1 APPENDIX 1

Table1: Summary of proteins identified by 2-D chromatography (MS/MS)

N	Unused	Total	% Cov	Accession #	Name	Species
1	2.76	2.76	21.7	BAC55342	AB086179 NID: - Anthoceros formosae	Anthoceros formosae
2	1.55	1.55	63.6	C84470	hypothetical protein At2g05580 [imported] - Arabidopsis thaliana	Arabidopsis thaliana
3	3.86	3.86	27.3	Q756R7_ASHGO	AER187Wp.- Ashbya gossypii (Yeast) (Eremothecium gossypii).	Ashbya gossypii
4	1.4	12.1	29.8	HATG	hemoglobin alpha-1 chains - Australian echidna (tentative sequence)	Australian echidna
5	1.55	12.5	34	HABDBM	hemoglobin alpha chain - beech marten	beech marten
6	2.98	2.98	23.4	AAI02942	BC102941 NID: - Bos Taurus	Bos taurus
7	2.82	2.82	10.5	Q1RMN3_BOVIN	Hypothetical protein.- Bos taurus (Bovine).	Bos taurus
8	2.01	2.01	4.8	Q32T06_BOVIN	Endopin 2C.- Bos taurus (Bovine).	Bos taurus
9	2	2	21.2	Q3ZEJ6_BOVIN	Muscle endopin 1b.- Bos taurus (Bovine).	Bos taurus
10	2	9.98	24.3	Q9N180_BOVIN	Ankyrin 1 (Fragment).- Bos taurus (Bovine).	Bos taurus
11	2	2	33.8	Q32PI5_BOVIN	Hypothetical protein.- Bos taurus (Bovine).	Bos taurus
12	1.7	1.7	10.3	Q5J801_BOVIN	Endopin 2B.- Bos taurus (Bovine).	Bos taurus
13	1.7	1.7	19.1	Q3SYR8_BOVIN	Immunoglobulin J chain.- Bos taurus (Bovine).	Bos taurus
14	2.08	2.08	25.5	cont|000097	gi|1351907|sp|P02769|ALBU_BOVIN Serum albumin precursor (Allergen Bos d 6) (BSA) [Bos taurus (contaminant)]	Bos taurus (contaminant)
15	2.05	2.05	12.3	cont|000070	gi|27806941|ref|NP_776307.1| serine (or cysteine) proteinase inhibitor, clade A (alpha-1antiproteinase, antitrypsin), member 1 [Bos taurus (contaminant)]	Bos taurus (contaminant)
16	2.1	7.87	39	HABO	hemoglobin alpha chain [validated] – bovine	bovine
17	2	2	24.2	S13188	apolipoprotein C-III - bovine (fragment)	bovine
18	1.4	3.2	24.8	HATPI	hemoglobin alpha-I chain – Brazilian tapir	Brazilian tapir

19	2.09	2.09	23.9	S55505	fatty-acid synthase (EC 2.3.1.85) - Brevibacterium ammoniagenes	Brevibacterium ammoniagenes
20	2.14	28.3	33.3	HAMQA	hemoglobin alpha chain - brown capuchin	brown capuchin
21	4.03	14.8	34.8	HALEF	hemoglobin alpha chain - brown lemur (tentative sequence)	brown lemur
22	2.98	30.3	42.6	HAMQF	hemoglobin alpha chain - brown-headed tamarin	brown-headed tamarin
23	1.4	1.4	6.9	A33977	myosin heavy chain, nonmuscle – chicken	chicken
24	2	2	35.6	JN0835	carbonate dehydratase (EC 4.2.1.1) I - chimpanzee	chimpanzee
25	1.52	9.57	66	HAGO3C	hemoglobin alpha-3 chain - chimpanzee (tentative sequence)	chimpanzee
26	1.34	1.34	31.2	Q2WGW0_CLOBE	Aspartyl aminopeptidase.- Clostridium beijerincki NCIMB 8052.	Clostridium beijerincki NCIMB
27	1.52	1.52	15.2	Q1NV99_9DELT	Hypothetical protein.- delta proteobacterium MLMS-1.	delta proteobacterium MLMS
28	2	2	8.2	Q54HE5_DICDI	Actin.- Dictyostelium discoideum AX4.	Dictyostelium discoideum AX
29	2.5	8.54	35.5	HAMNIF	hemoglobin alpha-I chain – domestic ferret	domestic ferret
30	1.7	1.7	15.4	Q291H8_DROPS	GA15593-PA (Fragment).- Drosophila pseudoobscura (Fruit fly).	Drosophila pseudoobscura
31	2.24	14.1	31.2	HAOL	hemoglobin alpha chain – Ehrenberg's mole-rat	Ehrenbergs mole-rat
32	2	6.12	34.2	HBOL	hemoglobin beta chain - Ehrenberg's mole-rat	Ehrenbergs mole-rat
33	1.4	1.4	9.2	Q5BC51_EMENI	Hypothetical protein.- Emericella nidulans (Aspergillus nidulans).	Emericella nidulans
34	3.34	20.5	71.9	HBBD	hemoglobin beta chain - Eurasian badger (tentative sequence)	Eurasian badger
35	6.55	9.55	51.1	A53880	hemoglobin alpha chain - European lynx	European lynx
36	2.43	8.12	56	HAUK2E	hemoglobin alpha-II chain - European polecat	European polecat
37	1.7	1.7	17.6	Q3W3V6_9ACTO	Hypothetical protein precursor.- Frankia sp. EAN1pec.	Frankia
38	2.01	9.78	44.8	HBBOG	hemoglobin beta chain – gayal	gayal
39	1.4	1.4	16.4	Q4IQV4_GIBZE	Hypothetical protein.- Gibberella zeae (Fusarium graminearum).	Gibberella zeae
40	2.07	13.1	41.1	HAHY	hemoglobin alpha chain - golden hamster	golden hamster
41	1.4	14.1	57.4	HAGW	hemoglobin alpha chain – guanaco	guanaco
42	1.4	1.4	11.3	Q5V3G6_HALMA	Cell division protein pelota.- Haloarcula marismortui (Halobacterium marismortui).	Haloarcula marismortui

43	2	12	41.8	HAMQP	hemoglobin alpha chain - hanuman langur	hanuman langur
44	55.59	55.6	77.5	AAK37554	AF349571 NID: - H. sapiens	H.sapiens
45	54.19	54.2	71.1	CAJ42703	CS185522 NID: - H. sapiens	H.sapiens
46	42.84	42.8	87.1	Q549N7_HUMAN	Mutant beta-globin.- H. sapiens (Human).	H.sapiens
47	24.7	24.7	24.6	SPTA1_HUMAN	Spectrin alpha chain, erythrocyte (Erythroid alpha-spectrin).- Homo sapiens (Human).	H.sapiens
48	21.34	21.3	34.5	Q4KKW9_HUMAN	Solute carrier family 4, anion exchanger, member 1 (Erythrocyte membrane protein band 3, Diego blood group).- Homo sapiens (Human).	H.sapiens
49	16	16	27.6	SPTB1_HUMAN	Spectrin beta chain, erythrocyte (Beta-I spectrin).- Homo sapiens (Human).	H.sapiens
50	10.9	10.9	17.2	Q59FP5_HUMAN	Spectrin, beta, erythrocytic (Includes spherocytosis, clinical type I) variant (Fragment).- Homo sapiens (Human).	H.sapiens
51	8.43	8.43	14.2	SPTA1_HUMAN	Spectrin alpha chain, erythrocyte (Erythroid alpha-spectrin).- Homo sapiens (Human).	H.sapiens
52	7.33	7.33	93.3	Q8IZI0_HUMAN	Hemoglobin beta chain variant Hb-I_Toulouse (Fragment).- Homo sapiens (Human).	H.sapiens
53	6.14	6.14	38.5	CAA31128	HSANTP NID: - Homo sapiens	H.sapiens
54	6	6	35.7	Q5VYL2_HUMAN	Spectrin, alpha, erythrocytic 1 (Elliptocytosis 2).- Homo sapiens (Human).	H.sapiens
55	5.62	5.62	35.3	AAA60578	HUMSPTB NID: - Homo sapiens	H.sapiens
56	4.96	4.96	14.7	AAA36401	HUMP42LA NID: - Homo sapiens	H.sapiens
57	4.74	4.74	16.8	UBP14_HUMAN	Ubiquitin carboxyl-terminal hydrolase 14 (EC 3.1.2.15) (Ubiquitin thioesterase 14) (Ubiquitin-specific-processing protease 14) (Deubiquitinating enzyme 14).- Homo sapiens (Human).	H.sapiens
58	4.64	4.64	7.6	Q4KKW9_HUMAN	Solute carrier family 4, anion exchanger, member 1 (Erythrocyte membrane protein band 3, Diego blood group).- Homo sapiens (Human).	H.sapiens
59	4.26	4.26	10.9	Q59F12_HUMAN	Protein 4.1 variant (Fragment).- Homo sapiens (Human).	H.sapiens
60	4.06	26.2	97.8	Q86YQ1_HUMAN	Hemoglobin alpha-2 (Fragment).- Homo sapiens (Human).	H.sapiens
61	4	4	37	Q59EH3_HUMAN	Acid phosphatase 1 isoform c variant (Fragment).- Homo sapiens (Human).	H.sapiens
62	3.7	3.7	10.5	SPTA1_HUMAN	Spectrin alpha chain, erythrocyte (Erythroid alpha-spectrin).- Homo sapiens (Human).	H.sapiens
63	3.31	34.6	45	CAJ42835	CS185654 NID: - Homo sapiens	H.sapiens

