

Supporting Information

Global proteomic analysis of the prenylated proteins in *Plasmodium falciparum* using an alkyne-modified isoprenoid analogue

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Table S1. List of total proteins identified in the proteomic analysis across three replicates. Proteins with putative prenylation motifs are highlighted in blue. Proteins with similar peptides identified are grouped into clusters. Undefined values in the spectral count and percent coverage columns are assigned with 1.

No.	Identified Proteins	Accession Number	Molecular Weight	Fold Change	Spectral counts					Percent Coverage				
					C15AikOPP		FPP		3	C15AikOPP		FPP		3
					1	2	3	1		1	2	3	1	
1	Cluster of Pfrab6, GTPase OS=Plasmodium falciparum (isolate 3D7) GN=RaB6 PE=3 SV=2 (Q8IHR8_PLAF7)	Q8IHR8_PLAF7	24 kDa	33	33	32	33	0	0	70.00%	69.60%	58.90%	1	0.00%
1.1	Pfrab6, GTPase OS=Plasmodium falciparum (isolate 3D7) GN=RaB6 PE=3 SV=2	Q8IHR8_PLAF7	24 kDa	33	33	32	33	0	0	70.00%	69.60%	58.90%	1	1
1.2	Ras-related protein Rab-44 OS=Homo sapiens GN=RaB44 PE=1 SV=1	A0A087W010_HUMAN	111 kDa	1	8	0	0	0	0	1.08%	1	1	1	0.00%
1.3	Ras-related protein Rab-39A OS=Homo sapiens GN=RaB39A PE=1 SV=2	RB39A_HUMAN	25 kDa	1	0	0	0	0	0	1	1	1	1	1
1.4	Ras-related protein Rab-6A OS=Homo sapiens GN=RaB6A PE=1 SV=3	RAB6A_HUMAN	24 kDa	1	0	0	0	0	0	1	1	1	1	1
1.5	Ras-related protein Rab-6B OS=Homo sapiens GN=RaB6B PE=1 SV=1	RAB6B_HUMAN	23 kDa	1	0	0	0	0	0	1	1	1	1	1
2	HSP40, subfamily A, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0359 PE=4 SV=1	Q8IL88_PLAF7	48 kDa	28	39	34	37	1	2	41.00%	34.70%	33.50%	1.89%	5.19%
3	Cluster of Pfrab7, GTPase OS=Plasmodium falciparum (isolate 3D7) GN=RaB7 PE=3 SV=1 (COH516_PLAF7)	COH516_PLAF7 [2]	24 kDa	26	25	27	25	0	0	58.70%	65.50%	65.50%	1	1
3.1	Pfrab7, GTPase OS=Plasmodium falciparum (isolate 3D7) GN=RaB7 PE=3 SV=1	COH516_PLAF7	24 kDa	26	25	27	25	0	0	58.70%	65.50%	65.50%	1	1
3.2	Ras-related protein Rab-7a OS=Homo sapiens GN=RaB7A PE=1 SV=1	C9J8S3_HUMAN	18 kDa	9.7	9	10	10	0	0	26.20%	26.90%	26.90%	1	1
4	Cluster of Rab1b, GTPase OS=Plasmodium falciparum (isolate 3D7) GN=RaB1b PE=4 SV=1 (Q7K6A8_PLAF7)	Q7K6A8_PLAF7 [2]	23 kDa	22	24	18	23	1	0	37.00%	35.50%	31.00%	6.79%	0.00%
4.1	Rab1b, GTPase OS=Plasmodium falciparum (isolate 3D7) GN=RaB1b PE=4 SV=1	Q7K6A8_PLAF7	23 kDa	16	19	12	17	1	0	37.00%	35.50%	31.00%	5.50%	1
4.2	Pfrab1a OS=Plasmodium falciparum (isolate 3D7) GN=RaB1a PE=3 SV=1	Q8I3W9_PLAF7	24 kDa	11	11	10	12	1	0	17.40%	21.30%	21.70%	5.31%	0.00%
4.3	Ras-related protein Rab-15 OS=Homo sapiens GN=RaB15 PE=1 SV=1	RAB15_HUMAN	24 kDa	1	11	0	9	0	0	14.60%	1	10.40%	1	1
4.4	Ras-related protein Rab-37 OS=Homo sapiens GN=RaB37 PE=1 SV=1	A8M2I4_HUMAN (+2)	22 kDa	1	7	0	7	0	0	5.76%	1	5.76%	1	1
4.5	Ras-related protein Rab-12 OS=Homo sapiens GN=RaB12 PE=1 SV=3	RAB12_HUMAN	27 kDa	1	7	0	7	0	0	4.51%	1	4.51%	1	1
4.6	Ras-related protein Rab-35 (Fragment) OS=Homo sapiens GN=RaB35 PE=1 SV=1	F5H157_HUMAN (+1)	23 kDa	1	0	0	0	0	0	1	1	1	1	1
4.7	Ras-related protein Rab-18 OS=Homo sapiens GN=RaB18 PE=1 SV=1	A0A087W011_HUMAN	19 kDa	1	13	7	0	0	0	24.70%	18.50%	1	1	1
4.8	Ras-related protein Rab-1A OS=Homo sapiens GN=RaB1A PE=1 SV=2	RAB1A_HUMAN	23 kDa	1	7	10	0	0	0	19.50%	14.60%	14.60%	1	1
4.9	Ras-related protein Rab-3A OS=Homo sapiens GN=RaB3A PE=1 SV=1	RAB3A_HUMAN	25 kDa	1	7	0	0	0	0	5.00%	1	1	1	1
4.1	Ras-related protein Rab-10 OS=Homo sapiens GN=RaB10 PE=1 SV=1	RAB10_HUMAN	23 kDa	1	0	0	0	0	0	1	1	1	1	1
4.11	Ras-related protein Rab-4B (Fragment) OS=Homo sapiens GN=RaB4B PE=1 SV=1	MOROX1_HUMAN (+1)	21 kDa	1	0	0	0	0	0	1	1	1	1	1
4.12	HCG1955540, isoform CRA_b OS=Homo sapiens GN=RaB4B PE=1 SV=1	Q6PIK3_HUMAN	14 kDa	1	0	6	0	0	0	1	19.80%	1	1	1
4.13	Ras-related protein Rab-8B (Fragment) OS=Homo sapiens GN=RaB8B PE=1 SV=1	HOYNE9_HUMAN (+1)	22 kDa	1	0	0	0	0	0	1	1	1	1	1
4.14	Ras-related protein Rab-1B OS=Homo sapiens GN=RaB1B PE=1 SV=1	RAB1B_HUMAN	22 kDa	1	0	0	0	0	0	1	1	1	1	1
4.15	Ras-related protein Rab-8A OS=Homo sapiens GN=RaB8A PE=1 SV=1	RAB8A_HUMAN	24 kDa	1	0	0	0	0	0	1	1	1	1	1
4.16	Ras-related protein Rab-15 (Fragment) OS=Homo sapiens GN=RaB15 PE=1 SV=1	QJQS4A_HUMAN	16 kDa	1	0	0	0	0	0	1	1	1	1	1
4.17	Ras-related protein Rab-30 (Fragment) OS=Homo sapiens GN=RaB30 PE=1 SV=1	E9PMJ1_HUMAN (+2)	19 kDa	1	0	0	0	0	0	1	1	1	1	1
4.18	Ras-related protein Rab-3B OS=Homo sapiens GN=RaB3B PE=1 SV=2	RAB3B_HUMAN	25 kDa	1	0	0	0	0	0	1	1	1	1	1
4.19	Ras-related protein Rab-14 OS=Homo sapiens GN=RaB14 PE=1 SV=4	RAB14_HUMAN (+1)	24 kDa	1	0	0	0	0	0	1	1	1	1	1
5	Cluster of Rab2, GTPase OS=Plasmodium falciparum (isolate 3D7) GN=RaB2 PE=3 SV=1 (Q8ISA9_PLAF7)	Q8ISA9_PLAF7	24 kDa	18	25	21	28	2	0	57.70%	56.30%	57.30%	10.80%	1
5.1	Rab2, GTPase OS=Plasmodium falciparum (isolate 3D7) GN=RaB2 PE=3 SV=1	Q8ISA9_PLAF7	24 kDa	18	25	21	28	2	0	57.70%	56.30%	57.30%	10.80%	1
5.2	Ras-related protein Rab-2A OS=Homo sapiens GN=RaB2A PE=1 SV=1	E9PKL7_HUMAN (+1)	21 kDa	1	0	0	0	0	0	1	1	1	1	1
5.3	Putative uncharacterized protein DKFp313C1541 OS=Homo sapiens GN=DKFp313C1541 PE=1 SV=1	QSHYI5_HUMAN (+1)	23 kDa	1	0	0	0	0	0	1	1	1	1	1
5.4	Ras-related protein Rab-2A (Fragment) OS=Homo sapiens GN=RaB2A PE=1 SV=1	HOYD31_HUMAN	16 kDa	1	0	0	0	0	0	1	1	1	1	1
6	Cluster of Rab5c, GTPase OS=Plasmodium falciparum (isolate 3D7) GN=RaB5c PE=3 SV=1 (Q8I274_PLAF7)	Q8I274_PLAF7	24 kDa	16	18	15	14	0	0	42.50%	34.60%	32.70%	1	1
6.1	Rab5c, GTPase OS=Plasmodium falciparum (isolate 3D7) GN=RaB5c PE=3 SV=1	Q8I274_PLAF7	24 kDa	16	18	15	14	0	0	42.50%	34.60%	32.70%	1	1
6.2	Ras-related protein Rab-5C OS=Homo sapiens GN=RaB5C PE=1 SV=2	RAB5C_HUMAN	23 kDa	1	6	4	4	0	0	5.09%	5.09%	5.09%	1	1
6.3	Ras-related protein Rab-5A OS=Homo sapiens GN=RaB5A PE=1 SV=2	RAB5A_HUMAN	24 kDa	1	0	0	0	0	0	1	1	1	1	0.00%
