c	Rab7
PB001163.00.0	PF14_0377	vesicle-associated membrane protein (VAMP)
PB000711.03.0	PF11_0052	Syn13*
PB001003.01.0	PF11_0098	calumenin
PB000994.03.0	PFB0450w	SEC61 gamma subunit
PB000782.00.0	PF08_0113	vacuolar proton-translocating ATPase subunit A
PB000723.02.0	PF14_0361	sec62*
PB001230.00.0	PFE1195w	Ran binding protein 5
PB001083.00.0	PF14_0493	sortilin*
PB000167.01.0	PFE0625w	Rab1
PB001177.00.0	PFI0875w	Bip
PB001126.00.0	PFL0930w	clathrin heavy chain*
AAF27978.1	PF11_0461	Rab6
PB105885.00.0	MAL8P1.104	coronin binding protein

PB001185.00.0	PFC0190c	EH-domain containing protein
PB001133.02.0	PFI1670c	vacuolar ATP synthase subunit E*
PB000844.02.0	PF13_0065	vacuolar ATP synthase catalytic subunit a
PB000642.03.0	PF13_0130	vacuolar ATP synthase subunit g
PB000507.01.0	PFC0140c	N-ethylmaleimide-sensitive fusion protein
PB000267.00.0	PFD0810w	sar1
PB000857.01.0	PF11_0183	Ran/TC4
PB000159.03.0	PF11_0465	dynamin-like protein
PB000600.00.0	PF07_0072	CDPK4
PB000158.03.0	PFB0815w	CDPK1*
PB000926.02.0	PFL1845c	calcyclin binding protein
PB000675.00.0	PFA0310c	calcium-transporting ATPase
PB000562.01.0	PFB0210c	monosaccharide transporter*
PB000394.02.0	PFL0590c	p-type ATPase
PB001115.00.0	PF10_0130	nicalin*
PB000910.02.0	PF14_0421	lysophosphatidic acid acyltransferase
PB000900.00.0	MAL8P1.69	14-3-3 protein
PB000878.03.0	PFL1110c	cAMP-dependent protein kinase regulatory subunit
PB000242.02.0	PF08_0019	RACK
PB001069.00.0	PF13_0233	myosin A
PB000857.00.0	PFD1050w	alpha tubulin
PB000164.02.0	PF10_0084	beta-tubulin
PB000323.01.0	PFL2215w	actin
PB000193.03.0	PFL2225w	MTIP
PB000803.00.0	PFE0165w	actin depolymerizing factor
PB000096.01.0	PF10_0039	IMC1
PB000314.00.0	PFL1030w	IMC3
PB300823.00.0	PF07_0029	heat shock protein 86
PB300387.00.0	PF11_0380	DnaJ*
PB001037.03.0	PF11_0331	t-complex protein 1, alpha subunit
PB000731.00.0	PFI0935w	DNAJ-like molecular chaperone protein*
PB000443.01.0	PF13_0102	Sec63 homologue
PB000053.00.0	PFL1070c	HSP90
PB300768.00.0	PF11_0099	DnaJ
PB000872.00.0	PF08_0063	ClpB
PB000330.03.0	PF11_0352	protein disulfide isomerase related protein
PB001598.02.0	PFL1545c	cpn60
PB001190.00.0	PF11_0175	clpB*
PB001516.02.0	PFF1415c	DNAJ domain protein
PB001532.02.0	PF07_0029	heat shock protein 81-2
PB001074.01.0	PF11_0351	hsp70
PB001185.02.0	PFB0595w	heat shock 40 kDa protein
PB001040.00.0	PF14_0359	DnaJ-like protein
PB000879.01.0	PF10_0153	hsp60
PB000876.00.0	MAL8P1.78	small heat shock protein
PB000831.01.0	PFC0350c	T-complex protein eta subunit
PB000817.02.0	PF08_0054	heat shock 70 kDa protein
PB000733.01.0	PFL0740c	10 kd chaperonin
PB000354.02.0	PFC0285c	T-complex protein beta subunit
PB000935.01.0	PF14_0700	DnaJ homologue*
PB000738.02.0	PF13_0322	falcilysin
PB000628.00.0	PF14_0517	peptidase
PB000298.03.0	PF14_0075	plasmepsin
PB300700.00.0	PF10_0334	flavoprotein subunit of succinate dehydrogenase
PB001222.02.0	MAL13P1.221	aspartate carbamoyltransferase*
PB001022.02.0	PFC0275w	FAD-dependent glycerol-3-phosphate dehydrogenase