64	3.1	37.6	73.9	AAN04486	AF536204 NID: - Homo sapiens	H.sapiens
65	2.66	25.5	96.6	Q86YQ4_HUMAN	Alpha-1 globin (Fragment).- Homo sapiens (Human).	H.sapiens
66	2.15	2.15	26.8	STOM_HUMAN	Erythrocyte band 7 integral membrane protein (Stomatin) (Protein 7.2b).- Homo sapiens (Human).	H.sapiens
67	2	2	6.9	Q59FP5_HUMAN	Spectrin, beta, erythrocytic (Includes spherocytosis, clinical type I) variant (Fragment).- Homo sapiens (Human).	H.sapiens
68	2	2	14.8	Q9ULP9_HUMAN	KIAA1171 protein (Fragment).- Homo sapiens (Human).	H.sapiens
69	2	2	20.3	ARK72_HUMAN	Aflatoxin B1 aldehyde reductase member 2 (EC 1.-.-.-) (AFB1-AR 1) (Aldoketoreductase 7).- Homo sapiens (Human).	H.sapiens
70	2	2	23.4	Q96M16_HUMAN	CDNA FLJ32899 fis, clone TESTI2005408, highly similar to SER/THR-RICH PROTEIN T10 IN DGCR REGION.- Homo sapiens (Human).	H.sapiens
71	2	2	24.2	Q2TSD0_HUMAN	Aging-associated gene 9 protein.- Homo sapiens (Human).	H.sapiens
72	2	26	42.3	Q1HDT5_HUMAN	Hemoglobin alpha 1-2 hybrid.- Homo sapiens (Human).	H.sapiens
73	2	2	43.6	Q2TSD0_HUMAN	Aging-associated gene 9 protein.- Homo sapiens (Human).	H.sapiens
74	1.96	30.1	87.1	Q6R7N2_HUMAN	Hemoglobin beta.- Homo sapiens (Human).	H.sapiens
75	1.74	50.3	76.7	Q6J1Z9_HUMAN	Hemoglobin alpha 1 (Fragment).- Homo sapiens (Human).	H.sapiens
76	1.7	1.7	5.1	TCPQ_HUMAN	T-complex protein 1 subunit theta (TCP-1-theta) (CCT-theta) (NY-REN-15 antigen).- Homo sapiens (Human).	H.sapiens
77	1.7	1.7	28.3	Q53YB8_HUMAN	Uroporphyrinogen decarboxylase.- Homo sapiens (Human).	H.sapiens
78	1.7	10.7	94.6	AAZ39780	DQ126305 NID: - Homo sapiens	H.sapiens
79	1.39	1.39	9.9	Q6B838_HUMAN	Transglutaminase 2 (C polypeptide, protein-glutamine-gamma- glutamyltransferase).- Homo sapiens (Human).	H.sapiens
80	18.09	18.1	60.3	6HBWB	hemoglobin beta mutant YES, chain B - human	human
81	11.69	11.7	20.3	SJHUK	ankyrin 1, erythrocyte splice form 1 – human	human
82	10.73	10.7	86.3	1GBVB	hemoglobin mutant CHAIN B, D, C112G alpha-oxy, beta-deoxy, t state, chain B - human	human
83	10	10	87.7	1GBUB	hemoglobin mutant CHAIN B, D, C93A, C112G deoxy, chain B - human	human
84	7.18	7.18	63	1HBAB	hemoglobin beta chain mutant (W37R) (deoxy, Hb Rothschild), chain B - human	human
85	5.4	5.4	40.5	SJHUB	spectrin beta chain – human	human
86	5.15	5.15	20.3	CRHU1	carbonate dehydratase (EC 4.2.1.1) I [validated] - human	human

87	5.11	28.7	72.6	HDHU	hemoglobin delta chain – human	human
88	4.57	4.57	48.1	JC2070	flavin reductase (EC 1.5.1.30) – human	human
89	2.54	2.54	20	SJHUA	spectrin alpha chain – human	human
90	2.1	35.3	85.6	1A01B	hemoglobin beta chain mutant (V1M, W37Y) (deoxy), chain B - human	human
91	2.07	2.07	21.1	B3HU	band 3 anion transport protein, erythrocyte - human	human
92	2	2	35.4	S00072	glycophorin B/glycophorin A mutant fusion protein Dantu - human	human
93	2	2	55.6	G02786	uroporphyrinogen decarboxylase – human	human
94	2	6.18	57.5	1GBUB	hemoglobin mutant CHAIN B, D, C93A, C112G deoxy, chain B - human	human
95	1.91	35.6	80.8	1QI8B	hemoglobin chain beta, chain B – human	human
96	1.7	1.7	55.8	JC2070	flavin reductase (EC 1.5.1.30) – human	human
97	2	2	26	Q28N87_JANSC	Monooxygenase, FAD-binding precursor.- Jannaschia sp. (strain CCS1).	Jannaschia
98	2.02	23.1	61	HAMQJ	hemoglobin alpha chain - Japanese macaque	Japanese macaque
99	2.29	16.7	48.2	S59496	hemoglobin alpha chain - lobe-lipped bat	lobe-lipped bat
100	2	19.9	63.8	HBA_MACSI	Hemoglobin subunit alpha-1/2 (Hemoglobin alpha-1/2 chain) (Alpha-1/2- globin).- Macaca sinica (Toque macaque) (Toque monkey).	Macaca sinica
101	4	4	9.8	S49155	heat shock protein 86 - malaria parasite (Plasmodium falciparum)	**malaria parasite**
102	2.9	2.9	37.5	S12628	actin - malaria parasite (Plasmodium falciparum)	**malaria parasite**
103	2.19	2.19	6.5	SAZQGM	major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (strain CAMP/Malaysia)	**malaria parasite**
104	2	2	8.1	S27833	rhoptry-associated protein 1 precursor - malaria parasite (Plasmodium falciparum)	**malaria parasite**
105	2	2	21.7	B71623	knob-associated His-rich protein PFB0100c - malaria parasite (Plasmodium falciparum)	**malaria parasite**
106	2	2	23.2	T18430	hypothetical protein PFC0350c - malaria parasite (Plasmodium falciparum)	**malaria parasite**
107	1.74	1.74	16.4	S40121	ras-related nuclear protein - malaria parasite (Plasmodium falciparum)	**malaria parasite**
108	2.01	3.39	39	S13280	hemoglobin alpha chain - masked palm civet	masked palm civet
109	2	2	16.2	Q9SST5_9ASTR	TAT-binding protein homolog.- Matricaria chamomilla.	Matricaria chamomilla

110	2.88	19.5	48.9	JC1099	hemoglobin alpha chain - moustached tamarind	moustached tamarin
111	2.7	14.2	41.5	Q61287_MOUSE	Alpha-globin.- Mus musculus (Mouse).	Mus musculus
112	2	2	7.5	Q7TMI0_MOUSE	Psmd11 protein (Fragment).- Mus musculus (Mouse).	Mus musculus
113	2	2	56.1	Q5SYK6_MOUSE	Cytokine receptor-like factor 3.- Mus musculus (Mouse).	Mus musculus
114	1.52	1.52	19.5	Q5DTQ8_MOUSE	MKIAA4056 protein (Fragment).- Mus musculus (Mouse).	Mus musculus
115	1.45	9.93	24.1	Q8BYM1_MOUSE	Adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A230090E05 product:similar to HAEMAGLOBIN THETA 1.- Mus musculus (Mouse).	Mus musculus
116	1.4	1.4	26.6	Q1D3U7_MYXXA	Hypothetical protein.- Myxococcus xanthus DK 1622.	Myxococcus xanthus DK
117	2.82	17.9	62.4	HARTNG	hemoglobin alpha chain - northern gundi	northern gundi
118	2	2	24.8	Q2G4K3_NOVAD	Glycerol-3-phosphate dehydrogenase (NAD(P)+) (EC 1.1.1.94).- Novosphingobium aromaticivorans (strain DSM 12444).	Novosphingobium aromaticivorans
119	2.24	2.24	10.4	RINI_PANTR	Ribonuclease inhibitor (Ribonuclease/angiogenin inhibitor 1).- Pan troglodytes (Chimpanzee).	Pan troglodytes
120	2	18.2	61.9	HBPG	hemoglobin beta chain [validated] – pig	pig
121	3.01	13.6	80.1	HAMQIP	hemoglobin alpha-I chain - pig-tailed macaque	pig-tailed macaque
122	4.02	15.5	31	HBA_PIPAB	Hemoglobin subunit alpha (Hemoglobin alpha chain) (Alpha-globin).- Pipistrellus abramus (Japanese pipistrelle) (Japanese house bat).	Pipistrellus abramus
123	2.12	3.52	20.8	Q8WT39_PLABE	Heat shock protein 70.- Plasmodium berghei.	**Plasmodium berghei**
124	6	6	31.1	Q8I0V4_PLAF7	Endoplasmin homolog, putative.- Plasmodium falciparum (isolate 3D7).	**Plasmodium falciparum**
125	4	4	21.1	Q8IDQ9_PLAF7	Phosphoethanolamine N-methyltransferase, putative (EC 2.1.1.103).- Plasmodium falciparum (isolate 3D7).	**Plasmodium falciparum**
126	3.52	3.52	21.9	Q8I0V4_PLAF7	Endoplasmin homolog, putative.- Plasmodium falciparum (isolate 3D7).	**Plasmodium falciparum**
127	3.16	3.16	21.4	Q8T6B1_PLAFA	Glyceraldehyde-3-phosphate dehydrogenase.- Plasmodium falciparum.	**Plasmodium falciparum**
128	2.32	3.05	22.5	Q8I2X4_PLAF7	Heat shock protein.- Plasmodium falciparum (isolate 3D7).	**Plasmodium falciparum**
129	2.2	2.2	9.4	CAG25330	CR382399 NID: - Plasmodium falciparum 3D7	**Plasmodium falciparum**
130	2.17	2.17	11.7	Q9U460_PLAFA	Membrane-associated calcium-binding protein.- Plasmodium falciparum.	**Plasmodium falciparum**