6.4	Ras-related protein Rab-5B (Fragment) OS=Homo sapiens GN=RaB5B PE=1 SV=1	F7VUAS_HUMAN (+2)	13 kDa	1	0	0	0	0	0	1	1	1	1	1
7	Cluster of Rab11a, GTPase OS=Plasmodium falciparum (isolate 3D7) GN=RaB11a PE=1 SV=1 (Q76NMA_PLAF7)	Q76NMA_PLAF7	25 kDa	14	12	17	12	0	0	40.70%	42.10%	41.20%	1	0.00%
7.1	Rab11a, GTPase OS=Plasmodium falciparum (isolate 3D7) GN=RaB11a PE=1 SV=1	Q76NMA_PLAF7	25 kDa	14	12	17	12	0	0	40.70%	42.10%	41.20%	1	1
7.2	Ras-related protein Rab-11A (Fragment) OS=Homo sapiens GN=RaB11A PE=3 SV=1	H3BMH2_HUMAN	18 kDa	1	0	0	0	0	0	1	1	1	1	0.00%
7.3	Ras-related protein Rab-25 OS=Homo sapiens GN=RaB25 PE=1 SV=1	A0A0C4DGX5_HUMAN (+1)	28 kDa	1	0	0	0	0	0	1	1	1	1	1
8	Rab5a, GTPase OS=Plasmodium falciparum (isolate 3D7) GN=RaB5a PE=1 SV=1	O96193_PLAF7	27 kDa	9.7	9	9	11	0	0	25.10%	28.50%	29.40%	1	1
9	Pfrab18, GTPase OS=Plasmodium falciparum (isolate 3D7) GN=RaB18 PE=3 SV=1	Q7K6B0_PLAF7	23 kDa	9	9	7	11	1	1	27.90%	24.40%	27.90%	5.47%	5.47%
10	Rab11b, GTPase (Fragment) OS=Plasmodium falciparum (isolate 3D7) GN=RaB11b PE=3 SV=1	COH5G2_PLAF7	24 kDa	9	8	10	9	0	0	30.30%	25.50%	30.80%	1	1
11	Karyopherin beta OS=Plasmodium falciparum (isolate 3D7) GN=PF1195W PE=4 SV=1	Q8I3M5_PLAF7	127 kDa	8.2	11	12	10	2	1	11.10%	12.50%	9.35%	2.05%	1.16%
12	SNARE protein, putative OS=Plasmodium falciparum (isolate 3D7) GN=PFYKt6.2 PE=4 SV=1	COH5D3_PLAF7	26 kDa	6	5	6	7	0	0	14.50%	17.60%	24.00%	1	1
13	Hexokinase OS=Plasmodium falciparum (isolate 3D7) GN=PF1155W PE=3 SV=1	C6K73L_PLAF7	55 kDa	5.8	10	9	10	3	1	12.80%	15.80%	13.00%	5.88%	2.43%
14	60S ribosomal protein L4, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF0530C PE=1 SV=1	Q8I431_PLAF7	46 kDa	5.4	10	9	8	3	1	19.20%	15.60%	16.10%	3.65%	1.95%
15	Adenosylhomocysteinase OS=Plasmodium falciparum (isolate 3D7) GN=PF1050W PE=1 SV=2	SAHH_PLAF7	54 kDa	5.4	11	8	8	2	1	9.39%	9.39%	9.39%	4.80%	2.71%
16	Glyceraldehyde-3-phosphate dehydrogenase OS=Plasmodium falciparum (isolate 3D7) GN=GAPDH PE=3 SV=1	Q8IKK7_PLAF7	37 kDa	5.3	23	17	18	6	1	38.30%	35.60%	30.60%	19.00%	2.67%
17	Eukaryotic translation initiation factor 3 subunit A OS=Plasmodium falciparum (isolate 3D7) GN=PFLO625C PE=3 SV=1	Q8IS56_PLAF7	166 kDa	5	2	8	5	0	0	1.82%	5.01%	4.21%	1	0.00%
18	Eukaryotic translation initiation factor 3 subunit L OS=Plasmodium falciparum (isolate 3D7) GN=PF0590C PE=3 SV=1	CKSW5_PLAF7	78 kDa	5	9	7	9	2	0	8.38%	10.70%	10.50%	4.27%	1
19	Cluster of Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=1 (A0A0C4DGB6_HUMAN)	A0A0C4DGB6_HUMAN	69 kDa	4.8	5	7	7	2	0	3.64%	2.48%	2.48%	2.48%	1
19.1	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	A0A0C4DGB6_HUMAN	69 kDa	1	5	7	7	2	0	3.64%	2.48%	2.48%	2.48%	1
19.2	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=1	A0A0C4DGB6_HUMAN	69 kDa	1	5	7	7	2	0	3.64%	2.48%	2.48%	2.48%	1
20	Serum albumin (Fragment) OS=Homo sapiens GN=ALB PE=1 SV=1	Q8I431_PLAF7	46 kDa	1	0	0	0	0	0	3.61%	2.46%	2.46%	2.46%	1
20.3	Helicase 45 OS=Plasmodium falciparum (isolate 3D7) GN=H45 PE=3 SV=1	H7C013_HUMAN	23 kDa	1	4	3	0	0	0	3.55%	0.00%	0.00%	1	1
21	Isoleucine-tRNA ligase, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF13_0179 PE=3 SV=1	Q8IKF0_PLAF7	45 kDa	4.4	14	9	8	4	1	24.40%	19.80%	17.60%	11.10%	2.51%
22	Falcipain OS=Plasmodium falciparum (isolate 3D7) GN=FIN PE=1 SV=1	Q8IDZ9_PLAF7	151 kDa	4.3	4	6	3	1	0	4.40%	4.64%	3.54%	0.71%	1
23	60S ribosomal protein L7-3, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0231 PE=1 SV=2	Q76NL8_PLAF7	139 kDa	4.3	2	4	7	0	0	2.77%	3.60%	6.62%	0.00%	1
24	60S ribosomal protein L13 OS=Plasmodium falciparum (isolate 3D7) GN=PF08_0075 PE=1 SV=1	Q8ILL2_PLAF7	33 kDa	4.3	5	2	6	1	0	1.60%	6.71%	9.54%	3.89%	0.00%
25	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=MAL3P1.237 PE=4 SV=1	Q8IAQ6_PLAF7	25 kDa	4.2	6	5	6	2	1	23.70%	20.50%	20.00%	6.98%	5.12%
26	Methionine-tRNA ligase, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF10_0340 PE=4 SV=1	Q8IDM3_PLAF7	42 kDa	4.2	8	6	7	2	0	24.20%	19.60%	24.70%	5.91%	1
27	Multidrug resistance protein OS=Plasmodium falciparum (isolate 3D7) GN=PFMDR1 PE=3 SV=1	Q8IU60_PLAF7	104 kDa	4.2	15	13	18	7	0	13.60%	13.20%	18.00%	5.96%	1
28	Methionine-tRNA ligase, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF05585C PE=4 SV=1	Q7K6A5_PLAF7	162 kDa	4	10	12	10	3	3	9.73%	8.67%	9.44%	2.89%	2.61%
29	Thioredoxin peroxidase 1 OS=Plasmodium falciparum (isolate 3D7) GN=TPx1 PE=4 SV=1	Q8IY8L_PLAF7	69 kDa	4	16	9	11	4	3	21.00%	13.10%	15.40%	7.95%	4.47%
30	40S ribosomal protein SA OS=Plasmodium falciparum (isolate 3D7) GN=PF10_0264 PE=1 SV=1	Q8IL80_PLAF7	22 kDa	4	8	5	3	2	0	26.70%	16.40%	8.21%	16.40%	1
31	Glutamine synthetase, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF1110W PE=3 SV=1	RSSA_PLAF7	30 kDa	4	3	5	4	0	0	6.84%	12.20%	10.60%	0.00%	1
32	Long-chain-fatty-acid-CoA ligase, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF11880W PE=4 SV=1	COH551_PLAF7	63 kDa	4	7	3	2	1	0	9.21%	4.97%	4.79%	2.03%	1
33	Long-chain-fatty-acid-CoA ligase, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF11880W PE=4 SV=1	Q8I535_PLAF7	92 kDa	3.8	6	4	5	2	0	8.08%	5.18%	6.69%	2.90%	1
34	Homocysteine adenosine transferase OS=Plasmodium falciparum (isolate 3D7) GN=PF0100C PE=4 SV=1	Q8IY99_PLAF7	71 kDa	3.7	5	13	15	4	4	6.42%	11.60%	8.26%	7.80%	4.74%
35	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=MAL8P1.95 PE=4 SV=1	HORN_HUMAN	282 kDa	3.7	2	4	5	0	0	1.40%	1.47%	3.12%	0.00%	1
36	Proteasome 26S regulatory subunit, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF80260W PE=4 SV=3	Q8HU4A_PLAF7	36 kDa	3.7	3	6	2	1	1	8.57%	11.70%	4.13%	4.13%	1
37	Asparagine-tRNA ligase, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF80525W PE=3 SV=1	O96153_PLAF7	108 kDa	3.7	3	5	3	1	0	2.59%	6.00%	2.80%	1.55%	0.00%