PB000966.02.0	PFL1550w	lipoamide dehydrogenase
PB000860.02.0	PF13_0121	dihydrolipoamide succinyltransferase
PB000370.02.0	PF08_0031	oxoglutarate/malate translocator protein*
PB000262.01.0	PF13_0272	thioredoxin-related protein
PB000185.00.0	PF13_0141	L-lactate dehydrogenase
PB000037.01.0	PF14_0368	2-Cys peroxiredoxin
PB001317.02.0	PF14_0192	glutathione reductase
PB000187.03.0	PFE1250w	long-chain fatty acid CoA ligase
PB000291.00.0	PF13_0044	carbamoyl phosphate synthetase II
PB000968.02.0	PFL1555w	cytochrome b5
PB000281.02.0	PF14_0295	ATP-specific succinyl-CoA synthetase beta subunit
PB000856.03.0	PF11_0174	cathepsin c
PB001143.00.0	PFI0695c	Phospholipid or glycerol acyltransferase*
PB000989.01.0	PFE1150w	multidrug resistance protein
PB000874.03.0	PF14_0334	NAD(P)H-dependent glutamate synthase
PB001294.02.0	PF08_0108	pepsinogen
PB300802.00.0	PF14_0615	ATP synthase (C/AC39) subunit
PB300223.00.0	PF14_0598	glyceraldehyde 3-phosphate dehydrogenase*
PB001331.02.0	PF14_0038	cytochrome c
PB000894.02.0	PFL1720w	Serine hydroxymethyltransferase
PB000613.00.0	PFF0825c	mitochondrial import receptor subunit tom40
PB000521.02.0	PFF1300w	pyruvate kinase
PB000456.03.0	PF10_0155	enolase
PB000318.00.0	PFI1105w	Phosphoglycerate kinase
PB000084.03.0	PF14_0598	glyceraldehyde-3-phosphate dehydrogenase
PB001437.02.0	PF10_0086	adenylate kinase
PB000896.02.0	PFL1725w	ATP synthase F1
PB001062.02.0	PF13_0070	branched-chain alpha keto-acid dehydrogenase
PB000990.01.0	PFE1155c	mitochondrial processing peptidase alpha subunit
PB000917.03.0	PF13_0242	isocitrate dehydrogenase (NADP), mitochondrial precursor
PB000824.00.0	PFB0795w	ATP synthase F1, alpha subunit
PB000183.00.0	PF13_0143	phosphoribosylpyrophosphate synthetase
PB000404.03.0	PF07_0047	Putative cell division cycle ATPase*
PB300214.00.0	PFB0895c	replication factor C*
PB300144.00.0	PFF0860c	histone h2a
PB000171.02.0	PFF0940c	cell division cycle protein 48
PB000338.02.0	PF14_0443	centrin
PB001391.02.0	PFA0345w	centrin*
PB001306.02.0	PF07_0054	histone h2b
PB001096.02.0	PFC0920w	histone H2A variant
PB000394.00.0	PF11_0250	high mobility group-like protein NHP2
PB000303.02.0	PFL0185c	nucleosome assembly protein 1
PB000272.03.0	PFB0445c	helicase
PB001284.02.0	PFI0930c	nucleosome assembly protein
PB001601.02.0	MAL8P1.72	high mobility group protein
PB000593.03.0	PFD0685c	chromosome-associated polypeptide
PB001018.00.0	PFF0510w	histone 3*
PB300781.00.0	PF11_0062	histone H2B
PB001051.00.0	PF11_0062	histone H2B
PB000540.03.0	PFL0145c	high mobility group protein*
PB001573.02.0	PFB0260w	proteasome 26S regulatory subunit
PB001114.01.0	PFI1085w	ubiquitin-like protein
PB000751.01.0	PF14_0632	26S proteasome subunit
PB001067.01.0	PF14_0477	signal recognition particle 54 kDa protein
PB000982.00.0	PF11_0164	peptidyl-prolyl cis-trans isomerase
PB000763.03.0	PFL0585w	Ubiquitin-like protein