131	2	2	5.6	Q9BHT6_PLAFA	Putative Rab2 GTPase.- Plasmodium falciparum.	**Plasmodium falciparum**
132	2	2	7.6	Q8IHR4_PLAF7	Dynamin-like protein.- Plasmodium falciparum (isolate 3D7).	**Plasmodium falciparum**
133	2	2	7.7	Q9NDT2_PLAFA	Elongation factor 2 (Fragment).- Plasmodium falciparum.	**Plasmodium falciparum**
134	2	2	13.1	Q8IE10_PLAF7	Glutaminyl-tRNA synthetase, putative (EC 6.1.1.18).- Plasmodium falciparum (isolate 3D7).	**Plasmodium falciparum**
135	2	2	17.8	Q8I0V4_PLAF7	Endoplasmin homolog, putative.- Plasmodium falciparum (isolate 3D7).	**Plasmodium falciparum**
136	2	2	21.2	Q8IDS5_PLAF7	Ribosomal protein L18.- Plasmodium falciparum (isolate 3D7).	**Plasmodium falciparum**
137	2	2	39.6	Q8I1S0_PLAF7	Small GTP-binding protein sar1.- Plasmodium falciparum (isolate 3D7).	**Plasmodium falciparum**
138	1.7	1.7	23.3	Q8I2S6_PLAF7	DNA-directed RNA polymerase II, putative (EC 2.7.7.6).- Plasmodium falciparum (isolate 3D7).	**Plasmodium falciparum**
139	1.62	1.62	19.3	Q71T02_PLAFA	L-lactate dehydrogenase (EC 1.1.1.27).- Plasmodium falciparum.	**Plasmodium falciparum**
140	50.05	50.1	56.7	HBA_PONPY	Hemoglobin subunit alpha (Hemoglobin alpha chain) (Alpha-globin).- Pongo pygmaeus (Orangutan).	Pongo pygmaeus
141	9.97	9.97	36.2	G3P_PONPY	Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH).- Pongo pygmaeus (Orangutan).	Pongo pygmaeus
142	4	30	47.2	Q3LRX5_PONPY	Alpha globin a3.- Pongo pygmaeus (Orangutan).	Pongo pygmaeus
143	2	2	21.3	Q3KED9_PSEPF	FAD dependent oxidoreductase.- Pseudomonas fluorescens (strain PfO-1).	Pseudomonas fluorescens
144	1.52	1.52	39.4	Q1FQW9_9GAMM	Diaminopimelate decarboxylase.- Psychromonas ingrahamii 37.	Psychromonas ingrahamii
145	2.09	14.9	33.3	HAMQB	hemoglobin alpha chain - red colobus (tentative sequence)	red colobus
146	2	2	10.8	CRMQ1R	carbonate dehydratase (EC 4.2.1.1) I - rhesus macaque (tentative sequence)	rhesus macaque
147	1.52	1.52	18.1	Q840T1_9NOCA	Aldehyde dehydrogenase (EC 1.2.1.3).- Rhodococcus ruber.	Rhodococcus ruber
148	4.2	15	31.2	HALEIR	hemoglobin alpha-I chain - ruffed lemur	ruffed lemur
149	2	2	6.9	ABSHS	serum albumin precursor – sheep	sheep
150	2.3	22	53.2	HALRS	hemoglobin alpha chain - slow loris	slow loris
151	2	7.52	46.1	HAMKS	hemoglobin alpha chain - sooty mangabey	sooty mangabey
152	2	2	26.4	AAB94053	AF017079 NID: - Sus scrofa	Sus scrofa
153	2	14.2	47.5	HAGC	hemoglobin alpha-I chain - thick-tailed bush baby (tentative sequence)	thick-tailed bush baby
154	2	2	14.7	Q9BKE2_TOXGO	Glyceraldehyde-3-phosphate dehydrogenase.- Toxoplasma gondii.	Toxoplasma gondii

155	2	2	56.8	Q1ZPE9_9VIBR	Putative MinD-related protein.- Vibrio angustum S14.	Vibrio angustum S
156	1.54	18.5	53.9	HATB	hemoglobin alpha chain - western tarsier (tentative sequence)	western tarsier
157	2.03	34.1	58.2	A25477	hemoglobin alpha chain - white-faced sapajou	white-faced sapajou
158	3.1	7.99	53.9	HABAY	hemoglobin alpha chain - yellow baboon	yellow baboon

Table 2: Summary of six protein mix identified by trypsin in-gel digestion

N	**Unused**	**Total**	**% Cov**	**Accession #**	**Name**	**Species**
1	29	29	43.6	TFHUP	transferrin precursor [validated] – human	human
2	22.09	22.1	28.8	cont|000097	gi|1351907|sp|P02769|ALBU_BOVIN Serum albumin precursor (Allergen Bos d 6) (BSA) [Bos taurus (contaminant)]	Bos taurus
3	18.93	18.9	19.8	cont|000160	gi|114939|sp|P00722|BGAL_ECOLI Beta-galactosidase (Lactase) [Escherichia coli]	Escherichia coli
4	10.02	10	74.7	1BSOA	bovine beta-lactoglobulin a – bovine	bovine
5	5.96	5.96	42.6	cont|000147	prf|630460A| lysozyme [Gallus gallus]	Gallus gallus
6	3.25	3.25	26	cont|000143	pdb|1FNI_A| A Chain A, Crystal Structure Of Porcine Beta Trypsin With 0.01% Polydocanol [Sus scrofa]	Sus scrofa
7	3.94	3.94	24.1	1BSQA	beta-lactoglobulin mutant YES – bovine	bovine
8	25	25	53	P02787	Serotransferrin precursor (transferrin)	human

Unused – A measure of the protein confidence for a detected protein (95% confidence); **N** – the rank of the specified protein relative to all other proteins in the list of detected proteins; **Total** – A measure of the total amount of evidence for a detected protein calculated using all of the peptides detected for the protein; **% Cov** – The percentage of matching amino acids from identified peptides having confidence greater than or equal to 95%, divided by the total number of amino acids in the sequence; **Accession number** – MSDB accession number assigned to protein; **Name** – MSDB name assigned to protein; **Species** – species origin of protein based on peptide sequences identified

2 APPENDIX 2

Table 1: Proteins identified using the PlasmoDB v 5.5 database

N	Unused	Total	% Cov	Accession #	Name	Species
1	2.45	2.45	24.4	pfa3D7predicted|chr11|chr11	coding) 26% identity to 52% of Q9MBF8: Dynein 1-beta heavy chain, flagellar inner arm I1 complex (1-beta DHC) (Dynein 1, subspecies f) Location= chr11	**118f|Genefinder|Plasmodium_ falciparum_TIGR|(protein**
2	2.55	2.55	63.7	pfa3D7predicted|chr5|chr5	coding) 100% identity to 100% of 1Q1G.C: Chain C, Crystal Structure Of Plasmodium Falciparum Pnp With 5'- Methylthio-Immucillin-H Location= chr5	**153|FullPhat|Plasmodium_ falciparum_Sanger|(protein**
3	1.55	1.58	45.9	pfa3D7predicted|chr8|chr8.	coding) 46% identity to 57% of 2116446C: ORF Location= chr8	**162f|Genefinder|Plasmodium_ falciparum_Sanger|(protein**
4	2.07	2.07	44.3	pfa3D7predicted|chr12|chr12	coding) null Location= chr12 complement	**162r|Genefinder|Plasmodium_ falciparum_Sanger|(protein**
5	5.37	5.37	74.5	pfa3D7predicted|chr9|chr9	coding) 100% identity to 100% of AAA93010.1: PBGRP Location= chr9	**173|FullPhat|Plasmodium_ falciparum_Sanger|(protein**
6	1.68	1.68	56.1	pfa3D7predicted|chr11|chr11.	coding) 100% identity to 100% of P38545: GTP-binding nuclear protein Ran (GTPase Ran) (Ras-like protein TC4) Location= chr11	**196|FullPhat|Plasmodium_ falciparum_TIGR|(protein**
7	1.9	1.9	33.3	pfa3D7predicted|chr13|chr13.	coding) 35% identity to 53% of AAO52024.1: similar to Dictyostelium discoideum (Slime mold). Homeobox-containing protein (Fragment) Location= chr13	**208|FullPhat|Plasmodium_ falciparum_Sanger|(protein**
8	1.9	1.94	34.6	pfa3D7predicted|chr1|chr1.	coding) 41% identity to 54% of 2116446C: ORF Location= chr1 join(29733..34985, 36111..37334, 37632..37805)	**21|FullPhat|Plasmodium_ falciparum_Sanger|(protein**

9	2.27	2.32	52.3	pfa3D7predicted|chr4|chr4.	coding) 40% identity to 57% of AAQ74128.1: A4tres CIDR1 [synthetic construct] Location= chr4 complement	**219|FullPhat|Plasmodium_falciparum_Sanger|(protein**
10	1.65	1.73	49.1	pfa3D7predicted|chr10|chr10.	coding) 36% identity to 49% of 2116446C: ORF Location= chr10	**23|FullPhat|Plasmodium_falciparum_TIGR|(protein**
11	1.61	1.61	65.9	pfa3D7predicted|chr12|chr12	coding) null Location= chr12	**232|FullPhat|Plasmodium_falciparum_Sanger|(protein**
12	9.44	9.44	62.3	pfa3D7predicted|chr13|chr13	coding) 100% identity to 100% of 1T26.A: Chain A, Plasmodium Falciparum Lactate Dehydrogenase Complexed With Nadh And 4-Hydroxy-1,2,5-Thiadiazole-3-Carboxylic Acid Location= chr13	**270|FullPhat|Plasmodium_falciparum_Sanger|(protein**