64	Cluster of Threonine--tRNA ligase, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF11_0270 PE=3 SV=1 (Q8IIA4, Q8IIA4_PLAF7	120 kDa	3	2	4	3	0	0	0	1.97%	4.15%	2.96%	1	1	1
64.1	Threonine--tRNA ligase, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF11_0270 PE=3 SV=1	120 kDa	3	2	4	3	0	0	0	1.97%	4.15%	2.96%	1	1	1
64.2	Threonine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=TARS PE=1 SV=3	83 kDa	1	0	0	0	0	0	0	1	1	1	1	1	1
65	4-methyl-5(β-hydroxyethyl)-thiazol monophosphate biosynthesizing enzyme OS=Plasmodium falciparum (isolate 3D7) GN=L6CKTB1_PLAF7	20 kDa	3	2	3	4	1	0	0	4.23%	16.40%	10.10%	4.23%	1	1
66	NAD synthase, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF1310w PE=4 SV=1	98 kDa	3	3	3	3	0	0	0	4.77%	4.77%	3.34%	1	1	1
67	T-complex protein 1 subunit delta OS=Plasmodium falciparum (isolate 3D7) GN=MAL13P1.283 PE=3 SV=1	58 kDa	3	3	3	3	0	0	0	7.37%	7.37%	7.37%	1	1	1
68	Rhoptery neck protein 3, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF12505c PE=4 SV=1	263 kDa	2.9	40	29	30	23	9	2	15.00%	13.80%	13.00%	10.50%	4.56%	1.40%
69	Cluster of Valine-tRNA ligase, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0589 PE=3 SV=1 (Q8IKL5_PLAI)Q8IKL5_PLAF7	128 kDa	2.8	3	4	7	2	1	2	3.49%	5.50%	4.40%	2.11%	2.11%	3.03%
69.1	Valine-tRNA ligase, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0589 PE=3 SV=1	128 kDa	2.8	3	4	7	2	1	2	3.49%	5.50%	4.40%	2.11%	2.11%	3.03%
69.2	Valine-tRNA ligase, OS=Homo sapiens GN=VARS PE=1 SV=4	140 kDa	1	1	0	0	0	0	0	1.19%	1	1	0.00%	0.00%	1
70	T-complex protein 1 subunit gamma OS=Plasmodium falciparum (isolate 3D7) GN=PF141425w PE=3 SV=1	61 kDa	2.8	4	3	4	0	0	2	7.56%	6.27%	7.75%	0.00%	1	4.43%
71	Pyridoxal 5'-phosphate synthase subunit PdxL OS=Plasmodium falciparum (isolate 3D7) GN=pdxL PE=1 SV=1	33 kDa	2.8	2	5	4	2	1	1	10.30%	12.30%	9.63%	7.97%	2.99%	2.99%
72	Cluster of Enolase OS=Plasmodium falciparum (isolate 3D7) GN=ENO PE=3 SV=1 (ENO_PLAF7)	49 kDa	2.7	21	19	23	12	8	3	24.20%	24.20%	24.20%	20.00%	10.80%	5.61%
72.1	Enolase OS=Plasmodium falciparum (isolate 3D7) GN=ENO PE=3 SV=1	49 kDa	2.7	21	19	23	12	8	3	24.20%	24.20%	24.20%	20.00%	10.80%	5.61%
72.2	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	47 kDa	1	0	2	2	0	0	0	1	4.15%	1.15%	1	1	1
72.3	Beta-enolase OS=Homo sapiens GN=ENO3 PE=1 SV=5	47 kDa	1	0	0	0	0	0	0	1	1	1	1	1	1
72.4	Enolase OS=Homo sapiens GN=ENO2 PE=1 SV=1	35 kDa	1	0	0	0	0	0	0	1	1	1	1	1	1
73	Cluster of Heat shock protein 86 OS=Plasmodium falciparum (isolate 3D7) GN=PF07_0029 PE=1 SV=1 (Q8IC05_PLAF7)	86 kDa	2.7	20	18	21	14	4	4	20.80%	15.70%	19.70%	16.50%	5.77%	6.71%
73.1	Heat shock protein 86 OS=Plasmodium falciparum (isolate 3D7) GN=PF07_0029 PE=1 SV=1	86 kDa	2.7	20	18	21	14	4	4	20.80%	15.70%	19.70%	16.50%	5.77%	6.71%
73.2	Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90A1 PE=1 SV=4	83 kDa	1	6	6	8	6	0	0	5.39%	5.39%	5.39%	5.39%	1	1
73.3	Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90A1 PE=1 SV=5	85 kDa	1	5	7	5	0	0	0	3.69%	3.69%	3.69%	3.69%	1	1
74	Carbamoyl phosphate synthetase OS=Plasmodium falciparum (isolate 3D7) GN=cpsII PE=4 SV=1	273 kDa	2.7	2	4	2	1	1	1	1.14%	1.68%	0.84%	0.46%	0.42%	0.51%
75	Peptidase, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0517 PE=3 SV=1	89 kDa	2.7	9	8	7	5	3	0	5.63%	7.98%	8.90%	5.37%	4.71%	0.00%
76	Adenosine deaminase, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF10_0289 PE=4 SV=1	42 kDa	2.7	10	6	8	7	1	1	19.90%	12.80%	15.30%	11.20%	3.27%	4.90%
77	Exportin 1, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF03135c PE=4 SV=2	148 kDa	2.7	3	2	0	0	0	0	2.87%	1.83%	1.91%	0.00%	1	1
78	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=PF0435w PE=4 SV=1	154 kDa	2.7	3	4	1	0	0	0	1.62%	3.01%	1.16%	0.00%	0.00%	1
79	Histidine-tRNA ligase, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0428 PE=3 SV=1	134 kDa	2.7	2	5	0	0	0	0	1.50%	3.27%	1	0.00%	1	1
80	DNAJ-like molecular chaperone protein, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF0935w PE=4 SV=1	43 kDa	2.7	4	3	1	1	1	0	11.10%	8.11%	4.86%	3.24%	3.24%	1
81	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=PF11_0191 PE=4 SV=1	69 kDa	2.7	2	3	3	0	0	0	4.88%	6.57%	6.73%	1	1	1
82	DEAD box helicase, UAP56 OS=Plasmodium falciparum (isolate 3D7) GN=UAP56 PE=4 SV=1	52 kDa	2.7	2	3	3	0	0	1	4.60%	5.91%	5.47%	1	1	2.41%
83	40S ribosomal protein S19, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF01055w PE=1 SV=1	20 kDa	2.7	3	4	1	0	0	0	11.20%	13.50%	5.29%	5.29%	1	1
84	M1-family aminopeptidase OS=Plasmodium falciparum (isolate 3D7) GN=MAL13P1.56 PE=1 SV=1	126 kDa	2.6	9	11	9	5	2	4	8.29%	7.93%	6.54%	4.24%	1.75%	4.61%
85	Heat shock protein 70 (HSP70) homologue OS=Plasmodium falciparum (isolate 3D7) GN=PF10875w PE=3 SV=1	72 kDa	2.6	29	29	26	21	4	7	33.10%	29.90%	26.80%	27.10%	6.90%	11.80%
86	Cluster of 14-3-3 protein, putative OS=Plasmodium falciparum (isolate 3D7) GN=MAL8P1.69 PE=3 SV=1 (C0H4V6_PLAF7)	30 kDa	2.6	12	11	11	9	3	1	23.30%	27.50%	23.30%	27.10%	13.00%	6.11%
86.1	14-3-3 protein, putative OS=Plasmodium falciparum (isolate 3D7) GN=MAL8P1.69 PE=3 SV=1	30 kDa	2.6	12	11	11	9	3	1	23.30%	27.50%	23.30%	27.10%	13.00%	6.11%
86.2	14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1	28 kDa	1	0	0	0	1	0	0	1	1	1	4.03%	0.00%	1
86.3	14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3	28 kDa	1	0	0	0	0	0	0	1	1	1	1	0.00%	1
86.4	14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1	28 kDa	1	0	0	0	1	0	0	1	1	1	4.08%	1	1
86.5	14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1	28 kDa	1	0	0	0	0	0	0	1	1	1	1	1	1
86.6	14-3-3 protein epsilon OS=Homo sapiens GN=YWHA E PE=1 SV=1	29 kDa	1	0	0	0	0	0	0	1	1	1	1	1	1
86.7	14-3-3 protein gamma OS=Homo sapiens GN=YWHA G PE=1 SV=2	28 kDa	1	0	0	0	0	0	0	1	1	1	1	1	1
86.8	14-3-3 protein eta OS=Homo sapiens GN=YWHA H PE=1 SV=4	28 kDa	1	0	0	0	0	0	0	1	1	1	1	1	1
87	Cell division cycle protein 48 homologue, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF0940c PE=3 SV=1	92 kDa	2.6	1	7	5	3	1	0	1.45%	9.30%	7.00%	4.59%	1.33%	1
88	Cytoadherence linked asexual protein 9 (CLAG9) OS=Plasmodium falciparum (isolate 3D7) GN=CLAG9 PE=4 SV=1	160 kDa	2.5	18	21	11	13	6	1	9.85%	9.40%	5.07%	5.45%	3.81%	0.60%
89	Glutamate--tRNA ligase, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF13_0257 PE=3 SV=1	101 kDa	2.5	9	8	8	5	3	2	10.80%	9.04%	9.04%	6.84%	4.17%	1.39%
90	Elongation factor 1-gamma, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF13_0214 PE=4 SV=2	48 kDa	2.5	4	2	4	2	0	0	5.11%	5.11%	8.03%	5.11%	1	2.43%
91	60S ribosomal protein L12, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF0850c PE=3 SV=2	18 kDa	2.5	4	2	4	2	0	0	27.90%	17.00%	22.40%	5.45%	1	7.88%
92	Merozoite surface protein 1 OS=Plasmodium falciparum (isolate 3D7) GN=MSP1 PE=4 SV=1	196 kDa	2.4	21	11	19	18	0	2	12.30%	6.98%	12.60%	10.00%	0.00%	1.28%
93	Cluster of Selenin-binding protein 1 OS=Homo sapiens GN=SELENBP1 PE=1 SV=2 (SBP1_HUMAN)	52 kDa	2.4	3	5	4	3	1	0	6.57%	9.75%	9.75%	6.57%	5.88%	1
93.1	Selenin-binding protein 1 OS=Homo sapiens GN=SELENBP1 PE=1 SV=2	52 kDa	2.4	3	5	4	3	1	0	6.57%	9.75%	9.75%	6.57%	5.88%	1
94	Calcium-binding protein 1 (Fragment) OS=Homo sapiens GN=SELENBP1 PE=1 SV=7	34 kDa	1	2	0	1	0	0	0	5.88%	1	5.88%	1	1	1
94	Calcium-binding protein 1 (Fragment) OS=Homo sapiens GN=SELENBP1 PE=1 SV=7	34 kDa	1	2	0	1	0	0	0	5.88%	1	5.88%	1	1	1
95	ADP/ATP transporter on adenylate translocase OS=Plasmodium falciparum (isolate 3D7) GN=PF10_0366 PE=3 SV=1	Q8IU34_PLAF7	2.3	4	1	2	1	0	1	7.97%	4.32%	4.32%	4.32%	0.00%	4.32%
96	Eukaryotic translation initiation factor 3 subunit C OS=Plasmodium falciparum (isolate 3D7) GN=PF10310c PE=3 SV=1	Q8ISV3_PLAF7	116 kDa	2.3	4	2	1	0	0	4.57%	2.13%	1.12%	1.12%	1	1
97	Sortilin, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0493 PE=4 SV=1	Q8IKV8_PLAF7	102 kDa	2.3	2	2	3	0	1	2.57%	1.33%	1.47%	1	1.79%	1
98	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=PF12120w PE=4 SV=1	Q8I4Y9_PLAF7	155 kDa	2.3	3	2	2	0	0	2.47%	1.23%	1.47%	0.00%	0.00%	1
99	Suprabasin OS=Homo sapiens GN=SBSN PE=1 SV=2	SBSN_HUMAN	61 kDa	2.3	0	3	3	0	0	0.00%	8.47%	9.15%	0.00%	1	1
100	6-phosphogluconate dehydrogenase, decarboxylating OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0520 PE=3 SV=1	Q8IKT2_PLAF7	53 kDa	2.3	3	2	2	1	0	5.56%	5.56%	4.70%	2.99%	1	1
101	Casein kinase 1, PCK1 OS=Plasmodium falciparum (isolate 3D7) GN=PFCK1 PE=3 SV=1	CS63F7_PLAF7 (+1)	38 kDa	2.3	3	1	3	0	0	6.79%	4.01%	9.26%	1	1	1
102	Eukaryotic translation initiation factor 3 subunit M OS=Plasmodium falciparum (isolate 3D7) GN=PF08080w PE=3 SV=1	Q8II05_PLAF7	51 kDa	2.3	4	2	0	0	0	10.50%	4.66%	0.00%	1	1	1
103	SNARE protein, putative OS=Plasmodium falciparum (isolate 3D7) GN=PFYtk6.1 PE=4 SV=1	Q8I346_PLAF7	23 kDa	2.3	3	2	2	0	0	16.60%	12.60%	11.10%	1	1	1
104	Cluster of Eukaryotic translation initiation factor 2 gamma subunit, putative OS=Plasmodium falciparum (isolate 3D7) GN=Q8ILY9_PLAF7	51 kDa	2.3	4	1	2	1	0	0	8.82%	2.80%	4.09%	2.80%	1	1
104.1	Eukaryotic translation initiation factor 2 gamma subunit, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0141 PE=4 SV=1	Q8ILY9_PLAF7	51 kDa	2.3	4	1	2	1	0	8.82%	2.80%	4.09%	2.80%	1	1
104.2	Putative eukaryotic translation initiation factor 2 subunit 3-like protein OS=Homo sapiens GN=EIF2S3L PE=5 SV=2	IF2GL_HUMAN (+1)	51 kDa	1	0	0	0	0	0	1	1	1	1	1	1
105	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=PF01110w PE=4 SV=1	Q8IFN1_PLAF7	43 kDa	2.3	3	2	2	0	0	11.00%	2.96%	7.26%	1	1	1
106	Obg-like ATPase 1 OS=Plasmodium falciparum (isolate 3D7) GN=MAL7P1.122 PE=3 SV=1	Q8IBM9_PLAF7	45 kDa	2.3	3	2	2	0	0	9.41%	5.85%	5.85%	1	1	2.80%
107	60S ribosomal protein L26, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF0535w PE=1 SV=1	Q77364_PLAF7	15 kDa	2.3	3	3	1	1	0	8.73%	8.73%	7.94%	8.73%	1	1
108	Proteasome subunit alpha type OS=Plasmodium falciparum (isolate 3D7) GN=MAL13P1.270 PE=3 SV=1	Q8IDG2_PLAF7	27 kDa	2.3	3	2	2	1	0	12.40%	9.13%	9.13%	4.56%	1	1
109	Importin subunit alpha OS=Plasmodium falciparum (isolate 3D7) GN=PF08_0087 PE=3 SV=1	Q8IAW0_PLAF7	61 kDa	2.3	2	2	3	0	0	2.20%	4.59%	4.59%	1	1	1
110	Lactate dehydrogenase OS=Plasmodium falciparum (isolate 3D7) GN=PF10H PE=1 SV=1	Q76M33_PLAF7	35 kDa	2.3	6	8	7	2	1	23.10%	16.10%	19.90%	16.50%	3.48%	2.48%
111	Fructose-bisphosphate aldolase OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0425 PE=1 SV=1	ALF_PLAF7	40 kDa	2.3	2	15	6	3	7	29.30%	39.00%	26.60%	21.10%	19.20%	7.59%
112	60S ribosomal protein L27, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0579 PE=1 SV=2	Q8IKM5_PLAF7	17 kDa	2.3	5	6	5	4	2	15.80%	15.80%	15.80%	15.10%	15.10%	8.22%
113	40S ribosomal protein S15A, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF03735w PE=1 SV=1	Q77395_PLAF7	15 kDa	2.2	3	3	3	1	2	13.10%	16.90%	16.90%	6.15%	6.92%	13.10%
114	Phosphoribosylpyrophosphate synthetase OS=Plasmodium falciparum (isolate 3D7) GN=PF13_0143 PE=4 SV=1	Q8IE67_PLAF7	49 kDa	2.2	1	5	3	1	2	2.97%	9.38%	6.86%	2.92%	1	1
115	Cluster of 60S ribosomal protein L27a, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF0885w PE=1 SV=1 (CGK C6K723_PLAF7)	17 kDa	2.2	3	8	9	6	2	1	23.60%	29.10%	29.10%	29.10%	10.80%	10.80%
115.1	60S ribosomal protein L27a, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF0885w PE=1 SV=1	C6K723_PLAF7	17 kDa	2.2	3	8	9	6							