PB000601.02.0	PF10_0081	26S proteasome subunit 4-like protein
PB001133.00.0	PF13_0063	26S proteasome regulatory subunit 7
PB300974.00.0	PFL2405c	hypothetical protein
PB300837.00.0	PF11_0384	hypothetical protein*
PB000031.02.0	PF14_0593	hypothetical protein*
PB000883.00.0	MAL13P1.540	hypothetical protein
PB300696.00.0	MAL13P1.342	hypothetical protein*
PB108442.00.0	MAL13P1.308	hypothetical protein
PB106275.00.0		hypothetical protein
PB105866.00.0		hypothetical protein
PB105143.00.0	PF10_0257	hypothetical protein
PB102173.00.0		hypothetical protein
PB000915.00.0	PFA0430c	hypothetical protein
PB001012.01.0	PF14_0616	hypothetical protein
PB000701.00.0	PFA0195w	hypothetical protein
PB001102.00.0	PF13_0355	hypothetical protein
PB000110.02.0	PFI1270w	hypothetical protein
PB402680.00.0	MAL8P1.66	hypothetical protein
PB000129.01.0	PF08_0008	hypothetical protein
PB001346.02.0	PFC0730w	hypothetical protein*
PB001294.00.0	PFL1685w	hypothetical protein
PB001258.02.0	MAL13P1.288	hypothetical protein*
PB001130.02.0	PFB0760w	hypothetical protein*
PB001081.01.0	PF11_0246	hypothetical protein
PB000878.02.0	PF10_0063	hypothetical protein
PB000851.02.0	PFA0490w	hypothetical protein*
PB000842.01.0	MAL13P1.121	hypothetical protein*
PB000730.02.0	PF14_0344	hypothetical protein
PB000722.00.0	MAL8P1.73	hypothetical protein*
PB000693.03.0	PFE0785c	hypothetical protein*
PB000658.00.0	PF14_0467	hypothetical protein*
PB000637.00.0	PF14_0350	hypothetical protein*
PB000607.00.0	PF08_0032	hypothetical protein*
PB000505.01.0	PFD0355c	hypothetical protein*
PB000489.03.0	PFF0835w	hypothetical protein
PB000440.03.0	PF13_0196	hypothetical protein*
PB000309.01.0	PF07_0087	hypothetical protein*
PB000253.02.0	PF11_0069	hypothetical protein
PB000248.02.0	PFL0795c	hypothetical protein*
PB000198.00.0	PF07_0089	hypothetical protein
PB000066.01.0	PF14_0159	hypothetical protein*
PB000041.00.0	PF10_0104	hypothetical protein*
PB000652.03.0	MAL13P1.203	hypothetical protein
PB000562.02.0	PF11_0262	hypothetical protein*
PB000003.00.0	MAL8P1.105	hypothetical protein*
PB000317.00.0	PF08_0008	hypothetical protein*
PB106367.00.0		hypothetical protein*
PB402566.00.0	PFA0585w	hypothetical protein*
PB402439.00.0		hypothetical protein*
PB300655.00.0	PF14_0117	hypothetical protein
PB001312.02.0	PF14_0510	hypothetical protein
PB000924.02.0	PFL1835w	hypothetical protein*
PB001440.02.0	PF13_0134	hypothetical protein*
PB001066.03.0	PF11_0055	hypothetical protein
PB000814.03.0	PFI0205w	hypothetical protein*
PB000792.02.0	PFI0230c	hypothetical protein*

PB000622.01.0	PF11_0046	hypothetical protein*
PB000616.00.0	PFL2405c	hypothetical protein
PB000587.02.0	PFL2135c	hypothetical protein*
PB000504.03.0	PFE0680w	hypothetical protein
PB000393.03.0	PFI0605c	hypothetical protein*
PB000642.01.0	MAL13P1.237	hypothetical protein
PB107535.00.0	PFI0610w	hypothetical protein
PB107035.00.0		hypothetical protein
PB101372.00.0		hypothetical protein*
PB000605.01.0	PFF0860c	hypothetical protein
PB000002.03.0	MAL13P1.336	hypothetical protein
PB403836.00.0	PFB0161c	hypothetical protein
PB000623.02.0	PFL1450c	hypothetical protein
PB001125.00.0	PF08_0033	hypothetical protein
PB001586.02.0	PF11_0374	hypothetical protein
PB001555.02.0	PF13_0058	hypothetical protein
PB001186.00.0	PFC0185w	hypothetical protein
PB001055.02.0	PF11_0437	hypothetical protein
PB001051.02.0	PF11_0440	hypothetical protein
PB000908.00.0	PFI0770c	hypothetical protein
PB000870.02.0	PFD1065c	hypothetical protein*
PB000862.00.0	PF08_0074	hypothetical protein
PB000842.03.0	PF14_0301	hypothetical protein*
PB000840.00.0	MAL8P1.95	hypothetical protein
PB000801.02.0	PF11_0485	hypothetical protein*
PB000768.03.0	PF14_0717	hypothetical protein
PB000740.02.0	PFI1455c	hypothetical protein
PB000737.02.0	PFD0520c	hypothetical protein
PB000674.01.0	PF13_0058	hypothetical protein
PB000672.02.0	PF14_0228	hypothetical protein*
PB000508.03.0	PF08_0119	hypothetical protein
PB000481.03.0	PF13_0225	hypothetical protein*
PB000419.00.0	PFF0325c	hypothetical protein*
PB000418.03.0	PFI0945w	hypothetical protein
PB000314.02.0	PFI0460w	hypothetical protein
PB000214.02.0	PFI0705w	hypothetical protein
PB000190.00.0	PFB0640c	hypothetical protein
PB000124.02.0	PFL1660c	hypothetical protein*
PB000120.01.0	PFC1065w	hypothetical protein
PB000034.01.0	PF11_0325	hypothetical protein
PB000011.03.0	MAL7P1.119	hypothetical protein
PB404179.00.0		hypothetical protein*
PB000828.02.0	PFL1660c	hypothetical protein*
PB000801.03.0	PF07_0014	hypothetical protein*
PB000592.02.0	PF14_0329	hypothetical protein
PB000536.02.0	PFA0420w	hypothetical protein*
PB000140.01.0	PF11_0207	hypothetical protein
PB000898.02.0	PFI0855w	hypothetical protein
PB000553.03.0	PF13_0161	hypothetical protein
PB000372.02.0	PF08_0030	hypothetical protein
PB000221.03.0	PF08_0075	60S ribosomal protein L13
PB001359.02.0	PF14_0448	ribosomal protein S2
PB000776.00.0	PF14_0104	eukaryotic translation initiation factor 2 gamma subunit
PB000669.01.0	PFL0460w	u6 snRNA-associated Sm-like protein
PB000541.02.0	PFE0350c	60S ribosomal subunit protein L4/L1
PB000219.02.0	PF11_0171	RNA binding protein*