13	2.58	2.58	41.1	pfa3D7predicted|chr13|chr13.	coding) 44% identity to 61% of 2116222A: variant surface protein Location= chr13	**345r|Genefinder|Plasmodium_falciparum_Sanger|(protein**
14	4.2	4.2	49.4	pfa3D7predicted|chr8|chr8.	coding) 44% identity to 57% of 2116446C: ORF Location= chr8 complement(join	**346|FullPhat|Plasmodium_falciparum_Sanger|(protein**
15	2.14	2.14	30.7	pfa3D7predicted|chr12|chr12.	coding) null Location= chr12 join	**347|FullPhat|Plasmodium_falciparum_Sanger|(protein**
16	1.86	1.87	27.5	pfa3D7predicted|chr12|chr12.	coding) null Location= chr12 join	**34f|Genefinder|Plasmodium_falciparum_Sanger|(protein**
17	2.08	2.08	41.4	pfa3D7predicted|chr6|chr6.	coding) 100% identity to 100% of Q07805: Ornithine aminotransferase (Ornithine--oxo-acid aminotransferase) Location= chr6	**42f|Genefinder|Plasmodium_falciparum_Sanger|(protein**
18	4.5	4.5	71.8	pfa3D7predicted|chr12|chr12.	coding) null Location= chr12 1920770..1921900	**460|FullPhat|Plasmodium_falciparum_Sanger|(protein**
19	3.3	3.34	46.3	pfa3D7predicted|chr11|chr11.	coding) 52% identity to 66% of 2116446C: ORF Location= chr11	**4f|Genefinder|Plasmodium_falciparum_TIGR|(protein**
20	2.34	2.34	29.7	pfa3D7predicted|chr12|chr12	coding) null Location= chr12 complement	**628|GlimmerM|Plasmodium_falciparum_Sanger|(protein**
21	2.63	2.63	39.7	pfa3D7predicted|chr6|chr6.	coding) 39% identity to 54% of 2116446C: ORF Location= chr6 complement	**79r|Genefinder|Plasmodium_falciparum_Sanger|(protein**
22	1.52	1.52	30.9	pfa3D7predicted|chr12|chr12.	coding) null Location= chr12	**836|GlimmerM|Plasmodium_falciparum_Sanger|(protein**
23	3.01	3.01	37.5	pfa3D7predicted|chr14|chr14.	coding) 33% identity to 55% of XP_396228.1: similar to dynein, axonemal, heavy chain 8; dynein, axon, heavy chain 8 [Apis mellifera] Location= chr14	Apis mellifera
24	1.48	1.48	29.6	pfa3D7predicted|chr10|chr10.	coding) 39% identity to 59% of NP_176917.2: DNA polymerase family B protein [Arabidopsis thaliana] Location= chr10	Arabidopsis thaliana
25	4.2	4.2	42	pfa3D7predicted|pfal_chr2|pfal_chr2.	coding) 100% identity to 100% of AAA29714.1: parasitophorous vacuole antigen Location= pfal_chr2 complement	**chr2|pfal_chr2.genefinder_74r|Genefinder|Plasmodium_ falciparum TIGR|(protein**
26	1.49	1.49	40.5	pfa3D7predicted|chr5|chr5.	coding) 32% identity to 53% of EAL38034.1: karyopherin beta [Cryptosporidium hominis] Location= chr5	Cryptosporidium hominis
27	1.61	1.63	35.1	pfa3D7predicted|chr11|chr11.	coding) 40% identity to 61% of CAD98495.1: putative transcription regulatory protein, possible [Cryptosporidium parvum] Location= chr11	Cryptosporidium parvum
28	1.47	1.47	43	pfa3D7predicted|chr13|chr13.	coding) 28% identity to 52% of CAD98262.1: hypothetical predicted Armadillo/beta-catenin-like repeat protein, unknown function Location= chr13	Cryptosporidium parvum
29	3.29	3.29	33.9	pfa3D7predicted|chr14|chr14.	coding) 29% identity to 45% of AAO53180.1: hypothetical protein [Dictyostelium discoideum] Location= chr14 complement	Dictyostelium discoideum
30	1.42	1.42	29.5	pfa3D7predicted|chr14|chr14.	coding) 28% identity to 43% of AAO53180.1: hypothetical protein [Dictyostelium discoideum] Location= chr14	Dictyostelium discoideum

31	1.78	1.78	50.8	pfa3D7predicted|chr8|chr8	coding) 46% identity to 68% of BAD15737.1: putative DegP2 protease [Oryza sativa (japonica cultivar-group)] Location= chr8 complement	Oryza sativa (japonica cultivar-group)
32	11.38	11.38	81.9	pfa3D7predicted|chr14|chr14.	coding) 84% identity to 95% of CAH99235.1: glyceraldehyde-3-phosphate dehydrogenase, putative [Plasmodium berghei]	Plasmodium berghei
33	4.11	4.16	32.6	pfa3D7predicted|chr14|chr14	coding) 37% identity to 52% of CAH97021.1: conserved hypothetical protein [Plasmodium berghei] Location= chr14 complement	Plasmodium berghei
34	3.01	3.01	56.8	pfa3D7predicted|chr9|chr9	coding) 80% identity to 92% of CAH95224.1: conserved hypothetical protein [Plasmodium berghei] Location= chr9 complement	Plasmodium berghei
35	2.87	2.87	94.2	pfa3D7predicted|chr5|chr5.	coding) 97% identity to 97% of CAH97256.1: 40S ribosomal subunit protein S14, putative [Plasmodium berghei] Location= chr5 complement	Plasmodium berghei
36	2.67	2.67	77.3	pfa3D7predicted|chr13|chr13.	coding) 91% identity to 98% of CAH98214.1: small GTPase Rab11, putative [Plasmodium berghei] Location= chr13	Plasmodium berghei
37	2.48	2.48	38	pfa3D7predicted|chr6|chr6.	coding) 48% identity to 63% of CAI04669.1: hypothetical protein PB105705.00.0 [Plasmodium berghei] Location= chr6	Plasmodium berghei
38	2.15	2.15	74.8	pfa3D7predicted|chr13|chr13	coding) 80% identity to 88% of CAH93761.1: phosphoribosylpyrophosphate synthetase, putative [Plasmodium berghei] Location= chr13 complement	Plasmodium berghei
39	1.96	1.96	38.2	pfa3D7predicted|chr5|chr5.	coding) 73% identity to 84% of CAH96435.1: hypothetical protein PB000785.01.0 [Plasmodium berghei] Location= chr5	Plasmodium berghei
40	1.94	1.94	26.7	pfa3D7predicted|chr8|chr8.	coding) 33% identity to 51% of CAH96228.1: hypothetical protein PB000644.01.0 [Plasmodium berghei] Location= chr8	Plasmodium berghei
41	1.76	1.76	25.2	pfa3D7predicted|chr11|chr11	coding) 36% identity to 55% of CAH95499.1: conserved hypothetical protein [Plasmodium berghei] Location= chr11 join	Plasmodium berghei
42	1.63	1.65	19.6	pfa3D7predicted|chr13|chr13.	coding) 36% identity to 55% of CAH98689.1: conserved hypothetical protein [Plasmodium berghei] Location= chr13	Plasmodium berghei
43	1.46	1.46	36.7	pfa3D7predicted|chr4|chr4.	coding) 37% identity to 54% of CAH97882.1: conserved hypothetical protein [Plasmodium berghei] Location= chr4	Plasmodium berghei
44	1.41	1.41	31.6	pfa3D7predicted|chr5|chr5.	coding) 43% identity to 61% of CAH96070.1: asparagine--tRNA ligase, putative [Plasmodium berghei] Location= chr5	Plasmodium berghei
45	1.4	1.4	26.3	pfa3D7predicted|chr13|chr13.	coding) 46% identity to 64% of CAH96693.1: hypothetical protein PB103910.00.0 [Plasmodium berghei] Location= chr13	Plasmodium berghei
46	5.39	5.39	38.8	pfa3D7predicted|chr5|chr5	coding) 46% identity to 62% of CAH79456.1: conserved hypothetical protein [Plasmodium chabaudi] Location= chr5	Plasmodium chabaudi
47	3.3	3.32	34.5	pfa3D7predicted|chr7|chr7.	coding) 48% identity to 62% of CAH77899.1: conserved hypothetical protein [Plasmodium chabaudi] Location= chr7 complement	Plasmodium chabaudi
48	2.94	2.94	38.8	pfa3D7predicted|chr14|chr14.	coding) 49% identity to 69% of CAH78083.1: conserved hypothetical protein	Plasmodium chabaudi

49	2.93	2.93	39.3	pfa3D7predicted|chr7|chr7.	coding) 31% identity to 49% of CAH81594.1: Cg7 protein, putative [Plasmodium chabaudi] Location= chr7 complement(join	Plasmodium chabaudi
50	2.11	2.11	39.2	pfa3D7predicted|chr9|chr9.	coding) 78% identity to 89% of CAH78643.1: conserved hypothetical protein [Plasmodium chabaudi] Location= chr9 complement	Plasmodium chabaudi
51	1.76	1.76	63.5	pfa3D7predicted|chr9|chr9.	coding) 90% identity to 96% of CAH80397.1: conserved hypothetical protein [Plasmodium chabaudi] Location= chr9	Plasmodium chabaudi
52	1.53	1.53	35	pfa3D7predicted|chr5|chr5.	coding) 82% identity to 89% of CAH76772.1: conserved hypothetical protein [Plasmodium chabaudi] Location= chr5	Plasmodium chabaudi
53	1.45	1.47	32.7	pfa3D7predicted|chr11|chr11.	coding) 53% identity to 65% of CAH76892.1: conserved hypothetical protein [Plasmodium chabaudi] Location= chr11	Plasmodium chabaudi
54	1.32	1.32	28.1	pfa3D7predicted|chr14|chr14.	coding) 40% identity to 53% of CAH74620.1: conserved hypothetical protein [Plasmodium chabaudi] Location= chr14	Plasmodium chabaudi
55	2.24	2.24	31.5	pfa3D7predicted|chr8|chr8.	coding) 84% identity to 92% of AAV36000.1: protein disulfide isomerase [Plasmodium chabaudi chabaudi] Location= chr8 complement	Plasmodium chabaudi chabaudi
56	2.8	2.8	71.1	pfa3D7predicted|chr8|chr8.	coding) 100% identity to 100% of AAC17515.1: 14-3-3 protein [Plasmodium knowlesi] Location= chr8	Plasmodium knowlesi
57	2.79	2.84	26.2	pfa3D7predicted|chr4|chr4.	coding) 23% identity to 44% of AAO38039.1: reticulocyte binding-like protein 2b [Plasmodium reichenowi] Location= chr4	Plasmodium reichenowi
58	1.52	1.52	26.4	pfa3D7predicted|chr8|chr8	coding) 32% identity to 55% of CAB96701.1: Pvstp1 [Plasmodium vivax] Location= chr8	Plasmodium vivax
59	6.2	6.2	94.8	pfa3D7predicted|chr13|chr13.	coding) 100% identity to 100% of EAA15302.1: translation elongation factor EF-1, subunit alpha [Plasmodium yoelii yoelii] Location= chr13	Plasmodium yoelii yoelii
60	4.73	4.73	64.3	pfa3D7predicted|chr10|chr10.	coding) 93% identity to 96% of EAA18207.1: ribosomal protein S2, putative [Plasmodium yoelii yoelii] Location= chr10	Plasmodium yoelii yoelii
61	3.21	3.21	33.3	pfa3D7predicted|chr13|chr13.	coding) 32% identity to 51% of EAA21279.1: chloroquine resistance marker protein [Plasmodium yoelii yoelii] Location= chr13 complement	Plasmodium yoelii yoelii
62	2.73	2.73	39.3	pfa3D7predicted|chr14|chr14	coding) 36% identity to 52% of EAA16501.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr14	Plasmodium yoelii yoelii
63	2.49	2.51	29.5	pfa3D7predicted|chr14|chr14	coding) 34% identity to 51% of EAA15702.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr14	Plasmodium yoelii yoelii
64	2.48	2.48	63	pfa3D7predicted|chr7|chr7	coding) 51% identity to 65% of EAA20598.1: Drosophila melanogaster LD15209p [Plasmodium yoelii yoelii] Location= chr7	Plasmodium yoelii yoelii
65	2.35	2.35	39	pfa3D7predicted|pfal_chr2|pfal_chr2	coding) 23% identity to 41% of EAA18039.1: hypothetical protein [Plasmodium yoelii yoelii] Location= pfal_chr2 complement	Plasmodium yoelii yoelii
66	2.28	2.29	41.3	pfa3D7predicted|chr1|chr1.	coding) 41% identity to 57% of EAA20533.1: Ubiquitin carboxyl-terminal hydrolase	Plasmodium yoelii yoelii
67	2.11	2.11	67.4	pfa3D7predicted|chr10|chr10	coding) 96% identity to 98% of EAA18347.1: 26S proteasome subunit 4-like protein [Plasmodium yoelii yoelii] Location= chr10 complement	Plasmodium yoelii yoelii
68	2.09	2.09	50	pfa3D7predicted|chr13|chr13	coding) 29% identity to 47% of EAA21778.1: chloroquine resistance marker protein	Plasmodium yoelii yoelii