139	Glucose-6-phosphate isomerase OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0341 PE=1 SV=1	Q8ILA4_PLA7	67 kDa	2	1	4	1	0	0	0	2.07%	5.53%	2.07%	0.00%	1	1
140	40S ribosomal protein S2, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0448 PE=1 SV=1	Q8ILO2_PLA7	30 kDa	2	3	0	2	1	0	0	10.30%	0.00%	5.88%	2.57%	1	0.00%
141	Annexin A7 OS=Homo sapiens GN=ANXA7 PE=1 SV=3	ANXA7_HUMAN	53 kDa	2	2	4	2	1	2	0	5.12%	8.61%	6.76%	3.48%	3.48%	1
142	Proteasome subunit, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0025 PE=4 SV=1	Q8IM66_PLA7	78 kDa	2	2	2	2	0	1	0	3.75%	3.75%	3.75%	0.00%	1.80%	1
143	GTP cyclohydrolase 1 OS=Plasmodium falciparum (isolate 3D7) GN=PF11155w PE=4 SV=1	Q8ISH7_PLA7	46 kDa	2	2	3	1	1	0	0	6.17%	6.17%	2.83%	2.83%	0.00%	1
144	Dsmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2	DSG1_HUMAN	114 kDa	2	0	3	4	2	1	0	0.00%	2.57%	6.29%	2.57%	1.81%	1
145	Tudor staphyloccal nuclease OS=Plasmodium falciparum (isolate 3D7) GN=TSN PE=4 SV=1	Q8IOI1_PLA7	129 kDa	2	0	3	2	1	1	0	1	3.28%	1.91%	1.46%	1.46%	1
146	Eukaryotic translation initiation factor 2, beta, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF10_0103 PE=4 SV=1	Q8IU79_PLA7	25 kDa	2	2	2	2	1	0	0	5.86%	10.80%	10.80%	5.86%	1	1
147	Protein disulfide isomerase related protein OS=Plasmodium falciparum (isolate 3D7) GN=PF11_0352 PE=4 SV=1	Q8IU23_PLA7	49 kDa	2	1	2	3	1	0	1	2.60%	5.44%	7.80%	2.84%	1	2.60%
148	Ubiquitin-activating enzyme e1, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF1245w PE=4 SV=1	Q8ISF9_PLA7	132 kDa	2	0	2	3	0	0	0	0.00%	2.28%	3.33%	1	1	1
149	Cysteinyl-HRNA synthetase, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF10_0149 PE=3 SV=2	Q8IUP7_PLA7	80 kDa	2	2	2	2	0	0	0	2.81%	3.25%	2.81%	0.00%	1	1
150	Multidrug resistance protein 2 (Heavy metal transport family) OS=Plasmodium falciparum (isolate 3D7) GN=PFMDR2 PE=3 SV=3	Q8IKZ6_PLA7	119 kDa	2	3	2	0	1	0	0	2.05%	2.73%	1	1.46%	1	1
151	T-complex protein 1, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF80635w PE=3 SV=3	Q96220_PLA7	61 kDa	2	3	2	0	1	0	0	5.90%	4.43%	1	2.21%	1	1
152	Eukaryotic translation initiation factor 3 subunit 5, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF10895c PE=4 SV=1	Q8IX20_PLA7	37 kDa	2	2	2	2	0	1	0	6.88%	6.88%	6.88%	1	3.12%	1
153	T-complex protein 1 epsilon subunit, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF0900w PE=3 SV=1	Q97282_PLA7	59 kDa	2	3	1	2	1	0	0	4.11%	2.24%	3.74%	2.24%	1	1
154	Band 3 anion transport protein OS=Homo sapiens GN=SLC4A1 PE=1 SV=3	B3AT_HUMAN	102 kDa	1.9	46	35	34	19	15	5	22.70%	21.60%	18.80%	24.10%	17.90%	6.15%
155	Cluster of Actin-1 OS=Plasmodium falciparum (isolate 3D7) GN=PF12215w PE=3 SV=1 (ACT1_PLA7)	ACT1_PLA7 [4]	42 kDa	1.9	26	19	29	10	9	46.50%	51.20%	37.40%	22.90%	20.80%	12.50%	
155.1	Actin-1 OS=Plasmodium falciparum (isolate 3D7) GN=PF12215w PE=3 SV=1	ACT1_PLA7	42 kDa	3.2	9	5	12	5	2	1	21.80%	14.90%	24.70%	11.20%	7.18%	4.26%
155.2	Actin-2 OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0124 PE=3 SV=1	ACT2_PLA7	43 kDa	2	3	1	2	0	0	0	9.04%	4.79%	9.04%	1	1	1
155.3	Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1	ACTG_HUMAN	42 kDa	1.6	15	9	14	13	6	5	29.90%	20.80%	30.70%	22.90%	20.80%	12.50%
155.4	Putative beta-actin-like protein 3 OS=Homo sapiens GN=POTEKP PE=5 SV=1	ACTBM_HUMAN	42 kDa	1.2	4	3	4	3	3	3	7.73%	7.73%	7.73%	7.73%	11.70%	7.73%
155.5	POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3	POTEE_HUMAN	121 kDa	1	6	4	5	4	4	4	4.47%	3.63%	3.63%	3.63%	5.02%	3.72%
155.6	POTE ankyrin domain family member F OS=Homo sapiens GN=POTEF PE=4 SV=1	AOA0095FL1_HUMAN	44 kDa	1	0	0	0	0	1	1	0.00%	0.00%	1	0.00%	3.81%	2.79%
155.7	POTE ankyrin domain family member C OS=Homo sapiens GN=POTEC PE=1 SV=1	AOA087WXQ2_HUMAN	43 kDa	1	0	0	0	0	0	0	1	1	1	1	1	1
155.8	POTE ankyrin domain family member B3 OS=Homo sapiens GN=POTEB3 PE=4 SV=1	AOA0G2JMU2_HUMAN	66 kDa	1	0	0	0	0	0	1	1	0.00%	1	0.00%	1	1.89%
155.9	Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2	ACTBL_HUMAN	42 kDa	1	7	2	5	4	1	1	9.31%	7.18%	7.18%	6.38%	4.26%	4.26%
155.1	POTE ankyrin domain family member I OS=Homo sapiens GN=POTEI PE=3 SV=1	POTEI_HUMAN	121 kDa	1	4	3	2	3	2	2	2.98%	2.14%	2.14%	2.14%	2.14%	1.21%
155.11	POTE ankyrin domain family member B2 OS=Homo sapiens GN=POTE2 PE=3 SV=1	POTB2_HUMAN	62 kDa	1	0	0	0	0	0	1	1	1	1	0.00%	1	2.02%
155.12	Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1	ACTC_HUMAN	42 kDa	1	13	7	9	8	3	3	21.50%	14.10%	14.10%	16.20%	9.81%	8.49%
155.13	Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1	ACTG_HUMAN	42 kDa	1	13	7	9	8	3	3	21.50%	14.10%	14.10%	16.20%	9.84%	8.51%
155.14	Actin, cytoplasmic 1 (Fragment) OS=Homo sapiens GN=ACTA PE=1 SV=1	C9JUM1_HUMAN	11 kDa	1	7	2	4	0	0	0	46.50%	21.20%	37.40%	1	1	1
155.15	Actin, cytoplasmic 2 (Fragment) OS=Homo sapiens GN=ACTG1 PE=1 SV=7	I3L4N8_HUMAN	27 kDa	1	7	5	7	8	3	2	25.20%	15.70%	22.30%	19.00%	15.70%	7.44%
155.16	Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1	J3K765_HUMAN	22 kDa	1	8	0	0	0	0	0	32.30%	1	1	1	1	9.09%
155.17	Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=3	AE6NL76_HUMAN	28 kDa	1	9	0	0	0	2	2	22.40%	1	1	1	1	6.30%
155.18	POTE ankyrin domain family member I OS=Homo sapiens GN=POTEI PE=4 SV=1	AOA0D9SF8_HUMAN	42 kDa	1	0	0	0	0	0	0	1	1	1	0.00%	1	0.00%
155.19	POTE ankyrin domain family member D OS=Homo sapiens GN=POTED PE=2 SV=2	POTED_HUMAN	66 kDa	1	0	0	0	0	0	1	1	1	1	1	1	1.88%
156	Spectrin alpha chain, erythrocytic OS=Homo sapiens GN=SPTA1 PE=1 SV=1	AOA087WZE4_HUMAN	281 kDa	1.9	95	92	99	93	38	16	26.00%	26.00%	26.20%	22.30%	12.50%	6.67%
157	Cluster of Cytochrome linked asexual protein OS=Plasmodium falciparum (isolate 3D7) GN=MAL7P1.229 PE=4 SV=1 (C0H4J7_PLA7 [3])	C0H4J7_PLA7 [3]	166 kDa	1.9	15	10	10	9	3	6	8.68%	7.48%	7.34%	6.99%	1.84%	5.01%
157.1	Cytoadherence linked asexual protein 3.1 OS=Plasmodium falciparum (isolate 3D7) GN=RhopH1(3.1) PE=4 SV=2	O77310_PLA7	167 kDa	1.8	14	9	10	9	3	6	8.68%	7.48%	7.34%	6.99%	1.83%	5.01%
157.2	Cytoadherence linked asexual protein OS=Plasmodium falciparum (isolate 3D7) GN=MAL7P1.229 PE=4 SV=1	C0H4J7_PLA7	166 kDa	1.7	2	2	0	1	0	0	1.51%	1.51%	0.00%	0.72%	1	1
157.3	Cytoadherence linked asexual protein 3.2 OS=Plasmodium falciparum (isolate 3D7) GN=RhopH1(3.2) PE=4 SV=3	O77309_PLA7	167 kDa	1.4	8	6	9	8	3	5	5.65%	4.45%	6.14%	5.79%	1.84%	3.81%
157.4	Cytoadherence linked asexual protein 2 OS=Plasmodium falciparum (isolate 3D7) GN=PF80935w PE=4 SV=2	O96279_PLA7	171 kDa	1	0	0	0	1	0	0	0.00%	0.00%	1	0.69%	1	1
158	Ornithine aminotransferase OS=Plasmodium falciparum (isolate 3D7) GN=OAT PE=1 SV=1	OAT_PLA7	46 kDa	1.9	21	15	18	13	10	5	17.40%	13.80%	17.60%	13.80%	8.94%	6.28%
159	Rhophy-associated protein 1, RAP1 OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0102 PE=4 SV=1	Q8ILZ1_PLA7	90 kDa	1.9	9	8	8	5	7	10	11.60%	11.50%	11.80%	5.50%	8.44%	1
160	Erythrocyte membrane protein band 4.2 OS=Homo sapiens GN=EPB42 PE=1 SV=3	EPB42_HUMAN	77 kDa	1.9	13	11	12	12	6	1	12.70%	13.50%	15.10%	10.70%	8.10%	1.88%
161	60S ribosomal protein L21e, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0240 PE=1 SV=1	Q8ILK3_PLA7	19 kDa	1.9	5	7	5	6	1	2	18.00%	24.80%	11.20%	24.20%	4.97%	12.40%
162	Nucleic acid binding protein, putative OS=Plasmodium falciparum (isolate 3D7) GN=MAL13P1.233 PE=4 SV=1	Q8IDN4_PLA7	25 kDa	1.9	3	4	6	2	3	2	20.90%	17.50%	19.00%	5.90%	9.00%	11.40%
163	60S ribosomal protein L18a OS=Plasmodium falciparum (isolate 3D7) GN=PF13_0224 PE=1 SV=1	Q8ID56_PLA7	22 kDa	1.9	3	6	4	5	1	0	16.80%	16.80%	16.80%	22.30%	4.35%	1
164	40S ribosomal protein S11, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF0C0775w PE=1 SV=2	O77381_PLA7	19 kDa	1.9	5	3	3	3	0	3	18.00%	11.80%	12.40%	18.00%	18.00%	1
165	Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	DSP_HUMAN	332 kDa	1.8	0	4	6	3	2	0	0.00%	1.30%	2.44%	0.70%	0.70%	1
166	Protein disulfide-isomerase OS=Plasmodium falciparum (isolate 3D7) GN=PF10_0149 PE=3 SV=2	C0H4Y6_PLA7	56 kDa	1.8	9	7	6	7	4	0	17.80%	14.30%	15.70%	17.00%	6.42%	0.00%
167	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=PF08_0091 PE=4 SV=1	Q8IAV1_PLA7	144 kDa	1.8	7	2	2	4	1	1	7.02%	1.98%	1.98%	3.97%	0.66%	0.91%
168	Serine hydroxymethyltransferase OS=Plasmodium falciparum (isolate 3D7) GN=PF1720w PE=1 SV=1	Q8I566_PLA7	50 kDa	1.8	6	4	1	2	0	3	8.82%	8.82%	2.49%	4.98%	1	4.30%
169	Aquaporin-1 OS=Homo sapiens GN=AQP1 PE=1 SV=3	AQP1_HUMAN (+1)	29 kDa	1.8	4	4	3	3	2	0	13.00%	13.00%	13.00%	13.00%	13.00%	1
170	Elongation factor 1-beta OS=Plasmodium falciparum (isolate 3D7) GN=PF8F-1beta PE=4 SV=1	Q8I320_PLA7	32 kDa	1.8	4	4	3	1	4	0	13.00%	16.30%	13.00%	8.33%	13.00%	1
171	GTP-binding nuclear protein rat/tc4 OS=Plasmodium falciparum (isolate 3D7) GN=PF11_0183 PE=4 SV=1	Q7KQK6_PLA7	25 kDa	1.8	7	8	5	5	4	2	21.50%	22.90%	26.60%	22.90%	15.90%	10.70%
172	Endoplasmic reticulum, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF11070c PE=1 SV=1	Q8IOV4_PLA7	95 kDa	1.8	11	15	12	13	6	2	14.00%	15.10%	14.60%	11.90%	5.12%	2.92%
173	V-type H(+)-translocating pyrophosphatase, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0541 PE=3 SV=3	Q8IKR1_PLA7	76 kDa	1.8	7	6	5	5	4	1	5.44%	5.58%	3.91%	5.58%	4.60%	1.26%
174	Phosphoglycerate kinase, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF11_0208 PE=1 SV=1	Q8IIG6_PLA7	29 kDa	1.8	3	3	3	2	0	2	18.00%	9.20%	9.20%	13.20%	1	8.80%
175	Hexose transporter, PHHT1 OS=Plasmodium falciparum (isolate 3D7) GN=HT1 PE=3 SV=1	Q7KWJ5_PLA7	56 kDa	1.8	3	3	3	2	1	2	5.95%	4.96%	4.96%	4.96%	2.98%	5.95%
176	Spectrin beta chain, non-erythrocytic 2 OS=Homo sapiens GN=SPTBN2 PE=1 SV=3	SPTN2_HUMAN	271 kDa	1.8	10	13	9	6	11	0	1.05%	1.42%	0.71%	0.71%	3.39%	0.00%
177	High molecular weight rhoptry protein-2 OS=Plasmodium falciparum (isolate 3D7) GN=RhopH2 PE=4 SV=1	C0H571_PLA7	163 kDa	1.8	46	28	26	38	13	6	22.90%	16.30%	17.40%	17.60%	9.00%	4.35%
178	Cluster of V-type proton ATPase catalytic subunit A OS=Plasmodium falciparum (isolate 3D7) GN=vapa PE=3 SV=1 (VATA VATA_PLA7)	VATA_PLA7	69 kDa	1.7	2	3	2	2	0	0	4.75%	6.55%	3.76%	3.76%	1	1
178.1	V-type proton ATPase catalytic subunit A OS=Plasmodium falciparum (isolate 3D7) GN=vapa PE=3 SV=1	VATA_PLA7	69 kDa	1.7	2	3	2	2	0	0	4.75%	6.55%	3.76%	3.76%	1	1
178.2	V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=1 SV=2	VATA_HUMAN	68 kDa	1	1	1	0	0	0	0	2.76%	2.76%	0.00%	0.00%	1	1
179	M17 leucyl aminopeptidase OS=Plasmodium falciparum (isolate 3D7) GN=LAP PE=1 SV=1	Q8IL11_PLA7	68 kDa	1.7	2	2	3	2	0	1	5.79%	3.80%	5.45%	3.31%	1.98%	1
180	Nucleoside transporter 1 OS=Plasmodium falciparum (isolate 3D7) GN=nt1 PE=4 SV=1	Q8IDM6_PLA7	48 kDa	1.7	1	4	2	2	1	0	4.27%	6.64%	6.64%	6.16%	1.90%	1
181	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=PF13_0219 PE=4 SV=1	Q8IDT3_PLA7	114 kDa	1.7	3	2	2	0	0	2	3.35%	2.51%	2.51%	0.00%	1	2.51%
182	PfESP2 erythrocyte surface protein OS=Plasmodium falciparum (isolate 3D7) GN=PF0E060w PE=4 SV=1	Q8I488_PLA7	49 kDa	1.7	3	1	3	2	0	0	6.37%	3.92%	5.85%	5.39%	0.00%	0.00%
183	Spermidine synthase OS=Plasmodium falciparum (isolate 3D7) GN=PF11_0301 PE=1 SV=1	Q8I773_PLA7	32 kDa	1.7	3	2	2	0	0	0	7.79%	8.10%	4.36%	6.60%	1	1
184	60S ribosomal protein L23g, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF13_0132 PE=1 SV=1	O8IE82_PLA7	22 kDa	1.7	3	2	4	3	2	1	13.20%	8.84%	17.00%	6.84%	6.84%	1
185	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=PF10_0325 PE=1 SV=1	Q8IU74_PLA7	33 kDa	1.7	2	3	2	2	1	0	11.80%	1				