PB000417.00.0	PF10_0272	ribosomal protein L3
PB000920.03.0	PF11_0065	ribosomal protein S4
PB000686.02.0	PF13_0213	60S ribosomal subunit protein L6e
PB000636.03.0	PF14_0230	ribosomal protein family L5
PB000511.03.0	PFE0975c	40S ribosomal subunit protein S24
PB000282.02.0	PF14_0296	ribosomal protein L14
PB000275.02.0	PF11_0106	60S ribosomal protein L36
PB000265.03.0	PF14_0205	ribosomal protein S25
PB001103.02.0	PF14_0391	ribosomal protein L1
PB000169.03.0	PF13_0224	60S ribosomal subunit protein L18
PB001583.02.0	PF13_0262	lysine-tRNA ligase
PB001285.00.0	PF14_0096	ribonucleoprotein homolog F21B7.26
PB001286.00.0	PFL1170w	polyadenylate-binding protein
PB001002.03.0	PF14_0241	basic transcription factor 3b
PB000296.01.0	PF11_0266	small nuclear ribonucleoprotein D1
PB000119.00.0	PFE0870w	transcriptional regulator*
PB000533.00.0	PF13_0346	ubiquitin/ribosomal fusion protein uba52
PB001107.01.0	PFE0845c	60S ribosomal protein L8
PB000603.01.0	PFC0915w	ATP-dependent RNA Helicase
PB001643.02.0	PFC1020c	40S ribosomal protein S3A
PB001521.02.0	PF13_0268	ribosomal protein L17
PB001366.02.0	MAL8P1.83	eukaryotic translation initiation factor
PB001184.00.0	PFC0290w	40S ribosomal protein S23
PB001182.00.0	PFC0300c	60S ribosomal protein L7
PB001087.02.0	MAL13P1.92	40S ribosomal protein S15
PB001076.01.0	PF10_0103	eukaryotic translation initiation factor 2, beta
PB001067.00.0	PFE1005w	40S ribosomal subunit protein S9
PB001054.02.0	PF11_0438	ribosomal protein
PB000999.03.0	PFB0830w	ribosomal protein S26e
PB000998.02.0	PFD1055w	ribosomal protein S19s
PB000967.01.0	PFF0885w	60S ribosomal protein L27a
PB000958.03.0	PFC0870w	elongation factor 1 (EF-1)
PB000942.03.0	PF13_0228	40S ribosomal subunit protein S6
PB000918.01.0	PF11_0043	60S acidic ribosomal protein p1
PB000822.02.0	PF14_0627	ribosomal protein S3
PB000761.03.0	PF14_0141	ribosomal protein L10
PB000672.01.0	PFF0700c	60S ribosomal protein L19
PB000560.01.0	PF11_0272	ribosomal protein S18
PB000550.03.0	PFL2095w	translation initiation factor SUI1
PB000523.01.0	PFC0400w	60S Acidic ribosomal protein P2
PB000465.03.0	PFL0210c	eukaryotic initiation factor 5a
PB000391.01.0	PF11_0313	ribosomal phosphoprotein P0
PB000272.01.0	PFD0770c	ribosomal protein l15
PB000222.03.0	PF08_0076	40S ribosomal protein S16
PB000194.03.0	PF13_0049	60S ribosomal protein L24
PB000180.03.0	PF13_0014	40S ribosomal protein S7 homologue
PB000178.02.0	PFE0810c	40S ribosomal subunit protein S14
PB000126.03.0	PF14_0655	RNA helicase-1
PB000148.02.0	PF10_0187	ribosomal protein L30e
PB000414.01.0	PFE0160c	Ser/Arg-rich splicing factor
PB000088.03.0	PF11_0293	multiprotein bridging factor type 1
PB104904.00.0	PF13_0171	60S ribosomal protein L23
PB001324.02.0	PF14_0579	ribosomal protein L27
PB001143.02.0	PF14_0083	ribosomal protein
PB001042.03.0	PFI0190w	ribosomal protein L32
PB000800.00.0	PF14_0486	elongation factor 2