69	1.86	1.88	44.7	pfa3D7predicted|chr8|chr8.	coding) 22% identity to 41% of EAA18039.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr8	Plasmodium yoelii yoelii
70	1.85	1.87	26.4	pfa3D7predicted|chr8|chr8.	coding) 26% identity to 45% of EAA18589.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr8	Plasmodium yoelii yoelii
71	1.81	1.81	27.3	pfa3D7predicted|chr4|chr4.	coding) 29% identity to 48% of EAA16876.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr4	Plasmodium yoelii yoelii
72	1.77	1.77	38.4	pfa3D7predicted|chr10|chr10.	coding) 53% identity to 71% of EAA17496.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr10	Plasmodium yoelii yoelii
73	1.76	1.76	29	pfa3D7predicted|chr5|chr5	coding) 27% identity to 44% of EAA18442.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr5	Plasmodium yoelii yoelii
74	1.65	1.65	34.3	pfa3D7predicted|chr9|chr9.	coding) 24% identity to 44% of EAA17393.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr9	Plasmodium yoelii yoelii
75	1.6	1.61	50.5	pfa3D7predicted|chr11|chr11.	coding) 26% identity to 46% of EAA19159.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr11	Plasmodium yoelii yoelii
76	1.59	1.59	18.1	pfa3D7predicted|chr7|chr7.	coding) 33% identity to 52% of EAA22516.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr7	Plasmodium yoelii yoelii
77	1.57	1.57	71.9	pfa3D7predicted|chr5|chr5.	coding) 95% identity to 99% of EAA16191.1: 60S ribosomal protein L8 [Plasmodium yoelii yoelii] Location= chr5 complement	Plasmodium yoelii yoelii
78	1.56	1.89	92.7	pfa3D7predicted|chr5|chr5.	coding) 100% identity to 100% of EAA20993.1: ribosomal protein S11, putative [Plasmodium yoelii yoelii] Location= chr5 complement	Plasmodium yoelii yoelii
79	1.56	1.56	34.6	pfa3D7predicted|chr4|chr4.	coding) 49% identity to 67% of EAA16412.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr4	Plasmodium yoelii yoelii
80	1.52	1.52	16.8	pfa3D7predicted|chr11|chr11.	coding) 28% identity to 45% of EAA22581.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr11	Plasmodium yoelii yoelii
81	1.51	1.51	34.5	pfa3D7predicted|chr5|chr5.	coding) 49% identity to 67% of EAA22286.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr5	Plasmodium yoelii yoelii
82	1.47	1.47	57.4	pfa3D7predicted|chr13|chr13	coding) 26% identity to 45% of EAA17051.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr13	Plasmodium yoelii yoelii
83	1.46	1.46	33	pfa3D7predicted|chr14|chr14.	coding) 25% identity to 44% of EAA17366.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr14	Plasmodium yoelii yoelii
84	1.4	1.41	38.3	pfa3D7predicted|chr3|chr3	coding) 34% identity to 52% of EAA21337.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr3	Plasmodium yoelii yoelii
85	1.39	1.4	37.5	pfa3D7predicted|chr3|chr3	coding) 29% identity to 47% of EAA21938.1: putative protein kinase [Plasmodium yoelii yoelii] Location= chr3	Plasmodium yoelii yoelii
86	1.37	1.39	33.2	pfa3D7predicted|chr13|chr13.	coding) 29% identity to 48% of EAA22695.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr13	Plasmodium yoelii yoelii
87	1.33	1.35	39.2	pfa3D7predicted|chr10|chr10	coding) 49% identity to 68% of EAA16713.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr10	Plasmodium yoelii yoelii

88	1.31	1.31	15.5	pfa3D7predicted|chr14|chr14.	coding) 42% identity to 59% of EAA17764.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr14	Plasmodium yoelii yoelii
89	4.13	4.13	38.9	pfa3D7predicted|chr7|chr7.	coding) 29% identity to 51% of BAA97048.1: cytoplasmic dynein heavy chain [Rattus norvegicus] Location= chr7	Rattus norvegicus
90	1.72	1.72	27.1	pfa3D7predicted|chr9|chr9.	coding) 33% identity to 54% of XP_220603.2: similar to 1-beta dynein [Rattus norvegicus] Location= chr9	Rattus norvegicus
91	2.88	2.92	75.8	pfa3D7predicted|chr8|chr8.	coding) 81% identity to 90% of AAC72001.1: heat shock protein 70 [Toxoplasma gondii] Location= chr8	Toxoplasma gondii

Table 2: Proteins identified using the MSDB database

N	Unused	Total	% Cov	Accession #	Name	Species
1	1.4	2.81	55.3	HAEMA	hemoglobin alpha chain - Amazon manatee	Amazon manatee
2	2.08	2.08	24.4	Q5TV98_ANOGA	ENSANGP00000028216.- Anopheles gambiae str. PEST.	Anopheles gambiae str
3	2.04	2.04	34.8	Q7PY43_ANOGA	ENSANGP00000011557.- Anopheles gambiae str. PEST.	Anopheles gambiae str
4	1.7	1.7	14.4	Q5P754_AZOSE	Hypothetical protein.- Azoarcus sp. (strain EbN1).	Azoarcus
5	2.02	2.02	20.3	Q8AAK3_BACTN	Beta-galactosidase.- Bacteroides thetaiotaomicron.	Bacteroides thetaiotaomicron
6	7.83	7.83	48.2	AAC71048	Immunoglobulin heavy chain constant region (Fragment).- Bos taurus (Bovine).	Bos taurus
7	5.36	5.36	38	Q2KIQ9_BOVIN	SERPINA3 protein.- Bos taurus (Bovine).	Bos taurus
8	4.76	4.76	41.7	AAN17824	AF542068 NID: - Bos taurus	Bos taurus
9	4.68	4.68	52.1	AAI02942	BC102941 NID: - Bos Taurus	Bos taurus
10	3.23	3.23	52.1	Q1RMN8_BOVIN	Hypothetical protein.- Bos taurus (Bovine).	Bos taurus
11	2.17	2.17	35.3	Q5J801_BOVIN	Endopin 2B.- Bos taurus (Bovine).	Bos taurus
12	1.71	1.71	44.1	AAI11226	BC111225 NID: - Bos Taurus	Bos taurus
13	1.38	1.38	22.9	AAI10173	BC110172 NID: - Bos Taurus	Bos taurus
14	1.32	1.32	12.3	Q6RKJ5_BOTCI	Polyketide synthase.- Botrytis cinerea (Noble rot fungus) (Botryotinia fuckeliana).	Botrytis cinerea
15	3.56	3.56	23.3	S21097	alpha-1-antitrypsin precursor – bovine	bovine
16	1.7	1.7	25.2	Q5RG12_BRARE	Novel protein similar to heat shock protein 90-alpha (Hsp90a).- Brachydanio rerio (Zebrafish) (Danio rerio).	Brachydanio rerio