216	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0567 PE=4 SV=1	Q8IKN7_PLAF7	40 kDa	1.7	2	0	2	1	1	0	7.35%	1	7.35%	3.53%	2.35%	1	
217	Small ubiquitin-related modifier, putative OS=Plasmodium falciparum (isolate 3D7) GN=PSUMO4 PE=4 SV=1	Q8I444_PLAF7	11 kDa	1.7	0	2	2	0	0	0	1	19.00%	19.00%	1	1	1	
218	Plasmeprin IV OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0075 PE=1 SV=1	Q8IM16_PLAF7	51 kDa	1.7	2	2	1	1	0	0	4.45%	4.68%	4.68%	4.68%	1	1	
219	Cluster of Spectrin beta chain, erythrocytic OS=Homo sapiens GN=SPTB PE=1 SV=5 (SPTB1_HUMAN)	SPTB1_HUMAN	246 kDa	1.6	147	##	170	163	80	40	36.40%	37.70%	40.50%	39.20%	25.30%	15.30%	
219.1	Spectrin beta chain, erythrocytic OS=Homo sapiens GN=SPTB PE=1 SV=5	SPTB1_HUMAN	246 kDa	1.6	147	##	170	163	80	40	36.40%	37.70%	40.50%	39.20%	25.30%	15.30%	
219.2	Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTB1 PE=1 SV=1	A0A087WU23_HUMAN	275 kDa	1	11	16	13	7	11	1	1.48%	1.86%	1.14%	1.14%	1.52%	0.42%	
219.3	Spectrin beta chain, erythrocytic (Fragment) OS=Homo sapiens GN=SPTB PE=1 SV=1	HOYIE6_HUMAN	117 kDa	1	42	41	54	61	24	16	25.50%	22.90%	33.30%	30.00%	17.40%	13.70%	
220	Mature parasite-infected erythrocyte surface antigen (MESA) or PEMP2 OS=Plasmodium falciparum (isolate 3D7) GN=M	Q8I492_PLAF7	168 kDa	1.6	11	15	8	12	8	0	7.53%	9.97%	5.93%	9.14%	17.60%	1	
221	Dna/SEC63 protein, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF13_0102 PE=4 SV=1	Q8IEC8_PLAF7	76 kDa	1.6	3	2	3	3	0	0	5.22%	4.61%	6.30%	6.14%	1	1	
222	60S ribosomal protein L17, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF13_0268 PE=1 SV=1	Q8ID15_PLAF7	23 kDa	1.6	2	4	2	3	1	0	3.94%	8.37%	3.94%	3.94%	1	1	
223	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=PF10_0028 PE=4 SV=1	Q8IK13_PLAF7	30 kDa	1.6	2	4	2	3	0	0	7.66%	13.30%	13.30%	13.30%	1	1	
224	Solute carrier family 2, facilitated glucose transporter member 1 OS=Homo sapiens GN=SLC2A1 PE=1 SV=2	GTR1_HUMAN	54 kDa	1.6	7	7	8	8	4	2	7.32%	8.74%	10.40%	10.40%	8.54%	4.67%	
225	Small GTP-binding protein sar1 OS=Plasmodium falciparum (isolate 3D7) GN=sar1 PE=3 SV=1	Q8I150_PLAF7	22 kDa	1.6	5	5	4	4	3	2	28.10%	32.30%	28.10%	22.40%	6.77%	12.50%	
226	Heat shock protein 101, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF11_0175 PE=1 SV=1	Q8IU8_PLAF7	103 kDa	1.5	7	8	5	6	6	0	9.38%	10.20%	6.95%	7.84%	7.28%	0.00%	
227	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=PF10_0208 PE=4 SV=1	Q8IU9_PLAF7	74 kDa	1.5	5	4	3	6	0	0	7.50%	6.70%	5.26%	8.93%	0.00%	1	
228	Cluster of Sodium/potassium-transporting ATPase subunit alpha-3 OS=Homo sapiens GN=ATP1A3 PE=1 SV=1 (A0A0A0M	A0A0A0MT26_HUMAN	133 kDa	1.5	0	4	0	0	0	2	1	3.43%	0.00%	0.00%	0.00%	1.47%	1
228.1	Sodium/potassium-transporting ATPase subunit alpha-3 OS=Homo sapiens GN=ATP1A3 PE=1 SV=1	A0A0A0MT26_HUMAN	133 kDa	1.5	0	4	0	0	0	2	1	3.43%	0.00%	0.00%	0.00%	1.22%	1
228.2	Sodium/potassium-transporting ATPase subunit alpha-2 OS=Homo sapiens GN=ATP1A2 PE=1 SV=1	AT1A2_HUMAN (+1)	112 kDa	1	0	3	0	0	0	2	1	1.47%	0.00%	1	1	1.47%	1
228.3	Potassium-transporting ATPase alpha chain 1 OS=Homo sapiens GN=ATP4A PE=2 SV=5	ATP4A_HUMAN	114 kDa	1	0	0	0	0	0	0	1	1	1	1	0.00%	1	
228.4	Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens GN=ATP1A1 PE=1 SV=1	AT1A1_HUMAN	113 kDa	1	0	3	0	0	0	2	1	1.47%	1	0.00%	1	1.47%	1
229	Cluster of Flotillin-1 OS=Homo sapiens GN=FLOT1 PE=1 SV=3 (FLOT1_HUMAN)	FLOT1_HUMAN	47 kDa	1.5	3	1	2	2	0	0	4.92%	2.58%	6.09%	7.56%	0.00%	1	
229.1	Flotillin-1 OS=Homo sapiens GN=FLOT1 PE=1 SV=3	FLOT1_HUMAN	47 kDa	1.5	3	1	2	2	0	0	4.92%	2.58%	6.09%	6.56%	0.00%	1	
229.2	Flotillin-1 (Fragment) OS=Homo sapiens GN=FLOT1 PE=1 SV=1	A2AB09_HUMAN	27 kDa	1	0	0	0	0	0	0	1	1	1	1	1	1	
230	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=PFD0080c PE=4 SV=1	Q8I207_PLAF7	60 kDa	1.5	2	2	2	0	2	0	3.75%	3.75%	3.75%	0.00%	1.79%	1	
231	3-oxo-5-alpha-steroid 4-dehydrogenase, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF11_0370 PE=4 SV=2	Q8II05_PLAF7	35 kDa	1.5	3	2	1	2	0	0	7.09%	2.70%	2.70%	7.09%	1	1	
232	Cluster of Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2 (HBB_HUMAN)	HBB_HUMAN [2]	16 kDa	1.5	27	27	22	24	16	11	61.90%	61.90%	61.20%	68.00%	59.20%	38.10%	
232.1	Hemoglobin subunit delta OS=Homo sapiens GN=HBD PE=1 SV=2	HBD_HUMAN	16 kDa	1.7	15	17	13	15	9	2	49.00%	40.80%	48.30%	55.10%	38.80%	17.00%	
232.2	Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2	HBB_HUMAN	16 kDa	1.5	23	25	18	21	14	10	61.90%	61.90%	61.20%	68.00%	59.20%	38.10%	
232.3	Hemoglobin subunit gamma-2 OS=Homo sapiens GN=HBG2 PE=1 SV=1	E9PBW4_HUMAN (+1)	15 kDa	1	0	0	0	0	0	0	1	1	1	1	1	1	
233	Cluster of Ankyrin-1 OS=Homo sapiens GN=ANK1 PE=1 SV=3 (ANK1_HUMAN)	ANK1_HUMAN [2]	135 kDa	1.5	94	76	75	101	41	23	25.70%	24.90%	23.00%	27.40%	14.90%	10.50%	
233.1	Ankyrin-1 OS=Homo sapiens GN=ANK1 PE=1 SV=3	ANK1_HUMAN	206 kDa	1.5	94	76	75	101	39	22	25.70%	24.90%	23.00%	27.40%	14.90%	10.50%	
233.2	Ankyrin-3 OS=Homo sapiens GN=ANK3 PE=1 SV=3	ANK3_HUMAN	480 kDa	1.1	7	3	6	7	5	3	0.46%	0.46%	1.07%	0.75%	1.28%	0.80%	
233.3	Ankyrin-2 OS=Homo sapiens GN=ANK2 PE=1 SV=4	ANK2_HUMAN (+1)	434 kDa	1	7	3	4	6	2	0	0.51%	0.51%	0.51%	0.51%	0.48%	1	
233.4	Ankyrin-3 (Fragment) OS=Homo sapiens GN=ANK3 PE=1 SV=1	A0A087WTF3_HUMAN	180 kDa	1	0	0	0	0	0	0	1	1	1	1	1	1	
233.5	Ankyrin-2 (Fragment) OS=Homo sapiens GN=ANK2 PE=1 SV=1	D6RHE1_HUMAN	176 kDa	1	0	0	0	0	0	0	1	1	1	1	1	1	
233.6	Ankyrin-3 (Fragment) OS=Homo sapiens GN=ANK3 PE=1 SV=1	A0A087WZ65_HUMAN	109 kDa	1	0	0	0	0	0	0	1	1	1	1	1	1	
233.7	Ankyrin-2 (Fragment) OS=Homo sapiens GN=ANK2 PE=1 SV=1	E9PHW9_HUMAN	189 kDa	1	0	0	0	0	0	0	1	1	1	1	1	1	
234	Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2	HBA_HUMAN	15 kDa	1.5	15	15	11	14	9	5	48.60%	36.60%	36.60%	31.00%	23.20%	31.00%	
235	60S ribosomal protein L13, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF10_0043 PE=1 SV=1	Q8IU27_PLAF7	24 kDa	1.4	5	3	5	4	3	2	15.30%	10.90%	18.80%	15.30%	5.94%	10.90%	
236	Protein 4.1 OS=Homo sapiens GN=EPB41 PE=1 SV=4	41_HUMAN	97 kDa	1.4	19	16	20	23	12	4	19.60%	15.50%	15.50%	19.90%	12.30%	6.37%	
237	Carbonic anhydrase 1 OS=Homo sapiens GN=CA1 PE=1 SV=2	CAH1_HUMAN	29 kDa	1.4	7	3	4	8	0	1	28.70%	10.30%	19.20%	31.80%	1	6.13%	
238	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=PFE1605w PE=4 SV=1	Q8I3F0_PLAF7	61 kDa	1.4	3	2	2	3	0	0	6.63%	3.98%	3.79%	4.92%	0.00%	1	
239	Sec61 alpha subunit, PfSEC61 OS=Plasmodium falciparum (isolate 3D7) GN=Sec61 PE=3 SV=1	Q8IDN6_PLAF7	52 kDa	1.4	2	3	2	3	0	0	2.54%	6.78%	4.45%	4.78%	1	1	
240	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=PF11590c PE=4 SV=1	Q8I2I8_PLAF7	159 kDa	1.4	6	2	3	3	0	4	5.22%	2.01%	3.58%	2.87%	1	2.68%	
241	Cluster of Pre-mRNA splicing factor, putative OS=Plasmodium falciparum (isolate 3D7) GN=PFD0265w PE=4 SV=1 (Q8I1X	Q8I1X5_PLAF7	366 kDa	1.3	2	1	0	0	1	1	0.79%	0.29%	0.00%	0.00%	0.32%	0.70%	
241.1	Pre-mRNA splicing factor, putative OS=Plasmodium falciparum (isolate 3D7) GN=PFD0265w PE=4 SV=1	Q8I1X5_PLAF7	366 kDa	1.3	2	1	0	0	1	1	0.57%	0.29%	0.00%	0.00%	0.32%	0.70%	
241.2	Pre-mRNA-processing-splicing factor 8 (Fragment) OS=Homo sapiens GN=PRPF8 PE=1 SV=7	I3LOI9_HUMAN	120 kDa	1	1	0	0	0	0	0	0.79%	1	0.00%	1	1	0.00%	
241.3	Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2	PRP8_HUMAN	274 kDa	1	0	0	0	0	0	0	1	1	1	1	1	1	
242	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0649 PE=4 SV=1	Q8IKF6_PLAF7	296 kDa	1.3	0	2	0	0	0	0	0.00%	1.09%	0.00%	0.00%	0.00%	0.00%	
243	DEAD/DEAH box helicase, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF10165c PE=4 SV=1	Q8I3B4_PLAF7	301 kDa	1.3	1	2	0	0	0	0	0.36%	0.83%	0.00%	1	0.99%	1	
244	Asparagine-N-acetyltransferase OS=Plasmodium falciparum (isolate 3D7) GN=PF11_0111 PE=4 SV=1	Q8IIQ7_PLAF7	174 kDa	1.3	1	2	0	0	0	0	0.74%	0.00%	1.48%	0.00%	0.00%	1	
245	Cluster of 55 kDa erythrocyte membrane protein OS=Homo sapiens GN=MPP1 PE=1 SV=2 (EM55_HUMAN)	EM55_HUMAN	52 kDa	1.3	2	2	4	4	0	0	4.51%	5.15%	7.08%	10.90%	1	1	
245.1	55 kDa erythrocyte membrane protein OS=Homo sapiens GN=MPP1 PE=1 SV=2	EM55_HUMAN	52 kDa	1.3	2	2	4	4	0	0	4.51%	5.15%	7.08%	10.90%	1	1	
245.2	55 kDa erythrocyte membrane protein (Fragment) OS=Homo sapiens GN=MPP1 PE=1 SV=1	ABMTM1_HUMAN	27 kDa	1	0	0	0	0	0	0	1	1	1	1	1	1	
246	Protein doxey homologue PFC0245c OS=Plasmodium falciparum (isolate 3D7) GN=PFC0245c PE=2 SV=1	DOP1_PLAF7	468 kDa	1.3	2	0	0	0	0	0	0.53%	0.00%	0.00%	0.00%	0.00%	1	
247	AcyL-CoA synthetase, PfACS12 OS=Plasmodium falciparum (isolate 3D7) GN=PFACS12 PE=4 SV=1	GCKT35_PLAF7	164 kDa	1.3	2	1	1	0	1	0	1.51%	0.79%	0.79%	1	0.79%	1	
248	US small nuclear ribonucleoprotein-specific protein, putative OS=Plasmodium falciparum (isolate 3D7) GN=PFD1060w	Q8I3F1_PLAF7	338 kDa	1.3	2	1	0	0	0	0	0.84%	0.38%	0.00%	0.00%	0.00%	1	
249	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=MAL8P1.73 PE=4 SV=1	Q8I4V4_PLAF7	134 kDa	1.3	2	0	0	0	0	0	1.64%	1	0.00%	0.00%	0.00%	0.00%	
250	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=PF08_0137 PE=4 SV=1	COH49A_PLAF7	147 kDa	1.3	0	1	2	0	0	0	0.00%	0.90%	1.72%	0.00%	0.00%	1	
251	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=PFL0340w PE=4 SV=1	Q8I5X7_PLAF7	86 kDa	1.3	1	2	1	0	0	1	1.24%	3.30%	1.24%	0.00%	1	1.93%	
252	60S ribosomal protein L35Ae, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF11_0438 PE=1 SV=1	Q8IHT9_PLAF7	16 kDa	1.3	2	1	1	1	0	0	15.00%	8.57%	8.57%	8.57%	1	1	
253	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0546 PE=4 SV=1	Q8IKQ7_PLAF7	76 kDa	1.3	2	0	0	0	0	0	2.66%	0.00%	0.00%	1	1	1	
254	Serine-repeat antigen protein OS=Plasmodium falciparum (isolate 3D7) GN=SERA PE=1 SV=1	SERA_PLAF7	112 kDa	1.3	1	2	1	1	0	0	1.10%	2.91%	1.10%	1.10%	1	1	
255	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=MAL8P1.53 PE=4 SV=1	Q8IB44_PLAF7	61 kDa	1.3	1	2	1	0	0	0	1.75%	3.89%	2.14%	0.00%	1	1	
256	Leucyl tRNA synthase OS=Plasmodium falciparum (isolate 3D7) GN=PF11095w PE=3 SV=1	GCKT64_PLAF7	170 kDa	1.3	1	2	0	0	0	0	0.83%	2.07%	1	0.00%	1	1	
257	Myosin-A OS=Plasmodium falciparum (isolate 3D7) GN=PF13_0233 PE=1 SV=1	MYOA_PLAF7	92 kDa	1.3	2	0	0	1	1	0	3.42%	0.00%	1	1.71%	1.71%	1	
258	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=PF08_0035 PE=4 SV=1	Q8IB63_PLAF7	138 kDa	1.3	2	0	0	1	1	0	2.30%	0.00%	1	0.68%	2.81%	1	
259	Aspartate carbamoyltransferase OS=Plasmodium falciparum (isolate 3D7) GN=atcasE PE=3 SV=1	Q8IDP8_PLAF7	43 kDa	1.3	2	1	0	0	0	1	5.87%	2.93%	1	1	2.93%	1	
260	Phosphatidyl choline acyltransferase OS=Plasmodium falciparum (isolate 3D7) GN=PCNA PE=3 SV=1	PCNA_PLAF7	31 kDa	1.3	1	2	0	0	1	0	4.74%	9.85%	1	4.01%	1	0.00%	
261	WD-repeat protein, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF08_0130 PE=4 SV=1	Q8IAN3_PLAF7	190 kDa	1.3	2	1	0	0	0	1	1	2.94%	0.00%	1	0.98%	1	
262	RNA binding protein, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0401 PE=4 SV=1	Q8I4I8_PLAF7	46 kDa	1.3	1	2	0	0	0	0	2.49%	4.73%	2.49%	0.00%	1	1	
263	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=MAL7P1.202 PE=4 SV=1	Q8I4L1_PLAF7	146 kDa	1.3	2	1	0	0	0	0	1.95%	0.98%	0.00%	0.00%	1	1	
264	Nucleotide reductase small subunit, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF10_0154 PE=4 SV=2	Q8IUN8_PLAF7	40 kDa	1.3	1	2	1	0	0	0	2.69%	5.97%	2.69%	0.00%	1		