PB000782.02.0	PFB0545c	ribosomal protein L7/L12*
PB000676.03.0	PF13_0316	40S ribosomal protein S13
PB000510.00.0	MAL13P1.209	60S ribosomal subunit porotein L18
PB000393.01.0	PF11_0312	ribosomal protein L38e
PB000367.02.0	PFE0185c	60S ribosomal subunit protein L31
PB000303.03.0	PFL2055w	40S ribosomal protein S17
PB000172.01.0	PFI1475w	merozoite surface protein 1
PB000173.03.0	PFE0120c	merozoite surface protein 8*
PB000442.03.0	PF13_0197	merozoite surface protein 7*
PB000668.01.0	PFL1385c	merozoite surface protein 9*
CAD12774.1	PFB0120w	Small exported protein 3*
PB301475.00.0	PFE0075c	rhoptry-associated protein*
PB103628.00.0	MAL7P1.208	rhoptry associated membrane antigen*
PB001562.02.0	PFI1445w	RhopH2*
PB000779.00.0	PF14_0102	rhoptry-associated protein 1
PB000405.02.0	PFC0110w	CLAG*
PB300291.00.0	PFI0265c	high molecular weight rhoptry protein 3
PB000821.01.0	PF11_0344	apical membrane antigen-1*
PB100384.00.0	PFB0120w	small exported protein 1

falciparum (Pf) orthologue. All proteins identified were manually
verage detected are indicated. The predicted localisation of
Nuc (nuclear), GPI linked or C (cytoplasmic). Multiple localisation

MIPs function	Peptide count	Spectrum count	Sequence coverage	Predicted localisation
micronemal protein	44	196	44	Sec
micronemal protein	61	1094	68.9	Sec/Api
micronemal protein	60	168	27	Sec/Api
micronemal protein	8	29	30.2	Sec
micronemal protein	12	43	34	Sec
micronemal protein	13	29	16.9	Sec/Api
micronemal protein	59	438	58.9	Sec
apical oranelles and surface	3	4	5.7	Sec
apical oranelles and surface	2	2	6.3	Sec
apical oranelles and surface	13	24	36.2	Sec
apical oranelles and surface	9	21	38.1	Sec
apical oranelles and surface	6	12	21	Sec
apical oranelles and surface	15	18	15.2	Sec
apical oranelles and surface	8	34	16.8	Sec
apical oranelles and surface	2	3	30.6	Sec
apical oranelles and surface	2	3	2	Sec
apical oranelles and surface	12	52	67.2	Sec
apical oranelles and surface	2	4	4.5	Sec
apical oranelles and surface	4	5	7.8	Sec
apical oranelles and surface	7	20	17.5	Sec/Api
apical oranelles and surface	15	30	13.5	Sec/Api
apical oranelles and surface	5	8	5	Sec/Api
apical oranelles and surface	12	54	40.5	Sec/Api
apical oranelles and surface	6	17	39	C
apical oranelles and surface	6	17	12.1	C
apical oranelles and surface	7	13	13.5	C
apical oranelles and surface	3	3	7	C
apical oranelles and surface	3	5	4.2	C
apical oranelles and surface	4	7	5.4	Mito
apical oranelles and surface	13	23	13.5	Nuc/Mito
apical oranelles and surface	9	16	13.5	Nuc
vesicle traffick	5	7	22	Sec
vesicle traffick	6	10	22.8	Sec
vesicle traffick	3	7	24	Sec
vesicle traffick	2	2	6.2	Sec
vesicle traffick	52	175	77.1	Sec
vesicle traffick	1	18	1800	Sec
vesicle traffick	10	20	13	Sec
vesicle traffick	3	3	8.6	Sec
vesicle traffick	5	13	7.5	Sec
vesicle traffick	3	4	3.2	Sec
vesicle traffick	3	4	15.1	Sec/Api
vesicle traffick	80	585	51.9	Sec/Api
vesicle traffick	3	5	4.7	C
vesicle traffick	3	4	16.4	C
vesicle traffick	2	8	10.9	C