17	1.43	1.43	17.6	AAM18908	IGF-IRb receptor.- Brachydanio rerio (Zebrafish) (Danio rerio).	Brachydanio rerio
18	1.75	1.75	38	Q35F02_9BRAD	Hypothetical protein.- Bradyrhizobium sp. BTAi1.	Bradyrhizobium
19	1.4	1.4	6.5	Q89M96_BRAJA	Blr4297 protein.- Bradyrhizobium japonicum.	Bradyrhizobium japonicum
20	1.51	1.51	29.9	Q60MX8_CAEBR	Hypothetical protein CBG22961.- Caenorhabditis briggsae.	Caenorhabditis briggsae
21	1.58	1.58	11.1	T26313	hypothetical protein W09D6.6 - Caenorhabditis elegans	Caenorhabditis elegans
22	1.41	1.41	24	Q4ANE5_9CHLB	Hypothetical protein.- Chlorobium phaeobacteroides BS1.	Chlorobium phaeobacteroides BS
23	2.04	2.04	14.2	Q4CDY5_CLOTM	ATP-binding region, ATPase-like.- Clostridium thermocellum ATCC 27405.	Clostridium thermocellum ATCC
24	4.59	10.9	93.8	HBD_COLPO	Hemoglobin subunit delta (Hemoglobin delta chain) (Delta-globin).- Colobus polykomos (Western black-and-white colobus monkey).	Colobus polykomos
25	1.53	1.53	28.9	Q4BXP9_CROWT	Phycobilisome linker polypeptide:Phycobilisome protein.- Crocosphaera watsonii.	Crocosphaera watsonii
26	2	2	15.2	Q6BSH7_DEBHA	Debaryomyces hansenii chromosome D of strain CBS767 of Debaryomyces hansenii.- Debaryomyces hansenii (Yeast) (Torulaspora hansenii).	Debaryomyces hansenii
27	7.2	17.4	97.3	HDMKDU	hemoglobin delta chain - douroucouli (tentative sequence)	douroucouli
28	1.52	1.52	16	Q295W8_DROPS	GA21900-PA (Fragment).- Drosophila pseudoobscura (Fruit fly).	Drosophila pseudoobscura
29	1.31	1.31	18.3	Q29NG1_DROPS	GA18401-PA (Fragment).- Drosophila pseudoobscura (Fruit fly).	Drosophila pseudoobscura
30	1.31	8.7	66.7	HABTF	hemoglobin alpha chain - Egyptian rousette (tentative sequence)	Egyptian rousette
31	1.88	3.73	80.7	HBBOG	hemoglobin beta chain – gayal	gayal
32	3.37	6.05	86.5	HAGW	hemoglobin alpha chain – guanaco	guanaco
33	1.33	1.33	26.9	G84315	cobalt transport protein [imported] - Halobacterium sp. NRC-1	Halobacterium
34	29.73	29.7	81.5	AAG41947	AF304164 NID: - Homo sapiens	H.sapiens
35	20.82	20.8	83.4	Q8N175_HUMAN	Keratin 10.- Homo sapiens (Human).	H.sapiens
36	18.58	18.6	41.7	SPTA1_HUMAN	Spectrin alpha chain, erythrocyte (Erythroid alpha-spectrin).- Homo sapiens (Human).	H.sapiens
37	18.07	18.1	44.8	Q59FP5_HUMAN	Spectrin, beta, erythrocytic (Includes spherocytosis, clinical type I) variant	H.sapiens
38	13.56	13.6	47.6	Q4KKW9_HUMAN	Solute carrier family 4, anion exchanger, member 1 (Erythrocyte membrane protein band 3, Diego blood group).- Homo sapiens (Human).	H.sapiens
39	12.39	15.1	81.4	Q4VAQ2_HUMAN	Keratin 2A (Epidermal ichthyosis bullosa of Siemens).- Homo sapiens (Human).	H.sapiens
40	6.68	6.68	43.8	AAA36401	HUMP42LA NID: - Homo sapiens	H.sapiens
41	5.85	5.85	64.6	CAG30024	CQ815085 NID: - Homo sapiens	H.sapiens
42	4.75	4.75	45.9	Q53F93_HUMAN	Palmitoylated membrane protein 1 variant (Fragment).- Homo sapiens (Human).	H.sapiens
43	4.68	4.68	43.6	Q9H7N4_HUMAN	FLJ00034 protein (Fragment).- Homo sapiens (Human).	H.sapiens
44	3	3	50.3	Q59EH3_HUMAN	Acid phosphatase 1 isoform c variant (Fragment).- Homo sapiens (Human).	H.sapiens
45	2.13	2.13	36.3	Q59F12_HUMAN	Protein 4.1 variant (Fragment).- Homo sapiens (Human).	H.sapiens
46	2.03	2.03	26.9	CAA40296	HSQAE1 NID: - Homo sapiens	H.sapiens
47	2.03	2.03	19.4	Q6B838_HUMAN	Transglutaminase 2 (C polypeptide, protein-glutamine-gamma- glutamyltransferase).- Homo sapiens (Human).	H.sapiens
48	2.01	2.01	29.4	Q4VX10_HUMAN	Pyruvate kinase, liver and RBC.- Homo sapiens (Human).	H.sapiens
49	2.01	2.01	45.9	CAA36235	HSGCI NID: - Homo sapiens	H.sapiens
50	1.52	21.3	100	Q8IUL9_HUMAN	Hemoglobin beta chain variant Hb.Sinai-Bel Air (Fragment).- Homo sapiens (Human).	H.sapiens
51	1.4	15.8	100	Q3LR79_HUMAN	Hemoglobin beta (Fragment).- Homo sapiens (Human).	H.sapiens
52	1.32	1.32	18.5	CAD97926	HSM806091 NID: - Homo sapiens	H.sapiens
53	18.91	18.9	51	SJHUK	ankyrin 1, erythrocyte splice form 1 – human	human

54	18.69	18.7	76.2	I37984	keratin 9, type I, cytoskeletal – human	human
55	14.94	14.9	100	1A3OA	hemoglobin alpha chain mutant (Y42H), chain A – human	human
56	7.18	7.18	55.6	CRHU1	carbonate dehydratase (EC 4.2.1.1) I [validated] – human	human
57	2.93	2.93	32.5	JC2070	flavin reductase (EC 1.5.1.30) – human	human
58	1.83	1.83	11.3	JC4246	platelet-activating factor acetylhydrolase (EC 3.1.1.-) gamma chain - human	human
59	1.72	1.72	22.7	A44224	DNA repair helicase ERCC6 – human	human
60	1.7	1.7	25.9	Q88VG2_LACPL	1-phosphofructokinase (EC 2.7.1.56).- Lactobacillus plantarum.	Lactobacillus plantarum
61	2.1	2.1	40.9	Q2PFZ3_MACFA	Hypothetical protein.- Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).	Macaca fascicularis
62	1.7	1.7	25.9	Q60BZ4_METCA	Putative SCO1/SenC family protein/methylamine utilization protein MauG.- Methylococcus capsulatus.	Methylococcus capsulatus
63	2.55	2.55	19.3	BAC98035	AK129225 NID: - Mus musculus	Mus musculus
64	2.42	2.42	40.6	Q2YD80_MOUSE	Expressed sequence AU021838.- Mus musculus (Mouse).	Mus musculus
65	2.4	2.4	43.2	2AAA_MOUSE	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform (PP2A, subunit A, PR65-alpha isoform) (PP2A, subunit A, R1-alpha isoform).- Mus	Mus musculus
66	1.78	1.78	39.9	Q3UB80_MOUSE	Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830022H06 product:t-complex protein 1, full insert sequence.- Mus musculus (Mouse).	Mus musculus
67	1.7	1.7	13.9	Q3TFE8_MOUSE	17 days embryo stomach cDNA, RIKEN full-length enr product:karyopherin (importin) beta 1, full insert sequence.- Mus musculus (Mouse).	Mus musculus
68	1.4	1.4	23	Q91WP1_MOUSE	Poliovirus receptor (Cd155).- Mus musculus (Mouse).	Mus musculus
69	2.04	2.04	54	Q9XEM7_ORYSA	Hypothetical protein.- Oryza sativa (indica cultivar-group).	Oryza sativa
70	1.4	1.4	22.6	Q8LIG5_ORYSA	Putative arabinoxylan narabinofuranohydrolase isoenzyme AXAH-I.	Oryza sativa
71	1.4	1.4	12.6	Q7XQU6_ORYSA	OSJNBa0043L09.1 protein.- Oryza sativa (japonica cultivar-group).	Oryza sativa
72	1.42	1.42	15.1	Q3B3U9_PELLD	Hypothetical protein precursor.- Pelodictyon luteolum (strain DSM 273) (Chlorobium luteolum (strain DSM 273)).	Pelodictyon luteolum
73	1.52	1.52	24.5	Q1X4D2_9FIRM	Coenzyme F390 synthetase.- Pelotomaculum thermopropionicum SI.	Pelotomaculum thermopropionicum SI
74	1.4	1.4	30.3	Q6LTU5_PHOPR	Putative NAD-dependent DNA ligase.- Photobacterium profundum (Photobacterium sp. (strain SS9)).	Photobacterium profundum
75	2.52	2.52	52.7	AAC34678	AF085278 NID: - Pichia angusta	Pichia angusta
76	12.76	12.8	48.9	TRPGTR	trypsin (EC 3.4.21.4) precursor - pig (tentative sequence)	pig
77	5.05	5.05	84.9	O77478_PLABE	Elongation factor 1 alpha.- Plasmodium berghei.	Plasmodium berghei
78	1.4	1.4	36.9	Q4Y4V5_PLACH	Uroporphyrinogen decarboxylase, putative.- Plasmodium chabaudi.	Plasmodium chabaudi
79	8.71	8.71	63.6	Q71T02_PLAFA	L-lactate dehydrogenase (EC 1.1.1.27).- Plasmodium falciparum.	Plasmodium falciparum
80	8.42	8.42	67.1	Q8T6B1_PLAFA	Glyceraldehyde-3-phosphate dehydrogenase.- Plasmodium falciparum.	Plasmodium falciparum
81	4.36	4.36	31.2	Q8IJD4_PLAF7	40S ribosomal protein, putative.- Plasmodium falciparum (isolate 3D7).	Plasmodium falciparum
82	3.3	3.3	50.2	Q07615_PLAFA	Heat shock protein.- Plasmodium falciparum.	**Plasmodium falciparum**
83	2.13	2.13	63.7	Q8IB17_PLAF7	14-3-3 protein homologue, putative.- Plasmodium falciparum (isolate 3D7).	**Plasmodium falciparum**
84	2.08	2.08	73.5	Q8I3U6_PLAF7	40S ribosomal subunit protein S14, putative.- Plasmodium falciparum	**Plasmodium falciparum**
85	2.05	2.05	18.4	CAG25330	CR382399 NID: - Plasmodium falciparum 3D7	**Plasmodium falciparum**
86	2.04	2.04	51.4	Q76NM4_PLAF7	Small GTPase Rab11.- Plasmodium falciparum (isolate 3D7).	**Plasmodium falciparum**

87	2.01	2.01	32	Q8IE67_PLAF7	Phosphoribosylpyrophosphate synthetase (EC 2.7.6.1).- Plasmodium falciparum (isolate 3D7).	**Plasmodium falciparum**
88	2.01	2.01	21.5	Q8I2X3_PLAF7	Acid phosphatase, putative (EC 3.1.3.2).- Plasmodium falciparum (isolate 3D7).	**Plasmodium falciparum**
89	2	2	19.4	Q8I2X0_PLAF7	Hypothetical protein PFI0895c.- Plasmodium falciparum (isolate 3D7).	**Plasmodium falciparum**
90	2	2	22	Q8I3X4_PLAF7	Uridine phosphorylase, putative (EC 2.4.2.3).- Plasmodium falciparum (isolate 3D7).	**Plasmodium falciparum**
91	2	2	17.4	Q6AAF8_PROAC	ABC transporter, putative molybdenum transport system.- Propionibacterium acnes.	Propionibacterium acnes
92	1.7	1.7	11.4	Q3K9R2_PSEPF	Rhodanese-like.- Pseudomonas fluorescens (strain PfO-1).	Pseudomonas fluorescens
93	2	2	15.1	Q8RQW1_PSEPA	ORF1 protein.- Pseudomonas paucimobilis (Sphingomonas paucimobilis).	Pseudomonas paucimobilis
94	1.42	1.42	31.2	Q1LH04_RALME	GTP-binding signal recognition particle SRP54, G-domain.- Ralstonia metallidurans (strain CH34 / ATCC 43123 / DSM 2839).	Ralstonia metallidurans
95	1.32	1.32	24.3	Q20YI5_RHOPB	ATPase AAA-2.- Rhodopseudomonas palustris (strain BisB18).	Rhodopseudomonas palustris
96	1.42	1.42	41.6	Q1RIB7_RICBR	Heat shock protein HslVU, ATPase subunit HslU.- Rickettsia bellii (strain RML369-C).	Rickettsia bellii
97	1.98	1.98	15.5	Q43S00_SOLUS	Peptidase M28 precursor.- Solibacter usitatus Ellin6076.	Solibacter usitatus Ellin
98	1.82	5.45	79.4	HAMKS	hemoglobin alpha chain - sooty mangabey	sooty mangabey
99	4.57	4.57	45	AAB94053	AF017079 NID: - Sus scrofa	Sus scrofa
100	1.4	1.4	22.3	Q5N1P4_SYNP6	NAD+ dependent glycerol-3-phosphate dehydrogenase.- Synechococcus sp. (strain PCC 6301) (Anacystis nidulans).	Synechococcus
101	1.4	1.4	6.3	Q7U4R7_SYNPX	Possible phycobilisome rod-core linker polypeptide (L-RC 28.5).- Synechococcus sp. (strain WH8102).	Synechococcus
102	34.18	34.2	100	1HDBB	hemoglobin (deoxy) beta-v67t mutant CHAIN B, D, V67T alpha-beta-alpha-beta tetramer, chain B – synthetic	Synthetic
103	3.33	3.33	68.9	Q1JSM2_TOXGO	Actin.- Toxoplasma gondii.	Toxoplasma gondii
104	2	2	14.6	Q4E1K3_TRYCR	Hypothetical protein.- Trypanosoma cruzi.	Trypanosoma cruzi
105	2	2	15.3	Q7ZTI8_XENLA	Kap beta 3 protein (Fragment).- Xenopus laevis (African clawed frog).	Xenopus laevis
106	2	2	19.2	CAG82196	CR382129 NID: - Yarrowia lipolytica CLIB122	Yarrowia lipolytica CLIB