301	Cluster of Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 (K2C1_HUMAN)	K2C1_HUMAN [7]	66 kDa	1.3	75	82	114	117	74	20	41.80%	41.00%	43.50%	42.40%	37.70%	14.10%
301.1	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6	K2C1_HUMAN	66 kDa	1.4	42	44	59	62	35	10	41.80%	41.00%	43.50%	42.40%	37.70%	13.00%
301.2	Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5	K2C6B_HUMAN	60 kDa	1.3	11	10	15	16	9	3	17.00%	14.90%	22.30%	22.50%	13.50%	5.14%
301.3	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2	K2ZE_HUMAN	65 kDa	1.2	18	24	33	33	21	8	29.10%	30.40%	29.70%	40.10%	26.90%	14.10%
301.4	Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3	K2C6A_HUMAN	60 kDa	1.2	10	16	21	9	3	3	20.00%	16.10%	24.10%	27.30%	15.20%	6.38%
301.5	Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3	K2C5_HUMAN	62 kDa	1.1	10	9	15	15	3	3	15.80%	17.50%	21.70%	19.50%	22.40%	7.97%
301.6	Keratin, type II cytoskeletal 79 OS=Homo sapiens GN=KRT79 PE=1 SV=2	K2C79_HUMAN	58 kDa	1.1	2	3	5	3	0	0	3.36%	3.93%	3.93%	5.42%	6.92%	1
301.7	Keratin, type II cuticular HB4 OS=Homo sapiens GN=KRT84 PE=2 SV=2	KRT84_HUMAN	65 kDa	1	1	1	0	2	0	0	1.50%	1.50%	1	1.50%	1	0.00%
301.8	Keratin, type II cytoskeletal 75 OS=Homo sapiens GN=KRT75 PE=1 SV=2	K2C75_HUMAN	60 kDa	1	0	0	0	5	5	0	1	1	1	5.26%	7.08%	1
301.9	Keratin, type II cytoskeletal 72 OS=Homo sapiens GN=KRT72 PE=1 SV=2	K2C72_HUMAN	56 kDa	1	0	0	0	2	0	0	1	1	1	1.76%	1	0.00%
301.1	Keratin, type II cytoskeletal 3 OS=Homo sapiens GN=KRT3 PE=1 SV=3	K2C3_HUMAN	64 kDa	1	0	3	0	5	0	0	1	3.34%	1	5.25%	1	1
301.11	Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=2 SV=3	K2C1B_HUMAN	62 kDa	1	0	0	0	0	0	0	1	1	1	1	1	1
301.12	Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5	K2C7_HUMAN	51 kDa	1	0	0	0	0	0	0	1	1	1	1	1	1
301.13	Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7	K2C8_HUMAN	54 kDa	1	2	1	0	0	0	0	3.93%	1.86%	1	1	1	1
301.14	Keratin, type II cytoskeletal 71 OS=Homo sapiens GN=KRT71 PE=1 SV=3	K2C71_HUMAN	57 kDa	1	0	1	0	0	0	0	1	1.72%	1	1	1	1
301.15	Keratin, type II cytoskeletal 73 OS=Homo sapiens GN=KRT73 PE=1 SV=1	K2C73_HUMAN	59 kDa	1	0	0	0	0	2	0	1	1	1	1	3.89%	1
301.16	Keratin, type II cytoskeletal 5 (Fragment) OS=Homo sapiens GN=KRT5 PE=1 SV=7	F8WOC6_HUMAN	21 kDa	1	0	0	8	0	5	0	1	1	27.90%	1	22.30%	1
301.17	Keratin, type II cytoskeletal 4 OS=Homo sapiens GN=KRT4 PE=1 SV=4	K2C4_HUMAN	57 kDa	1	0	0	0	0	1	0	1	1	1	1	2.25%	1
301.18	Keratin, type II cytoskeletal 74 OS=Homo sapiens GN=KRT74 PE=1 SV=1	F8W1S1_HUMAN (+1)	59 kDa	1	0	0	2	0	0	0	1	1	1.66%	1	1	1
301.19	Keratin, type II cytoskeletal 8 (Fragment) OS=Homo sapiens GN=KRT8 PE=1 SV=1	F8W1U3_HUMAN	33 kDa	1	0	0	0	0	0	0	1	1	1	1	1	1
301.2	Keratin, type II cytoskeletal 2 oral OS=Homo sapiens GN=KRT76 PE=1 SV=2	K22O_HUMAN	66 kDa	0.8	2	3	0	6	0	0	2.82%	3.29%	1	7.21%	1	1
302	Cluster of Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6 (K1C10_HUMAN)	K1C10_HUMAN [6]	59 kDa	1.3	38	54	63	60	50	11	37.00%	38.90%	37.00%	35.30%	31.50%	13.60%
302.1	Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4	K1C16_HUMAN	51 kDa	1.6	15	21	23	22	14	1	29.00%	38.90%	36.60%	35.30%	24.50%	2.33%
302.2	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4	K1C14_HUMAN	52 kDa	1.3	12	16	17	16	15	4	24.80%	34.30%	30.90%	24.80%	22.50%	13.60%
302.3	Keratin, type I cytoskeletal 12 OS=Homo sapiens GN=KRT12 PE=1 SV=1	K1C12_HUMAN	54 kDa	1.2	3	0	1	2	1	0	5.87%	1	1.82%	1.82%	1.82%	1
302.4	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6	K1C10_HUMAN	59 kDa	1.2	17	27	30	30	24	7	22.10%	30.30%	26.40%	25.00%	25.30%	13.50%
302.5	Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2	K1C17_HUMAN	48 kDa	1.1	8	9	9	9	12	2	14.60%	14.40%	15.50%	14.80%	20.60%	4.86%
302.6	Keratin, type I cuticular Ha5 OS=Homo sapiens GN=KRT35 PE=2 SV=5	KRT35_HUMAN	50 kDa	1	0	0	0	0	0	0	0.00%	1	0.00%	1	0.00%	0.00%
302.7	Keratin, type I cytoskeletal 28 OS=Homo sapiens GN=KRT28 PE=1 SV=2	K1C28_HUMAN	51 kDa	1	0	0	4	0	2	0	1	1	4.09%	1	2.16%	1
302.8	Keratin, type I cytoskeletal 20 OS=Homo sapiens GN=KRT20 PE=1 SV=1	K1C20_HUMAN	48 kDa	1	0	1	0	0	0	0	1	2.12%	1	1	1	1
302.9	Keratin, type I cytoskeletal 18 OS=Homo sapiens GN=KRT18 PE=1 SV=1	F8VZY9_HUMAN (+1)	44 kDa	1	0	0	0	0	0	0	1	1	1	1	0.00%	1
302.1	Keratin, type I cytoskeletal 15 OS=Homo sapiens GN=KRT15 PE=1 SV=3	K1C15_HUMAN	49 kDa	1	0	0	0	0	0	1	1	1	1	1	1	2.41%
302.11	Keratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13 PE=1 SV=4	K1C13_HUMAN (+1)	50 kDa	1	0	0	0	0	0	0	1	1	1	1	1	1
302.12	Keratin, type I cuticular Ha2 OS=Homo sapiens GN=KRT32 PE=2 SV=3	K1H2_HUMAN	50 kDa	1	0	0	0	0	0	0	1	1	1	1	1	1
302.13	Keratin-like protein KRT222 OS=Homo sapiens GN=KRT222 PE=2 SV=1	KT222_HUMAN	34 kDa	1	0	0	0	0	0	0	1	1	1	1	1	1
302.14	Keratin, type I cytoskeletal 27 OS=Homo sapiens GN=KRT27 PE=1 SV=2	K1C27_HUMAN	50 kDa	1	0	0	3	0	3	0	1	1	3.92%	1	4.36%	1
302.15	Keratin, type I cytoskeletal 16 (Fragment) OS=Homo sapiens GN=KRT16 PE=1 SV=1	K7ENW6_HUMAN	19 kDa	1	0	0	0	0	0	0	1	1	1	1	1	1
302.16	Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4	K1C19_HUMAN	44 kDa	1	0	0	0	0	0	0	1	1	1	1	1	1
302.17	Keratin, type I cuticular Ha3-II OS=Homo sapiens GN=KRT33B PE=1 SV=3	KT33B_HUMAN	46 kDa	1	0	0	0	0	0	0	1	1	1	1	1	1
302.18	Keratin, type I cuticular Ha7 OS=Homo sapiens GN=KRT37 PE=3 SV=3	KRT37_HUMAN (+1)	50 kDa	1	0	0	0	0	0	0	1	1	1	1	1	1
302.19	Keratin, type I cytoskeletal 24 OS=Homo sapiens GN=KRT24 PE=1 SV=1	K1C24_HUMAN	55 kDa	0.4	0	0	0	3	3	0	1	1	1	5.52%	2.10%	1
303	60S ribosomal protein L5, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0230 PE=1 SV=1	Q8ILL3_PLAF7	34 kDa	1.2	2	1	2	1	1	2	2.72%	3.06%	10.50%	3.06%	3.06%	6.12%
304	DNAJ protein, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF08_0032 PE=4 SV=1	Q8IB72_PLAF7	77 kDa	1.2	2	1	2	2	0	0	3.66%	1.98%	1.53%	3.66%	0.00%	1
305	60S ribosomal protein L19, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF0700C PE=1 SV=1	C6KSV6_PLAF7	22 kDa	1.2	3	1	1	1	2	1	18.70%	9.34%	4.95%	4.40%	9.34%	4.95%
306	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0186 PE=4 SV=2	Q8ILO8_PLAF7	80 kDa	1.2	2	2	1	1	2	0	3.58%	3.58%	1.94%	2.09%	3.58%	1
307	Merozoite capping protein 1 OS=Plasmodium falciparum (isolate 3D7) GN=PF10_0268 PE=4 SV=1	Q8IUD0_PLAF7	44 kDa	1.2	2	4	5	6	2	1	4.83%	8.91%	15.30%	15.00%	6.36%	4.07%
308	60S ribosomal protein L11a, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF07_0079 PE=1 SV=1	Q8IBQ6_PLAF7	20 kDa	1.2	2	2	2	2	2	1	12.10%	12.10%	8.09%	8.09%	8.09%	8.09%
309	Exported protein 2 OS=Plasmodium falciparum (isolate 3D7) GN=EXP-2 PE=4 SV=1	K8IKC8_PLAF7	33 kDa	1.2	2	3	2	3	2	1	9.06%	12.20%	9.06%	6.97%	3.83%	3.83%
310	DNA/RNA-binding protein Alba, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF08_0074 PE=4 SV=1	K8IAX8_PLAF7	27 kDa	1.2	5	5	5	7	4	2	16.90%	12.10%	12.50%	17.30%	12.90%	8.06%
311	Cluster of Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=2 (ADDA_HUMAN)	ADDA_HUMAN [3]	81 kDa	1.1	2	3	3	3	0	0	4.34%	3.75%	8.25%	10.80%	10.20%	1
311.1	Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=2	ADDA_HUMAN (+2)	81 kDa	1.1	2	3	3	3	0	0	4.34%	2.04%	4.48%	5.83%	5.56%	1
311.2	Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=1	ADDA00MSR2_HUMAN	44 kDa	1	0	2	3	3	3	1	3.75%	8.25%	10.80%	10.20%	1	1
312	40S ribosomal protein S3, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0627 PE=1 SV=1	K8IKH8_PLAF7	25 kDa	1.1	2	4	3	4	3	1	11.80%	21.30%	15.40%	21.30%	10.40%	5.88%
313	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=PF10_0047 PE=4 SV=1	Q8IUZ3_PLAF7	106 kDa	1	1	2	0	2	1	0	1.14%	2.27%	0.00%	2.39%	1.25%	0.00%
314	Formate-nitrate transporter, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF03725C PE=4 SV=2	Q77389_PLAF7	34 kDa	1	1	1	2	2	0	0	3.88%	3.56%	3.88%	6.15%	0.00%	1
315	60S ribosomal protein L44 OS=Plasmodium falciparum (isolate 3D7) GN=RPL44 PE=1 SV=3	RL44_PLAF7	12 kDa	1	1	1	2	2	1	1	10.60%	10.60%	10.60%	18.30%	10.60%	10.60%
316	Hypoxanthine phosphoribosyltransferase OS=Plasmodium falciparum (isolate 3D7) GN=PF10_0121 PE=4 SV=1	Q8JUS1_PLAF7	26 kDa	1	2	3	0	4	0	0	7.36%	15.60%	1	24.20%	1	1
317	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=PF11270w PE=4 SV=1	Q8IF54_PLAF7	33 kDa	1	2	1	2	2	2	0	8.81%	3.05%	7.80%	6.78%	4.41%	1
318	Protein phosphatase, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF11_0281 PE=4 SV=2	Q8I93_PLAF7	34 kDa	1	0	2	1	2	1	0	0.00%	10.50%	4.88%	3.14%	4.88%	1
319	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=PF0050w PE=4 SV=1	Q8I490_PLAF7	31 kDa	1	3	1	3	0	0	0	9.62%	5.77%	3.85%	9.62%	1	1
320	Peptidyl-prolyl cis-trans isomerase OS=Plasmodium falciparum (isolate 3D7) GN=PF09P19 PE=3 SV=1	Q76NN7_PLAF7	19 kDa	1	1	0	2	2	1	1	5.26%	1	11.70%	11.10%	5.85%	5.85%
321	Proteasome regulatory component, putative OS=Plasmodium falciparum (isolate 3D7) GN=MAL13P1.190 PE=4 SV=1	Q8IDV2_PLAF7	59 kDa	1	0	2	0	1	0	2	0.00%	4.77%	0.00%	2.19%	1	5.17%
322	Metabolite/drug transporter, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF0785C PE=4 SV=1	K8I3V1_PLAF7	52 kDa	1	1	2	1	2	1	0	1.75%	4.17%	1.75%	4.17%	1.75%	1
323	Phosphatidylserine synthase 1, putative OS=Plasmodium falciparum (isolate 3D7) GN=MAL13P1.335 PE=4 SV=1	Q8H5K9_PLAF7	42 kDa	1	2	1	1	0	2	1	10.90%	2.80%	2.80%	0.00%	2.52%	2.52%
324	Thioredoxin OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0545 PE=1 SV=1	THIO_PLAF7	12 kDa	1	1	2	1	1	1	2	9.62%	21.20%	11.50%	11.50%	11.50%	11.50%
325	Cluster of ADP-ribosylation factor 5 OS=Homo sapiens GN=ARF5 PE=1 SV=2 (ARF5_HUMAN)	ARF5_HUMAN	21 kDa	1	2	0	0	2	1	0	18.60%	1	1	18.60%	6.67%	1
325.1	ADP-ribosylation factor 5 OS=Homo sapiens GN=ARF5 PE=1 SV=2	ARF5_HUMAN (+1)	21 kDa	1	1	0	0	2	1	0	6.11%	1	1	6.11%	6.67%	1
325.2	ADP-ribosylation factor 1 OS=Plasmodium falciparum (isolate 3D7) GN=ARF1 PE=1 SV=1	ARF1_PLAF7	21 kDa	1	2	0	0	0	0	0	13.80%	1	1	1	1	1
325.3	Uncharacterized protein OS=Homo sapiens PE=3 SV=1	FSH423_HUMAN	23 kDa	1	2	0	0	0	0	0	11.90%	1	1	1	1	1
325.4	ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=1	FSH0B3_HUMAN	7 kDa	1	0	0	0	2	0	0	1	1	1	18.60%	1	1
326	Superoxide dismutase [Fe] OS=Plasmodium falciparum (isolate 3D7) GN=SODB PE=1 SV=1	SOFE_PLAF7	23 kDa	1	0	0	1	1	2	0	7.07%	13.10%	7.07%	6.06%	6.06%	1
327	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=PF0605C PE=4 SV=1	Q8I328_PLAF7	53 kDa	1	2	0	0	2	0	0	4.71%	1	1	4.71%	1	1
328	Histone H4 OS=Plasmodium falciparum (isolate 3D7) GN=PF11_0061 PE=3 SV=1	Q8IIV2_PLAF7	11 kDa	0.9	5	4	5	7	5	4	31.10%	31.10%	19.40%	42.70%	19.40%	21.40%
329	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=PF11_0302 PE=4 SV=1	Q8IUT2_PLAF7	52 kDa	0.9	1	2	3	4	2	0	2.43%	5.31%	7.08%	7.08%	2.43%	1
330	40S ribosomal protein S25, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0205 PE=1 SV=2	Q8ILN8_PLAF7	12 kDa	0.9	1	2	2	4	3	0	23.00%	21.90%	21.90%	17.10%		