vesicle traffick	3	3	9.1	C
vesicle traffick	2	2	9.7	C
vesicle traffick	4	6	9.5	C
vesicle traffick	3	8	28.6	C
vesicle traffick	2	2	7.4	C
vesicle traffick	4	5	25.4	C
vesicle traffick	4	5	21	C
vesicle traffick	4	6	7.8	Nuc/ER
Signalling	8	14	10.2	Sec
Signalling	2	2	5.7	Sec
Signalling	3	4	17.8	Sec
Signalling	6	9	8.7	Sec
Signalling	3	3	5.8	Sec
Signalling	8	14	9.1	Sec
Signalling	2	3	4.7	Sec/ER
Signalling	8	47	18.5	Sec/Api
Signalling	15	70	46.2	C
Signalling	2	5	3.5	C
Signalling	2	2	26.8	C
cytoskeleton	10	20	15.5	Sec
cytoskeleton	9	20	24.3	C
cytoskeleton	17	46	49	C
cytoskeleton	12	39	24.2	C
cytoskeleton	4	7	22.1	C
cytoskeleton	2	5	18	C
cytoskeleton	13	55	35	C
cytoskeleton	7	26	11.4	C
Chaperone	20	52	30.1	Sec
Chaperone	3	4	18.4	Sec
Chaperone	2	2	4.6	Sec
Chaperone	4	7	18.9	Sec
Chaperone	7	11	17.5	Sec
Chaperone	66	283	57.1	Sec
Chaperone	12	29	26.9	Sec
Chaperone	14	22	19.2	Sec
Chaperone	16	44	33.3	Sec/Api
Chaperone	18	46	25.6	Sec/Api
Chaperone	8	10	12.8	Sec/Api
Chaperone	16	27	36.8	Sec/Api
Chaperone	20	58	30.2	C
Chaperone	17	33	20.8	C
Chaperone	4	4	20.2	C
Chaperone	10	18	22.6	C
Chaperone	16	37	31.3	C
Chaperone	3	11	21.2	C
Chaperone	2	4	6.9	C
Chaperone	36	106	38	C
Chaperone	19	81	96.7	C
Chaperone	2	4	7	C
Chaperone	3	7	12	Nuc
metabolism	6	7	9.1	Sec
metabolism	9	15	12.3	Sec
metabolism	9	30	20.2	Sec
metabolism	2	2	5.1	Sec
metabolism	3	5	8.2	Sec
metabolism	13	26	23.6	Sec

metabolism	2	3	7.4	Sec
metabolism	4	8	9.2	Sec
metabolism	2	2	9.1	Sec
metabolism	3	9	12.1	Sec
metabolism	4	7	13	Sec
metabolism	5	14	30.9	Sec
metabolism	2	2	6.3	Sec
metabolism	6	8	9.4	Sec
metabolism	2	2	1.7	Sec
metabolism	3	4	43	Sec
metabolism	3	4	10.5	Sec
metabolism	18	53	31.5	Sec/Api
metabolism	3	6	9.1	Sec/Api
metabolism	20	42	17.4	Sec/ER
metabolism	3	5	1.7	Sec/ER
metabolism	9	29	21.7	C
metabolism	3	4	13.5	C
metabolism	12	33	35.6	C
metabolism	7	10	39.8	C
metabolism	2	2	6.4	C
metabolism	3	14	13	C
metabolism	8	14	19	C
metabolism	10	28	36.1	C
metabolism	8	12	20	C
metabolism	12	33	35.6	C
metabolism	14	52	59.1	C
metabolism	12	35	34	Mito
metabolism	2	3	6.8	Mito
metabolism	2	5	4.3	Mito
metabolism	3	4	10.9	Mito
metabolism	4	10	9.7	Mito
metabolism	5	11	10.5	Mito
nuclear/ cell cycle	6	7	9.4	Sec
nuclear/ cell cycle	2	4	37.9	Sec
nuclear/ cell cycle	20	146	68.4	C
nuclear/ cell cycle	10	21	13.5	C
nuclear/ cell cycle	3	7	29.8	C
nuclear/ cell cycle	3	5	15.5	C
nuclear/ cell cycle	19	572	62.6	C
nuclear/ cell cycle	11	242	34.2	C
nuclear/ cell cycle	2	5	13.9	C
nuclear/ cell cycle	3	3	10.7	C
nuclear/ cell cycle	5	11	15.2	C
nuclear/ cell cycle	5	8	14.6	C
nuclear/ cell cycle	9	33	38.9	Mito
nuclear/ cell cycle	2	3	3.4	Mito
nuclear/ cell cycle	14	44	55.9	Mito
nuclear/ cell cycle	27	379	75	Mito
nuclear/ cell cycle	27	379	75.4	Mito
nuclear/ cell cycle	3	5	32.3	Mito
Protein fate	3	3	4.3	Sec
Protein fate	4	4	4.9	Sec
Protein fate	2	2	2.2	Sec
Protein fate	2	3	5.4	Sec
Protein fate	15	83	65.4	Sec/Api
Protein fate	15	210	25.5	C