Key:
Unused – A measure of the protein confidence for a detected protein; **N** – the rank of the specified protein relative to all other proteins in the list of detected proteins; **Total** – A measure of the total amount of evidence for a detected protein calculated using all of the peptides detected for the protein; **% Cov** – The percentage of matching amino acids from identified peptides having confidence greater than or equal to 95%, divided by the total number of amino acids in the sequence; **Accession number** – MSDB accession number assigned to protein; **Name** – MSDB name assigned to protein; **Species** – species origin of protein based on peptide sequences identified

Table 3: Summary of proteins identified by trypsin in-gel digestion (6hr control) (1D RP-HPLC)

N	Unused	Total	% Cov	Accession #	Name	Species
1	2.45	2.45	24.4	pfa3D7predicted|chr11|chr11	coding) 26% identity to 52% of Q9MBF8: Dynein 1-beta heavy chain, flagellar inner arm I1 complex (1-beta DHC) (Dynein 1, subspecies f) Location= chr11	**118f|Genefinder|Plasmodium_ falciparum_TIGR|(protein**
2	2.55	2.55	63.7	pfa3D7predicted|chr5|chr5	coding) 100% identity to 100% of 1Q1G.C: Chain C, Crystal Structure Of Plasmodium Falciparum Pnp With 5'- Methylthio-Immucillin-H Location= chr5	**153|FullPhat|Plasmodium_ falciparum_Sanger|(protein**
3	1.55	1.58	45.9	pfa3D7predicted|chr8|chr8.	coding) 46% identity to 57% of 2116446C: ORF Location= chr8	**162f|Genefinder|Plasmodium_ falciparum_Sanger|(protein**
4	2.07	2.07	44.3	pfa3D7predicted|chr12|chr12	coding) null Location= chr12 complement	**162r|Genefinder|Plasmodium_ falciparum_Sanger|(protein**
5	5.37	5.37	74.5	pfa3D7predicted|chr9|chr9	coding) 100% identity to 100% of AAA93010.1: PBGRP Location= chr9	**173|FullPhat|Plasmodium_ falciparum_Sanger|(protein**
6	1.68	1.68	56.1	pfa3D7predicted|chr11|chr11.	coding) 100% identity to 100% of P38545: GTP-binding nuclear protein Ran (GTPase Ran) (Ras-like protein TC4) Location= chr11	**196|FullPhat|Plasmodium_ falciparum_TIGR|(protein**
7	1.9	1.9	33.3	pfa3D7predicted|chr13|chr13.	coding) 35% identity to 53% of AAO52024.1: similar to Dictyostelium discoideum (Slime mold). Homeobox-containing protein (Fragment) Location= chr13	**208|FullPhat|Plasmodium_ falciparum_Sanger|(protein**
8	1.9	1.94	34.6	pfa3D7predicted|chr1|chr1.	coding) 41% identity to 54% of 2116446C: ORF Location= chr1 join(29733..34985, 36111..37334, 37632..37805)	**21|FullPhat|Plasmodium_ falciparum_Sanger|(protein**
9	2.27	2.32	52.3	pfa3D7predicted|chr4|chr4.	coding) 40% identity to 57% of AAQ74128.1: A4tres CIDR1 [synthetic construct] Location= chr4 complement	**219|FullPhat|Plasmodium_falciparum_Sanger|(protein**
10	1.65	1.73	49.1	pfa3D7predicted|chr10|chr10.	coding) 36% identity to 49% of 2116446C: ORF Location= chr10	**23|FullPhat|Plasmodium_falciparum_TIGR|(protein**

11	1.61	1.61	65.9	pfa3D7predicted|chr12|chr12	coding) null Location= chr12	**232|FullPhat|Plasmodium_falciparum_Sanger|(protein**
12	9.44	9.44	62.3	pfa3D7predicted|chr13|chr13	coding) 100% identity to 100% of 1T26.A: Chain A, Plasmodium Falciparum Lactate Dehydrogenase Complexed With Nadh And 4-Hydroxy-1,2,5-Thiadiazole-3-Carboxylic Acid Location= chr13	**270|FullPhat|Plasmodium_falciparum_Sanger|(protein**

13	2.58	2.58	41.1	pfa3D7predicted|chr13|chr13.	coding) 44% identity to 61% of 2116222A: variant surface protein Location= chr13	**345r|Genefinder|Plasmodium_falciparum_Sanger|(protein**
14	4.2	4.2	49.4	pfa3D7predicted|chr8|chr8.	coding) 44% identity to 57% of 2116446C: ORF Location= chr8 complement(join	**346|FullPhat|Plasmodium_falciparum_Sanger|(protein**
15	2.14	2.14	30.7	pfa3D7predicted|chr12|chr12.	coding) null Location= chr12 join	**347|FullPhat|Plasmodium_falciparum_Sanger|(protein**
16	1.86	1.87	27.5	pfa3D7predicted|chr12|chr12.	coding) null Location= chr12 join	**34f|Genefinder|Plasmodium_falciparum_Sanger|(protein**
17	2.08	2.08	41.4	pfa3D7predicted|chr6|chr6.	coding) 100% identity to 100% of Q07805: Ornithine aminotransferase (Ornithine--oxo-acid aminotransferase) Location= chr6	**42f|Genefinder|Plasmodium_falciparum_Sanger|(protein**
18	4.5	4.5	71.8	pfa3D7predicted|chr12|chr12.	coding) null Location= chr12 1920770..1921900	**460|FullPhat|Plasmodium_falciparum_Sanger|(protein**
19	3.3	3.34	46.3	pfa3D7predicted|chr11|chr11.	coding) 52% identity to 66% of 2116446C: ORF Location= chr11	**4f|Genefinder|Plasmodium_falciparum_TIGR|(protein**
20	2.34	2.34	29.7	pfa3D7predicted|chr12|chr12	coding) null Location= chr12 complement	**628|GlimmerM|Plasmodium_falciparum_Sanger|(protein**
21	2.63	2.63	39.7	pfa3D7predicted|chr6|chr6.	coding) 39% identity to 54% of 2116446C: ORF Location= chr6 complement	**79r|Genefinder|Plasmodium_falciparum_Sanger|(protein**
22	1.52	1.52	30.9	pfa3D7predicted|chr12|chr12.	coding) null Location= chr12	**836|GlimmerM|Plasmodium_falciparum_Sanger|(protein**
23	3.01	3.01	37.5	pfa3D7predicted|chr14|chr14.	coding) 33% identity to 55% of XP_396228.1: similar to dynein, axonemal, heavy chain 8; dynein, axon, heavy chain 8 [Apis mellifera] Location= chr14	Apis mellifera
24	1.48	1.48	29.6	pfa3D7predicted|chr10|chr10.	coding) 39% identity to 59% of NP_176917.2: DNA polymerase family B protein [Arabidopsis thaliana] Location= chr10	Arabidopsis thaliana
25	4.2	4.2	42	pfa3D7predicted|pfal_chr2|pfal_chr2.	coding) 100% identity to 100% of AAA29714.1: parasitophorous vacuole antigen Location= pfal_chr2 complement	**chr2|pfal_chr2.genefinder_74r|Genefinder|Plasmodium_falciparum TIGR|(protein**
26	1.49	1.49	40.5	pfa3D7predicted|chr5|chr5.	coding) 32% identity to 53% of EAL38034.1: karyopherin beta [Cryptosporidium hominis] Location= chr5	Cryptosporidium hominis
27	1.61	1.63	35.1	pfa3D7predicted|chr11|chr11.	coding) 40% identity to 61% of CAD98495.1: putative transcription regulatory protein, possible [Cryptosporidium parvum] Location= chr11	Cryptosporidium parvum
28	1.47	1.47	43	pfa3D7predicted|chr13|chr13.	coding) 28% identity to 52% of CAD98262.1: hypothetical predicted Armadillo/beta-catenin-like repeat protein, unknown function Location= chr13	Cryptosporidium parvum
29	3.29	3.29	33.9	pfa3D7predicted|chr14|chr14.	coding) 29% identity to 45% of AAO53180.1: hypothetical protein [Dictyostelium discoideum] Location= chr14 complement	Dictyostelium discoideum
30	1.42	1.42	29.5	pfa3D7predicted|chr14|chr14.	coding) 28% identity to 43% of AAO53180.1: hypothetical protein [Dictyostelium discoideum] Location= chr14	Dictyostelium discoideum
31	1.78	1.78	50.8	pfa3D7predicted|chr8|chr8	coding) 46% identity to 68% of BAD15737.1: putative DegP2 protease [Oryza sativa (japonica cultivar-group)] Location= chr8 complement	Oryza sativa (japonica cultivar-group)