365	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=PFE1485w PE=4 SV=1	Q8I3H0_PLAF7	226 kDa	0.8	0	0	0	0	2	0	0.00%	0.00%	0.00%	0.00%	1.05%	1
366	Uncharacterized protein MAL13P1.304 OS=Plasmodium falciparum (isolate 3D7) GN=MAL13P1.304 PE=4 SV=1	YPF12_PLAF7	210 kDa	0.8	0	0	0	0	2	0	0.00%	0.00%	1	1	1.45%	1
367	Piwi-like protein 1 OS=Homo sapiens GN=PIWL1 PE=1 SV=1	PIWL1_HUMAN-DECOY	?	0.8	0	0	0	1	2	0	1	1	1	0.00%	0.00%	1
368	Uncharacterized protein MAL13P1.304 OS=Plasmodium falciparum (isolate 3D7) GN=MAL13P1.304 PE=4 SV=1	YPF12_PLAF7-DECOY	?	0.8	0	0	0	0	2	0	0.00%	0.00%	1	1	0.00%	1
369	PR domain zinc finger protein 15 OS=Homo sapiens GN=PRDM15 PE=1 SV=4	PRD15_HUMAN	169 kDa	0.8	0	0	0	0	2	0	1	1	0.00%	1	2.19%	0.00%
370	Glideosome-associated protein 50 OS=Plasmodium falciparum (isolate 3D7) GN=GAP50 PE=1 SV=1	Q8I2X3_PLAF7	45 kDa	0.8	1	1	1	2	1	1	2.78%	2.78%	2.78%	5.81%	2.78%	3.03%
371	DNA repair endonuclease, putative OS=Plasmodium falciparum (isolate 3D7) GN=MAL13P1.346 PE=4 SV=1	Q8I2D2_PLAF7-DECOY	?	0.8	0	0	0	0	2	0	0.00%	1	1	0.00%	0.00%	1
372	Cluster of Fibrillarin, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0068 PE=3 SV=1 (Q8IM23_PLAF7)	Q8IM23_PLAF7	34 kDa	0.8	0	0	0	0	2	0	0.00%	0.00%	0.00%	1	15.20%	1
372.1	Fibrillarin, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0068 PE=3 SV=1	Q8IM23_PLAF7	34 kDa	1	0	0	0	0	1	0	0.00%	1	0.00%	1	3.77%	1
372.2	rRNA 2'-O-methyltransferase fibrillarin (Fragment) OS=Homo sapiens GN=FBL PE=1 SV=1	MOR110_HUMAN	18 kDa	1	0	0	0	0	2	0	1	1	1	1	15.20%	1
372.3	rRNA 2'-O-methyltransferase fibrillarin (Fragment) OS=Homo sapiens GN=FBL PE=1 SV=1	MOR204_HUMAN	29 kDa	1	0	0	0	0	2	0	1	1	1	1	9.89%	1
373	Phosphatase, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0614 PE=4 SV=2	Q8IK11_PLAF7	170 kDa	0.8	0	0	0	2	0	0	1	0.00%	1	1.53%	0.00%	0.00%
374	Coiled-coil domain-containing protein 158 OS=Homo sapiens GN=CCDC158 PE=1 SV=2	CD158_HUMAN	127 kDa	0.8	0	0	0	0	2	0	1	1	0.00%	1	2.79%	1
375	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0652 PE=4 SV=1	Q8IKF3_PLAF7-DECOY	?	0.8	0	0	0	0	2	0	0.00%	1	1	0.00%	0.00%	1
376	Protein ELYS OS=Homo sapiens GN=AHCTF1 PE=1 SV=3	ELYS_HUMAN-DECOY	?	0.8	0	0	0	1	2	0	1	1	1	0.00%	0.00%	1
377	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0703 PE=4 SV=1	Q8IKA3_PLAF7	104 kDa	0.8	0	0	0	0	2	0	1	0.00%	0.00%	1	3.41%	1
378	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=PF11_0384 PE=4 SV=1	Q8IH22_PLAF7	82 kDa	0.8	1	1	1	2	0	0	1.60%	1.60%	1.60%	2.76%	1	1
379	Adenomatous polyposis coli protein 2 OS=Homo sapiens GN=APC2 PE=1 SV=1	APC2_HUMAN	244 kDa	0.8	0	0	0	2	1	0	1	1	1	1.48%	0.56%	1
380	Collagen alpha-5(VI) chain OS=Homo sapiens GN=COL6A5 PE=1 SV=1	CO6A5_HUMAN	290 kDa	0.8	0	0	0	0	2	0	1	1	1	1	1.15%	1
381	Protein FAM83H OS=Homo sapiens GN=FAM83H PE=1 SV=3	FAM83H_HUMAN	127 kDa	0.8	0	0	0	0	2	0	1	1	1	1	2.46%	0.00%
382	Pappalysin-1 OS=Homo sapiens GN=PAPPA PE=1 SV=3	PAPPI1_HUMAN-DECOY	?	0.8	0	0	0	0	2	1	0.00%	1	1	0.00%	0.00%	0.00%
383	40S ribosomal protein S14, putative OS=Plasmodium falciparum (isolate 3D7) GN=PFE0810c PE=1 SV=1	Q8I3U6_PLAF7	16 kDa	0.8	1	1	0	1	2	0	9.93%	9.93%	1	9.93%	18.50%	1
384	Ribosomal protein S20e, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF10_0038 PE=1 SV=1	Q8IK02_PLAF7	14 kDa	0.8	1	1	1	1	2	0	7.63%	7.63%	7.63%	7.63%	17.80%	1
385	Metallothionein-1L OS=Homo sapiens GN=MT1L PE=2 SV=1	MT1L_HUMAN-DECOY	?	0.8	0	0	1	0	2	0	1	1	0.00%	1	0.00%	1
386	Tubulin-tyrosine ligase-like protein 12 OS=Homo sapiens GN=TTLL12 PE=1 SV=2	TTLL12_HUMAN	74 kDa	0.8	0	0	0	2	1	0	1	0.00%	0.00%	3.73%	1.86%	1
387	A-kinase anchor protein 12 OS=Homo sapiens GN-AKAP12 PE=1 SV=4	AKA12_HUMAN	191 kDa	0.8	0	0	0	0	2	0	1	1	1	0.00%	2.75%	1
388	Structure specific recognition protein OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0393 PE=4 SV=1	Q8IL56_PLAF7	59 kDa	0.8	0	0	0	2	0	0	1	1	0.00%	4.55%	0.00%	1
389	Aquaglyceroporin OS=Plasmodium falciparum (isolate 3D7) GN=PF11_0338 PE=3 SV=1	Q8II36_PLAF7	28 kDa	0.8	1	0	1	2	0	0	3.88%	1	3.88%	6.98%	1	1
390	Hamartin OS=Homo sapiens GN=TSCT1 PE=1 SV=2	TSC1_HUMAN	130 kDa	0.8	0	0	0	0	2	0	1	1	1	1	3.09%	1
391	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=PF11870c PE=4 SV=1	Q8I377_PLAF7	46 kDa	0.8	1	0	1	2	0	0	3.56%	1	3.56%	6.87%	1	1
392	1-deoxy-D-xylulose 5-phosphate synthase OS=Plasmodium falciparum (isolate 3D7) GN=MAL13P1.186 PE=4 SV=1	Q8IDV0_PLAF7	140 kDa	0.8	0	0	0	0	2	0	1	1	1	1	1.99%	1
393	ARHGAP12 protein OS=Homo sapiens GN=ARHGAP12 PE=1 SV=1	Q1RLN5_HUMAN (+1)	91 kDa	0.8	0	0	0	0	2	0	1	0.00%	1	1	3.63%	1
394	Membrane associated histidine-rich protein, MAHRP1 OS=Plasmodium falciparum (isolate 3D7) GN=MAHRP1 PE=4 SV=1	COH519_PLAF7	29 kDa	0.8	0	1	1	2	0	0	1	4.02%	4.02%	10.80%	1	1
395	Keratin, type II cytoskeletal 80 OS=Homo sapiens GN=KRT80 PE=1 SV=2	K2C80_HUMAN	51 kDa	0.8	0	0	0	2	1	0	1	1	1	1	4.42%	2.21%
396	Kinesin-associated protein 3 OS=Homo sapiens GN=KIFAP3 PE=1 SV=2	KIFA3_HUMAN-DECOY	?	0.8	0	0	0	2	0	0	1	1	1	0.00%	1	1
397	Contactin-4 OS=Homo sapiens GN=CNTN4 PE=1 SV=1	CNTN4_HUMAN-DECOY	?	0.8	0	0	0	2	0	0	1	1	1	0.00%	1	1
398	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0105 PE=4 SV=1	Q8IILY_PLAF7	40 kDa	0.8	1	1	0	2	0	0	2.99%	2.99%	1	5.99%	1	1
399	phospholipase A2 inhibitor and Ly6/PLAUR domain-containing protein OS=Homo sapiens GN=PINLYP PE=2 SV=3	PINLY_HUMAN-DECOY	?	0.8	0	0	0	0	2	0	1	1	1	1	0.00%	1
400	WAP four-disulfide core domain protein 8 OS=Homo sapiens GN=WFD8 PE=2 SV=2	WFD8_HUMAN	28 kDa	0.8	0	0	0	0	2	0	1	1	1	0.00%	13.70%	1
401	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=PF10_0063 PE=4 SV=1	Q8IUX8_PLAF7	12 kDa	0.8	0	0	0	2	0	0	1	1	1	1	19.60%	1
402	D(1A) dopamine receptor OS=Homo sapiens GN=DRD1 PE=1 SV=1	DRD1_HUMAN-DECOY	?	0.8	0	0	0	0	2	0	1	1	1	1	0.00%	1
403	Conserved Plasmodium protein OS=Plasmodium falciparum (isolate 3D7) GN=PF10_0104 PE=4 SV=1	Q8IUT8_PLAF7	26 kDa	0.8	0	0	1	2	0	0	1	1	6.73%	12.10%	1	1
404	Fliotillin-2 OS=Homo sapiens GN=FLT02 PE=4 SV=1	J3QK24_HUMAN-DECOY	?	0.8	0	0	0	0	2	0	1	1	1	1	0.00%	1
405	Keratin, type I cytoskeletal 26 OS=Homo sapiens GN=KRT26 PE=1 SV=2	K1C26_HUMAN	52 kDa	0.8	0	0	0	2	0	0	1	1	1	1	4.49%	1
406	Flavin reductase (NADPH) OS=Homo sapiens GN=BLVRB PE=1 SV=3	BLVRB_HUMAN	22 kDa	0.7	3	0	1	5	1	0	11.70%	1	6.80%	19.90%	6.80%	1
407	Nucleosome assembly protein OS=Plasmodium falciparum (isolate 3D7) GN=PF10930c PE=3 SV=1	Q8I2W3_PLAF7	32 kDa	0.7	2	1	1	2	3	0	7.06%	3.72%	3.35%	7.43%	10.80%	1
408	Hydrolase, putative OS=Plasmodium falciparum (isolate 3D7) GN=PF13_0032 PE=4 SV=1	Q8IEQ3_PLAF7	57 kDa	0.7	1	2	1	4	1	0	2.93%	5.02%	2.09%	7.32%	2.09%	1
409	Ubiquitin carboxyl-terminal hydrolase, putative OS=Plasmodium falciparum (isolate 3D7) GN=MAL7P1.147 PE=4 SV=1	Q8IBJ1_PLAF7-DECOY	?	0.6	0	0	0	0	3	0	0.00%	0.00%	0.00%	0.00%	0.00%	1
410	Transcription factor TFIIB component B' homolog OS=Homo sapiens GN=BDP1 PE=1 SV=1	A0A0G2JNU3_HUMAN-D	?	0.6	0	0	0	3	0	0	0.00%	1	0.00%	0.00%	0.00%	0.00%
411	AF4/FMR2 family member 1 OS=Homo sapiens GN=AFF1 PE=1 SV=1	AF1_HUMAN	131 kDa	0.6	0	0	0	0	3	0	1	1	1	0.00%	2.73%	1
412	REX2 protein OS=Plasmodium falciparum (isolate 3D7) GN=REX2 PE=4 SV=1	COH592_PLAF7	11 kDa	0.6	1	1	0	2	0	0	13.80%	13.80%	1	25.50%	13.80%	1
413	Cluster of Keratin-associated protein 4-8 OS=Homo sapiens GN=KRTAP4-8 PE=2 SV=4 (KRA48_HUMAN-DECOY)	KRA48_HUMAN-DECOY	?	0.6	0	0	0	0	3	0	1	1	1	1	0.00%	0.00%
413.1	Keratin-associated protein 4-8 OS=Homo sapiens GN=KRTAP4-8 PE=2 SV=4	KRA48_HUMAN-DECOY	?	0.8	0	0	0	0	2	0	1	1	1	1	0.00%	0.00%
413.2	Keratin-associated protein 4-8 OS=Homo sapiens GN=KRTAP4-4 PE=2 SV=1	KRA44_HUMAN-DECOY	?	0.8	0	0	0	0	2	0	1	1	1	1	0.00%	1
414	Heat shock protein hsp70 homologue OS=Plasmodium falciparum (isolate 3D7) GN=PF11_0351 PE=3 SV=1	Q8II24_PLAF7	73 kDa	0.6	2	1	0	3	1	3	3.02%	1.51%	1	5.13%	1.81%	3.92%
415	Cluster of Ras and Rab interactor 3 OS=Homo sapiens GN=RIN3 PE=1 SV=1 (A0A087WWY9_HUMAN-DECOY)	A0A087WWY9_HUMAN-G3V217_HUMAN-DECOY	?	0.6	1	0	2	2	3	2	0.00%	1	0.00%	0.00%	0.00%	0.00%
415.1	Ras and Rab interactor 3 OS=Homo sapiens GN=RIN3 PE=1 SV=1	A0A087WWY9_HUMAN	?	1	1	0	0	0	0	1	0.00%	1	1	1	1	0.00%
415.2	Ras and Rab interactor 3 OS=Homo sapiens GN=RIN3 PE=1 SV=1	A0A087WWY9_HUMAN	?	0.6	1	0	2	2	3	2	0.00%	1	0.00%	0.00%	0.00%	0.00%
416	Cluster of Nebulin OS=Homo sapiens GN=NEB PE=1 SV=1 (A0A087X1N7_HUMAN)	A0A087X1N7_HUMAN	991 kDa	0.5	0	0	0	0	4	0	0.00%	0.00%	0.00%	0.00%	0.62%	0.00%
416.1	Nebulin OS=Homo sapiens GN=NEB PE=1 SV=5	NEBU_HUMAN	773 kDa	1	0	0	0	0	3	0	0.00%	1	1	0.00%	0.60%	0.00%
416.2	Nebulin OS=Homo sapiens GN=NEB PE=1 SV=1	A0A087X1N7_HUMAN	991 kDa	0.5	0	0	0	0	4	0	0.00%	0.00%	0.00%	0.00%	0.62%	0.00%
417	Cysteine repeat modular protein 4, putative OS=Plasmodium falciparum (isolate 3D7) GN=PCRM4 PE=4 SV=2	Q8IK84_PLAF7-DECOY	?	0.5	0	0	0	0	4	0	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
418	Cluster of Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5 (PRDX2_HUMAN)	PRDX2_HUMAN	22 kDa	0.5	1	1	1	3	2	0	5.05%	4.04%	4.04%	14.60%	9.60%	1
418.1	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1	A0A0A0MRO5_HUMAN	11 kDa	1	0	0	0	0	0	0	1	1	1	1	1	1
418.2	Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5	PRDX2_HUMAN	22 kDa	0.5	1	1	1	3	2	0	5.05%	4.04%	4.04%	14.60%	9.60%	1
419	Erythrocyte membrane protein 1, PEMP1 OS=Plasmodium falciparum (isolate 3D7) GN=VAR PE=4 SV=1	Q8ISL5_PLAF7-DECOY	?	0.5	0	0	0	0	4	0	1	1	0.00%	0.00%	0.00%	1
420	Tropomodulin-1 OS=Homo sapiens GN=TMOD1 PE=1 SV=1	TMOD1_HUMAN	41 kDa	0.5	1	2	0	6	0	0	2.79%	2.79%	1	13.60%	1	1
421	Biliverdin reductase A OS=Homo sapiens GN=BLVRA PE=1 SV=2	BIEA_HUMAN	33 kDa	0.5	0	0	0	4	1	1	1	1	1	12.50%	4.73%	3.04%
422	Uncharacterized protein OS=Plasmodium falciparum (isolate 3D7) GN=PF11_0179 PE=4 SV=1	Q8IIU4_PLAF7	15 kDa	0.4	1	1	1	5	1	0	7.81%	7.81%	7.81%	32.00%	7.03%	1
423	Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2	CAH2_HUMAN	29 kDa	0.4	1	3	0	7	6	1	3.46%	14.60%	1	15.40%	15.40%	4.62%
424	Cluster of Histone H2A OS=Plasmodium falciparum (isolate 3D7) GN=PF0920w PE=3 SV=1 (O97320_PLAF7)	O97320_PLAF7	16 kDa	0.3	2	0	1	7	4	0	12.00%	1	7.03%	26.60%	19.00%	1
424.1	Histone H2A OS=Plasmodium falciparum (isolate 3D7) GN=PF0860c PE=3 SV=1	C6KT18_PLAF7	14 kDa	1	1	0	1	2	2	0	6.82%	1	6.82%	6.82%	1	1
424.2	Histone H2A.J OS=Homo sapiens GN=H2AFJ PE=1 SV=1	H2AJ_HUMAN	14 kDa	1	1	0	0	2	2	0	6.98%	1	1	6.98%	6.98%	1
424.3	Histone H2A.Z OS=Homo sapiens GN=H2AFZ PE=1 SV=2	H2AZ_HUMAN	14 kDa	1	0	0	1	5	0	0	1	1	7.03%	18.00%	1	1
424.4	Histone H2A.X OS=Homo sapiens GN=H2AFX PE=1 SV=2	H2AX_HUMAN	15 kDa	1	0	0	0	0	0	0	1	1	1	1	1	1
424.5	Histone H2A OS=Plasmodium falciparum (isolate 3D7) GN=PF0920w PE=3 SV=1	O97320_PLAF7	16 kDa	0.3	2	0	1	7	4	0	12.00%	1	5.70%	26.60%	19.00%	1
425	Fliot															