Protein fate	4	4	17	C
Protein fate	2	2	7.4	C
unknown	2	2	11	Sec
unknown	3	7	12.6	Sec
unknown	5	7	7.8	Sec
unknown	22	47	20	Sec
unknown	3	19	25.2	Sec
unknown	3	3	2.8	Sec
unknown	7	26	17.4	Sec
unknown	5	8	22.7	Sec
unknown	3	3	19.1	Sec
unknown	4	6	25.7	Sec
unknown	2	2	4.3	Sec
unknown	2	2	4	Sec
unknown	2	4	3	Sec
unknown	54	434	23.4	Sec
unknown	8	11	25.7	Sec
unknown	5	8	29.3	Sec
unknown	20	88	30	Sec
unknown	2	2	8.4	Sec
unknown	3	5	27.6	Sec
unknown	2	7	30	Sec
unknown	10	35	18.7	Sec
unknown	9	72	11.8	Sec
unknown	8	19	49.5	Sec
unknown	2	2	14.9	Sec
unknown	2	2	14.6	Sec
unknown	11	21	28.4	Sec
unknown	3	4	2.4	Sec
unknown	2	2	5.9	Sec
unknown	5	19	21.8	Sec
unknown	4	7	13.8	Sec
unknown	6	11	14.2	Sec
unknown	2	3	15.3	Sec
unknown	11	13	31.5	Sec
unknown	2	5	22	Sec
unknown	3	6	14.4	Sec
unknown	3	11	15.9	Sec
unknown	17	37	57	Sec
unknown	28	96	33.7	Sec
unknown	3	4	5.9	Sec
unknown	3	3	22.8	Sec
unknown	31	99	59.7	Sec
unknown	3	6	13.1	Sec
unknown	3	5	5	Sec
unknown	14	78	63.8	Sec/GPI
unknown	4	25	23.8	Sec/Api
unknown	10	36	93.4	Sec/Api
unknown	4	9	54	Sec/Api
unknown	8	16	24.4	Sec/Api
unknown	3	7	6.7	Sec/Api
unknown	8	11	31.6	Sec/Api
unknown	4	5	10.9	Sec/Api
unknown	15	60	22.3	Sec/Api
unknown	5	8	19.7	Sec/Api
unknown	2	4	5.3	Sec/Api

unknown	3	3	17.9	Sec/Api
unknown	5	10	10.1	Sec/Api
unknown	3	8	7.3	Sec/Api
unknown	2	3	10.4	Sec/Api
unknown	2	2	8.3	Sec/Api
unknown	6	10	20.1	C
unknown	4	13	27	C
unknown	7	12	13.4	C
unknown	2	2	30.9	C
unknown	19	62	20	C
unknown	3	9	3.2	C
unknown	6	10	31	C
unknown	4	9	12.4	C
unknown	12	32	28.5	C
unknown	5	8	7.9	C
unknown	8	51	48	C
unknown	5	13	19.7	C
unknown	4	14	36.6	C
unknown	7	30	29	C
unknown	3	6	22.6	C
unknown	2	2	18.7	C
unknown	13	45	35.5	C
unknown	3	10	18.3	C
unknown	3	4	15	C
unknown	2	2	17.6	C
unknown	29	78	49.9	C
unknown	2	2	7.4	C
unknown	2	20	20.1	C
unknown	8	51	54.3	C
unknown	2	2	4.5	C
unknown	2	29	15.2	C
unknown	2	3	11	C
unknown	4	6	19.9	C
unknown	6	10	34.8	C
unknown	9	37	22.9	C
unknown	2	3	10.8	C
unknown	2	2	2.3	C
unknown	3	8	28.3	C
unknown	3	4	6	C
unknown	3	7	14.8	C
unknown	2	2	4	Mito
unknown	7	10	50	Mito
unknown	8	30	22.2	Mito
unknown	2	2	4.6	Mito
unknown	4	17	12.7	Mito
unknown	2	3	17.4	Mito
unknown	7	14	14.2	Nuc/Mito
unknown	2	3	4.5	Nuc
unknown	33	98	24.8	Nuc
unknown	4	5	11.1	Nuc/ER
probable contaminant	9	15	31.2	Sec
probable contaminant	6	12	27.1	Sec
probable contaminant	3	4	13.1	Sec
probable contaminant	3	8	56.5	Sec
probable contaminant	9	18	26	Sec
probable contaminant	4	5	16.8	Sec

probable contaminant	7	15	13.2	Sec
probable contaminant	3	3	12.3	Sec
probable contaminant	8	18	38.8	Sec
probable contaminant	5	10	22.8	Sec
probable contaminant	4	19	21.8	Sec
probable contaminant	6	11	44.1	Sec
probable contaminant	11	54	38.5	Sec/Api
probable contaminant	9	23	32	Sec/Api
probable contaminant	4	11	6	Sec/Api
probable contaminant	6	9	27.3	C
probable contaminant	2	2	6.4	C
probable contaminant	3	6	5.3	C
probable contaminant	6	27	8.2	C
probable contaminant	4	5	18.8	C
probable contaminant	2	7	17.9	C
probable contaminant	2	2	3	C
probable contaminant	4	24	33.8	C
probable contaminant	5	8	19.1	C
probable contaminant	8	20	16.1	C
probable contaminant	6	29	22.6	C
probable contaminant	3	10	12.1	C
probable contaminant	4	7	18	C
probable contaminant	3	7	14	C
probable contaminant	2	6	10.2	C
probable contaminant	3	16	11.8	C
probable contaminant	3	7	9.5	C
probable contaminant	5	11	33.7	C
probable contaminant	5	17	31.5	C
probable contaminant	4	29	22.4	C
probable contaminant	5	20	25.4	C
probable contaminant	3	17	20.9	C
probable contaminant	4	7	28	C
probable contaminant	16	63	36.1	C
probable contaminant	11	19	63	C
probable contaminant	8	36	43.1	C
probable contaminant	5	19	27.9	C
probable contaminant	7	19	20.2	C
probable contaminant	5	11	49.4	C
probable contaminant	2	2	21.7	C
probable contaminant	9	20	73.9	C
probable contaminant	5	10	35.4	C
probable contaminant	10	21	27.7	C
probable contaminant	2	5	10.5	C
probable contaminant	10	35	51.4	C
probable contaminant	4	5	21.8	C
probable contaminant	6	18	12.9	C
probable contaminant	18	56	64.7	C
probable contaminant	7	20	19.8	C/ER
probable contaminant	3	4	17.6	Mito
probable contaminant	2	2	8.4	Mito
probable contaminant	4	12	27.9	Mito
probable contaminant	3	8	24.5	Mito
probable contaminant	8	26	43.6	Mito
probable contaminant	10	23	51.2	Mito
probable contaminant	3	6	18.3	Mito
probable contaminant	15	48	17.5	Mito

probable contaminant	2	5	6.8	Mito
probable contaminant	5	10	33.3	Mito
probable contaminant	4	9	20.5	Mito
probable contaminant	4	9	42.5	Mito
probable contaminant	3	7	29.6	Mito
probable contaminant	4	9	33.6	Mito
probable BS contaminant	50	120	27.9	Sec
probable BS contaminant	14	50	29.2	Sec
probable BS contaminant	2	6	24.6	Sec
probable BS contaminant	3	4	30.3	Sec
probable BS contaminant	6	15	33.8	Sec
probable BS contaminant	3	6	12.5	Sec/Api
probable BS contaminant	2	3	11.5	Sec
probable BS contaminant	7	16	7.9	Sec
probable BS contaminant	2	3	9.9	Sec
probable BS contaminant	4	5	5.7	Sec
BS contamination confirmed by IFA	5	8	26.6	Sec
BS contamination confirmed by IFA	4	8	11	Sec
BS contamination confirmed by IFA	2	14	20.9	Sec/Api

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Supplementary Table 3. Spectral counts of rhoptry proteins detected in the *P. berghei* ookinete m

Protein		microneme proteome	whole cell proteome
Rhoptry associated protein 1	RAP1	4	63
Rhoptry associated protein 2/ 3	RAP2/3	6	90
Rhoptry associated membrane antigen	RAMA	2	0
High molecular mass complex H1	RhopH1	4	63
High molecular mass complex H2	RhopH2	14	159
High molecular mass complex H3	RhopH3	7	57

icroneme and mixed Asexual Blood Stage proteomes.