Figure S1. FASTA sequences of DEAD/DEAH box Helicase and Methionyl-tRNA formyltransferase in isolate 3D7 and other proteome databases from UniProt.

- A. FASTA sequence of Methionyl-tRNA formyltransferase from isolate 3D7 proteome database. The Cys is at the 5th position from the C-terminus.

```
>tr|Q8IEI1|Q8IEI1_PLAF7 Methionyl-tRNA formyltransferase, putative
OS=Plasmodium falciparum (isolate 3D7) GN=PF3D7_1313200 PE=4 SV=2
MYVKCFYVIQILFIIFLKCHCYKIKCFNILDNLKKKYYSFREHINCEHIRNSVNRNNLS
NVLLRRRTKNALVKELYVSKLKDNYKTHTNFIRTNNIFLEEDKKIQECNINNIINNNDVI
QENVEKYNILYKNQLDDINILYILLFNTLMIYKKKYDFFMNENYIRSYYYIYKNNLGRDK
KIYNTKNYFINTFSITWYNTIKPYMNNIFLEILNIIENTLGNKIFYIDIKQELNKNRDEI
INTLYNIYKGNFRKRDKKPIKLLFIGSNEYSNLCFKIILLIKRLRNDIILDNVITKSPR
RKGRNLILKKSNEVEDEAIKNNINVFYDKLKNNIHMLQNKMDLCISISFGEIFNCNFFK
TIKSNIFSLHPSLLPFYKGASPIQRSLLNNEILYGYSVFLTTLNIDSGNVIMKKPFWFNS
NYNFNDIITILFTQGTLSLLKNISYLANYNKDIPHKNIYNNNICEETKNNLNQNHVQNKY
DSEINIHNSNLENKNSRNNILPLNINNVLNNNYNNKMYIQNDYNINNNYAPKIKNDEKYV
CFFCSTSLFIHNKIRSFINWPKAECTFLLLQNEVIKPLEIKIKSSYDLNNNYKFIKYDG
LINTHDQHTCFDNIIPRFVYIQNDSLNILCKNNTLLKIYKLOQKNKKIVDAMSFINSINK
CSLLY
```

- B. FASTA sequence of DEAD/DEAH box helicase from isolate 3D7 proteome database. There is no putative prenylation motif at the C-terminus.

```
>tr|Q8I511|Q8I511_PLAF7 ATP-dependent RNA helicase DBP9, putative
OS=Plasmodium falciparum (isolate 3D7) GN=PF3D7_1241800 PE=4 SV=2
MNDQAQIKDMMNDEEEKEEIEIKENINDKINEIDDDDDDDGDDDDDEDEDESDNDND
DEDNDEDEDNDNDNDNDSDNDDDDHNDVKKSSKNKKKNEEMFDRSNHFDNFDNIMLDV
RLRKALLYLFKYQHPTIIQKMSICKILNGHDVIISSKTGSGKTMAYLIPVVHNLKIFNLN
EKDHLKFFYKCIICPTEELCLQIYDVTKKLCTYLKDIITVNHNVNNTFYEHPTILISTP
KDLCTHIIIEKKKKNNLDILMNLKILILDEADVLHTQEFQSYLKTLSYLPKKFNKKYQIV
MASATLKRNIIEKTKLFLHNPIYVSHEQKNESSEFEKKKNKTNTNSVIMKREEAGKNNIH
DEGNEGKTKYQKFTGKAFYVYKEELIKYIYLYNLIKIKIIPYKSIIFTTTHDAYKIKI
FLTYLVNVSILNPNHPILIRQNIISAFNNSKFHFLICPQYEKNNMKHVKGVLGSNKMDN
VDGGDDNDDDEDDGDYNDNDDDDNDDDDNDDDDNDDDDNDDDEDEDNDDDDGDDNDD
NDDNDDNDDNDDQTLNEPLSDNNSCRTYNSSDENKTDTTKLNEEKDFLYSRGLDFYD
VKCVNFDPSPDSETFIHRIGRTCLNNKGCISFVNELNYGEKEFLQKLIEDKNICTMI
KKNIQYNIVEKYRYRVESTLNKCTNKKIKLFIQKEILYQSLKSKELKDFNTNINEKRKI
NKIIKHFNKAVIPQKLIKDRNQSIPLNKSXVKNKIIQKNNTNNKNKNNNNNIPFALKNN
NGLVITEQGYESQLTKEPEREVADPSKLPPLCGQRLRNYMYLKYIKGKKNKNGSNMKNKY
NSNNKKRKNNNKYNRYNKYNKKGINKNHNKRNTNFNR
```

- C. FASTA sequence of DEAD/DEAH box helicase from isolate HB3 proteome database. The putative prenylation motif CMLQ is present.

```
>tr|A0A0L7KBA8|A0A0L7KBA8_PLAFX Uncharacterized protein OS=Plasmodium
falciparum (isolate HB3) GN=PFHG_02136 PE=4 SV=1
MNDQAQIKDMMNDEEEKEEIEIKENINDKINEIDDDGDDNDDNDDGDDDDDEDEDE
DNDNDDDEDNDNDEDNDDDEDNDDDEDNDEDEDNDDNDDNDDSDNDDDDHNDVKKSSKNK
KKNNEEMFDRSNHFDNFDNIMLDVRLRKALLYLFKYQHPTIIQKMSICKILNGHDVIISS
KTGSGKTMAYLIPVVHNLKIFNLNEKDHLKFFYKCIICPTEELCLQIYDVTKKLCTYLK
DIITVNHNVNNTFYEHPTILISTPKDLCTHIIIEKKKKNNLDILMNLKILILDEADVLHTQ
EFQSYLKTLSYLPKKFNKKYQIVMASATLKRNIIEKTKLFLHNPIYVSHEQKNESSEFEK
KKNKTNTNSVIMKREEAGKNNIHDEGNEGKTKYQKFTGKAFYVYKEELIKYIYLYNLI
KIKIIPYKSIIFTTTHDAYKIKIFLTYLVNVSILNPNHPILIRQNIISAFNNSKFHFL
ICPQYEKNNMKHVKGVLGSNKMDNVDGGDDNDDDEDDGDYNDNDDDDNDDDDNDDDDN
DDDEDNDEDEDNDEDEDNDDDDGDDNDDNDDQTLNEPLSDNNSCRTYNSSDENKTDTT
```

TKLNEEKDFLYSRGLDFYDVKCVVNFDMPSDSETFIHRIGRTCRLNNKGK CISFVNELNY
 GEKEFLQKLIEDKNICTMIKKNIQYNIVEKYRVRVESTLNKCTNKKIKLFIQKEILYQSL
 KSKELKDFNTNINEKRKINKIIKHFNKAVIPQKLIKDRNQSI FLNKS VKNKIIQKNNT
 NNKNKNNNNNNIKPFALKNNNGLVITEQGYESQLTKEPEREVADPSKLPPLCGQRLRNMY
 LKVIKGGKKNKNGSNMNNNSYNSNNKKRNNNNKYNRRYNKYNNKKGINKNNHNKRNTNFNRIQK
 KIIFLLSLF **CMLQ**

D. FASTA sequence of DEAD/DEAH box helicase from isolate Camp/Malaysia proteome database. The putative prenylation motif CMLQ is present.

>tr|A0A024X4J9|A0A024X4J9_PLAFC Uncharacterized protein (Fragment)
 OS=Plasmodium falciparum (isolate Camp / Malaysia) GN=PFMC_04004 PE=4
 SV=1 DDDNDNDQTLNEPLSDNNSCRTYNSDDENEKTD DTTKLNEEKDFLYSRGLDFYDVKCVV
 NFDMPDSETFIHRIGRTCRLNNKGK CISFVNELNYGEKEFLQKLIEDKNICTMIKKNIQ
 YNIVEKYRVRVESTLNKCTNKKIKLFIQKEILYQSLKSKELKDFNTNINEKRKINKIIK
 HFNKAVIPQKLIKDRNQSI FLNKS VKNKIIQKNNTNNKNKNNNNNNIKPFALKNNNGLVI
 TEQGYESQLTKEPEREVADPSKLPPLCGQRLRNMYLKYIKGGKKNKNGSNMNNNSYNSNNK
 KRKNNNNKYNRRYNKYNNKKGINKNNHNKRNTNFNRIQKKIIFLLSLF **CMLQ**

Figure S2. Comparison of peptide sequences identified between *P. falciparum* and human Rab protein homologs. *P. falciparum* proteins contain peptides present in human homologs but with statistically higher probabilities, spectral counts, and percent coverages.

A. Comparison of peptide sequences identified between Pf Rab7 and human Rab7a.

C0H516_PLAF7 (100%), 23,788.5 Da

PfRab7, GTPase OS=Plasmodium falciparum (isolate 3D7) GN=Rab7 PE=3 SV=1

7 exclusive unique peptides, 8 exclusive unique spectra, 25 total spectra, 121/206 amino acids (59% coverage)

MSNKKRTILK	VIILGDSGVG	KTSLMNQYVN	KKFTNQYKAT	IGADFLTKET
IVDNEQITMQ	IWDTAGQERF	QSLGVAFYRG	ADCCVLVFDL	TNYKTYESLE
SWKDEFILQA	SPKDPENFPF	VIIGNKVDET	NKRKVQSLKV	LQWCKSNNNI
PYFETS AKNA	INVDQAFDEI	ARKAMKQEHQ	EEQIYLPETF	ALNNQSEQKM
YKSRCC				

C9J8S3_HUMAN (99%), 18,026.8 Da

Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A PE=1 SV=1

0 exclusive unique peptides, 0 exclusive unique spectra, 10 total spectra, 43/160 amino acids (27% coverage)

MTSRKKVLLK	VIILGDSGVG	KTSLMNQYVN	KKFSNQYKAT	IGADFLTKEV
MVDDRLVTMQ	IWDTAGQERF	QSLGVAFYRG	ADCCVLVATK	RAQAWCYSKN
NIPYFETSAK	EA INVEQAFQ	TIARNALKQE	TEVELYNEFP	EPIKLDKNDR
AKASAESCSC				

B. Comparison of peptide sequences identified between Pf and human Rab1B.

Rab1b, GTPase OS=Plasmodium falciparum (isolate 3D7) GN=Rab1b PE=4 SV=1

3 exclusive unique peptides, 4 exclusive unique spectra, 19 total spectra, 74/200 amino acids (37% coverage)

MNDSYDSLFLK	ILLIGDSGVG	KSCLLLRFAD	DTYTDSYIST	IGVDFKIKTI
EIEDKIIKLQ	IWDTAGQERF	RTITSSYYRG	AQGIIIVYDV	TDRDSFN NVK
NWIIIEIKYA	SEDVQKILIG	NKIDLKNDNR	VSYEEGKELA	DSCNIQFLET
SAK IAHNVEQ	AFKTMAYEIK	NKSQHETINK	GKTNINLNAR	PIKDTKKKCC

A0A087WT11_HUMAN (36%), 18,678.1 Da

Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1

0 exclusive unique peptides, 0 exclusive unique spectra, 13 total spectra, 40/162 amino acids (25% coverage)

MNPEYDYLFK	LLIIGDSGVG	KSCLLLRFAD	DTYTESYIST	IGVDFKIRTI
ELDGKTIKLQ	IWDTAGQERF	RTITSSYYRG	AHGIIIVYDV	TDQESYANVK
QGCRRLTAMP	ARTSISSWWA	TRATSPRRRW	WTTTPQPRSLQ	TLWASPSWRR
APRMPPMSSR	RS			

C. Comparison of peptide sequences identified between Pf and human Rab1A.

Q8I3W9_PLAF7 (100%), 23,860.6 Da

PfRab1a OS=Plasmodium falciparum (isolate 3D7) GN=Rab1a PE=3 SV=1

2 exclusive unique peptides, 2 exclusive unique spectra, 12 total spectra, 45/207 amino acids (22% coverage)

MTENR	SRDYD	YLYKIILIGD	SGVGK	SCILL	RFSDDHFTES	YITTIGVDFR
FRTIKVDDKI	VKLQIWDTAG	QERFRTITSA	YYRGADGIII	IYDTTDR	NSF	
LHINDWMNEI	NKYTNEDTCK	LLVGNKADCK	DDIEITTMEG	QNKAKELNIS		
FIETSAKDAT	NVELAFTMIT	QELIKKKKKK	NFTSLKNNHA	KLKLSLTHDNS		
PQSFCSC						

RAB1A_HUMAN (27%), 22,678.5 Da

Ras-related protein Rab-1A OS=Homo sapiens GN=RAB1A PE=1 SV=3

0 exclusive unique peptides, 0 exclusive unique spectra, 13 total spectra, 40/205 amino acids (20% coverage)

MSSMNPEYDY	LFK	LLLIGDS	GVGK	SCLLLR	FADDTYTESY	ISTIGVDFK
RTIELDGKTI	K	LQIWDTAGQ	ERFR	TITSSY	YRGAHGIIIV	YDVTDQESFN
NVKQWLQEID	RYASENVNKL	LVGNKCDLTT	KKVVDYTTAK	EFADSLGIPF		
LETSAKNATN	VEQSFMMAA	EIKKRMGPGA	TAGGAEKSNNV	KIQSTPVKQS		
GGGCC						

D. Comparison of peptide sequences identified between Pf and human Rab5C.

Q8I274_PLAF7 (100%), 24,329.4 Da

Rab5c, GTPase OS=Plasmodium falciparum (isolate 3D7) GN=Rab5c PE=3 SV=1

7 exclusive unique peptides, 8 exclusive unique spectra, 18 total spectra, 91/214 amino acids (43% coverage)

MAYYLSNLNN	NEKYETNQSY	NSTKVFNSKL	VLLGDTSVGK	SCIVVRFAKN
EFYEYQUESTI	GAAFMTQLID	IGECTIKFEI	WDTAGQERYR	SLAPMYRGA
SAAVIVYDIT	NKKSFEAGAKG	WIHELKSVHS	NDIIIALAGN	KNDLEEHRV
DRELAESFAN	SNNILFIETS	AKTGQNVNEL	FLRIA KKLPL	HKKEQERCPA
IQINNTTEETK	KKCC			

RAB5C_HUMAN (47%), 23,482.7 Da

Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C PE=1 SV=2

0 exclusive unique peptides, 0 exclusive unique spectra, 6 total spectra, 11/216 amino acids (5% coverage)

MAGRGGGAARP	NGPAAGNKIC	QFKLVLLGES	AVGKSSLVLR	FVKGGFHEYQ
ESTIGAAFLT	QTVCLDDTTV	KFEIWDTAGQ	ERYHSLAPMY	YRGAQAAIVV
YDITNTDTFA	RAKNWVKELQ	RQASPNIVIA	LAGNKADLAS	KRAVEFQEAQ
AYADDNSLLF	METSAKTAMN	VNEIFMAIAK	KLPKNEPQNA	TGAPGRNRGV
DLQENNPASR	SQCCSN			

MS Analysis Parameters

Parameter	Value	
	<i>MS1 (Orbitrap)</i>	<i>MS 2 (Ion trap)</i>
Orbitrap resolution	30000	-
Mass range	normal	-
CID collision energy (%)	-	35
Activation Q	-	0.25
Scan range (m/z)	300-1500	auto
AGC Target	500,000	5,000
Max. Injection time (ms)	50	25
Microscans	1	1
Data type	centroid	centroid

MS Filters:

Charge state: 2-7

Exclude undetermined charge states

Dynamic exclusion duration (s): 90

Mass tolerance: 0.01 m/z for both high and low

Intensity threshold: 500