32	11.38	11.38	81.9	pfa3D7predicted|chr14|chr14.	coding) 84% identity to 95% of CAH99235.1: glyceraldehyde-3-phosphate dehydrogenase, putative [Plasmodium berghei]	Plasmodium berghei
33	4.11	4.16	32.6	pfa3D7predicted|chr14|chr14	coding) 37% identity to 52% of CAH97021.1: conserved hypothetical protein [Plasmodium berghei] Location= chr14 complement	Plasmodium berghei
34	3.01	3.01	56.8	pfa3D7predicted|chr9|chr9	coding) 80% identity to 92% of CAH95224.1: conserved hypothetical protein [Plasmodium berghei] Location= chr9 complement	Plasmodium berghei
35	2.87	2.87	94.2	pfa3D7predicted|chr5|chr5.	coding) 97% identity to 97% of CAH97256.1: 40S ribosomal subunit protein S14, putative [Plasmodium berghei] Location= chr5 complement	Plasmodium berghei
36	2.67	2.67	77.3	pfa3D7predicted|chr13|chr13.	coding) 91% identity to 98% of CAH98214.1: small GTPase Rab11, putative [Plasmodium berghei] Location= chr13	Plasmodium berghei
37	2.48	2.48	38	pfa3D7predicted|chr6|chr6.	coding) 48% identity to 63% of CAI04669.1: hypothetical protein PB105705.00.0 [Plasmodium berghei] Location= chr6	Plasmodium berghei
38	2.15	2.15	74.8	pfa3D7predicted|chr13|chr13	coding) 80% identity to 88% of CAH93761.1: phosphoribosylpyrophosphate synthetase, putative [Plasmodium berghei] Location= chr13 complement	Plasmodium berghei
39	1.96	1.96	38.2	pfa3D7predicted|chr5|chr5.	coding) 73% identity to 84% of CAH96435.1: hypothetical protein PB000785.01.0 [Plasmodium berghei] Location= chr5	Plasmodium berghei
40	1.94	1.94	26.7	pfa3D7predicted|chr8|chr8.	coding) 33% identity to 51% of CAH96228.1: hypothetical protein PB000644.01.0 [Plasmodium berghei] Location= chr8	Plasmodium berghei
41	1.76	1.76	25.2	pfa3D7predicted|chr11|chr11	coding) 36% identity to 55% of CAH95499.1: conserved hypothetical protein [Plasmodium berghei] Location= chr11 join	Plasmodium berghei
42	1.63	1.65	19.6	pfa3D7predicted|chr13|chr13.	coding) 36% identity to 55% of CAH98689.1: conserved hypothetical protein [Plasmodium berghei] Location= chr13	Plasmodium berghei
43	1.46	1.46	36.7	pfa3D7predicted|chr4|chr4.	coding) 37% identity to 54% of CAH97882.1: conserved hypothetical protein [Plasmodium berghei] Location= chr4	Plasmodium berghei
44	1.41	1.41	31.6	pfa3D7predicted|chr5|chr5.	coding) 43% identity to 61% of CAH96070.1: asparagine--tRNA ligase, putative [Plasmodium berghei] Location= chr5	Plasmodium berghei
45	1.4	1.4	26.3	pfa3D7predicted|chr13|chr13.	coding) 46% identity to 64% of CAH96693.1: hypothetical protein PB103910.00.0 [Plasmodium berghei] Location= chr13	Plasmodium berghei
46	5.39	5.39	38.8	pfa3D7predicted|chr5|chr5	coding) 46% identity to 62% of CAH79456.1: conserved hypothetical protein [Plasmodium chabaudi] Location= chr5	Plasmodium chabaudi
47	3.3	3.32	34.5	pfa3D7predicted|chr7|chr7.	coding) 48% identity to 62% of CAH77899.1: conserved hypothetical protein [Plasmodium chabaudi] Location= chr7 complement	Plasmodium chabaudi
48	2.94	2.94	38.8	pfa3D7predicted|chr14|chr14.	coding) 49% identity to 69% of CAH78083.1: conserved hypothetical protein [Plasmodium chabaudi] Location= chr14 join	Plasmodium chabaudi
49	2.93	2.93	39.3	pfa3D7predicted|chr7|chr7.	coding) 31% identity to 49% of CAH81594.1: Cg7 protein, putative [Plasmodium chabaudi] Location= chr7 complement(join	Plasmodium chabaudi

50	2.11	2.11	39.2	pfa3D7predicted|chr9|chr9.	coding) 78% identity to 89% of CAH78643.1: conserved hypothetical protein [Plasmodium chabaudi] Location= chr9 complement	Plasmodium chabaudi
51	1.76	1.76	63.5	pfa3D7predicted|chr9|chr9.	coding) 90% identity to 96% of CAH80397.1: conserved hypothetical protein [Plasmodium chabaudi] Location= chr9	Plasmodium chabaudi
52	1.53	1.53	35	pfa3D7predicted|chr5|chr5.	coding) 82% identity to 89% of CAH76772.1: conserved hypothetical protein [Plasmodium chabaudi] Location= chr5	Plasmodium chabaudi
53	1.45	1.47	32.7	pfa3D7predicted|chr11|chr11.	coding) 53% identity to 65% of CAH76892.1: conserved hypothetical protein [Plasmodium chabaudi] Location= chr11	Plasmodium chabaudi
54	1.32	1.32	28.1	pfa3D7predicted|chr14|chr14.	coding) 40% identity to 53% of CAH74620.1: conserved hypothetical protein [Plasmodium chabaudi] Location= chr14	Plasmodium chabaudi
55	2.24	2.24	31.5	pfa3D7predicted|chr8|chr8.	coding) 84% identity to 92% of AAV36000.1: protein disulfide isomerase [Plasmodium chabaudi chabaudi] Location= chr8 complement	Plasmodium chabaudi chabaudi
56	2.8	2.8	71.1	pfa3D7predicted|chr8|chr8.	coding) 100% identity to 100% of AAC17515.1: 14-3-3 protein [Plasmodium knowlesi] Location= chr8	Plasmodium knowlesi
57	2.79	2.84	26.2	pfa3D7predicted|chr4|chr4.	coding) 23% identity to 44% of AAO38039.1: reticulocyte binding-like protein 2b [Plasmodium reichenowi] Location= chr4	Plasmodium reichenowi
58	1.52	1.52	26.4	pfa3D7predicted|chr8|chr8	coding) 32% identity to 55% of CAB96701.1: Pvstp1 [Plasmodium vivax] Location= chr8	Plasmodium vivax
59	6.2	6.2	94.8	pfa3D7predicted|chr13|chr13.	coding) 100% identity to 100% of EAA15302.1: translation elongation factor EF-1, subunit alpha [Plasmodium yoelii yoelii] Location= chr13	Plasmodium yoelii yoelii
60	4.73	4.73	64.3	pfa3D7predicted|chr10|chr10.	coding) 93% identity to 96% of EAA18207.1: ribosomal protein S2, putative [Plasmodium yoelii yoelii] Location= chr10	Plasmodium yoelii yoelii
61	3.21	3.21	33.3	pfa3D7predicted|chr13|chr13.	coding) 32% identity to 51% of EAA21279.1: chloroquine resistance marker protein [Plasmodium yoelii yoelii] Location= chr13 complement	Plasmodium yoelii yoelii
62	2.73	2.73	39.3	pfa3D7predicted|chr14|chr14	coding) 36% identity to 52% of EAA16501.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr14	Plasmodium yoelii yoelii
63	2.49	2.51	29.5	pfa3D7predicted|chr14|chr14	coding) 34% identity to 51% of EAA15702.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr14	Plasmodium yoelii yoelii
64	2.48	2.48	63	pfa3D7predicted|chr7|chr7	coding) 51% identity to 65% of EAA20598.1: Drosophila melanogaster LD15209p [Plasmodium yoelii yoelii] Location= chr7	Plasmodium yoelii yoelii
65	2.35	2.35	39	pfa3D7predicted|pfal_chr2|pfal_chr2	coding) 23% identity to 41% of EAA18039.1: hypothetical protein [Plasmodium yoelii yoelii] Location= pfal_chr2 complement	Plasmodium yoelii yoelii
66	2.28	2.29	41.3	pfa3D7predicted|chr1|chr1.	coding) 41% identity to 57% of EAA20533.1: Ubiquitin carboxyl-terminal hydrolase	Plasmodium yoelii yoelii
67	2.11	2.11	67.4	pfa3D7predicted|chr10|chr10	coding) 96% identity to 98% of EAA18347.1: 26S proteasome subunit 4-like protein [Plasmodium yoelii yoelii] Location= chr10 complement	Plasmodium yoelii yoelii
68	2.09	2.09	50	pfa3D7predicted|chr13|chr13	coding) 29% identity to 47% of EAA21778.1: chloroquine resistance marker protein [Plasmodium yoelii yoelii] Location= chr13	Plasmodium yoelii yoelii
69	1.86	1.88	44.7	pfa3D7predicted|chr8|chr8.	coding) 22% identity to 41% of EAA18039.1: hypothetical protein [Plasmodium yoelii	Plasmodium yoelii yoelii

70	1.85	1.87	26.4	pfa3D7predicted|chr8|chr8.	coding) 26% identity to 45% of EAA18589.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr8	Plasmodium yoelii yoelii
71	1.81	1.81	27.3	pfa3D7predicted|chr4|chr4.	coding) 29% identity to 48% of EAA16876.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr4	Plasmodium yoelii yoelii
72	1.77	1.77	38.4	pfa3D7predicted|chr10|chr10.	coding) 53% identity to 71% of EAA17496.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr10	Plasmodium yoelii yoelii
73	1.76	1.76	29	pfa3D7predicted|chr5|chr5	coding) 27% identity to 44% of EAA18442.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr5	Plasmodium yoelii yoelii
74	1.65	1.65	34.3	pfa3D7predicted|chr9|chr9.	coding) 24% identity to 44% of EAA17393.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr9	Plasmodium yoelii yoelii
75	1.6	1.61	50.5	pfa3D7predicted|chr11|chr11.	coding) 26% identity to 46% of EAA19159.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr11	Plasmodium yoelii yoelii
76	1.59	1.59	18.1	pfa3D7predicted|chr7|chr7.	coding) 33% identity to 52% of EAA22516.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr7	Plasmodium yoelii yoelii
77	1.57	1.57	71.9	pfa3D7predicted|chr5|chr5.	coding) 95% identity to 99% of EAA16191.1: 60S ribosomal protein L8 [Plasmodium yoelii yoelii] Location= chr5 complement	Plasmodium yoelii yoelii
78	1.56	1.89	92.7	pfa3D7predicted|chr5|chr5.	coding) 100% identity to 100% of EAA20993.1: ribosomal protein S11, putative [Plasmodium yoelii yoelii] Location= chr5 complement	Plasmodium yoelii yoelii
79	1.56	1.56	34.6	pfa3D7predicted|chr4|chr4.	coding) 49% identity to 67% of EAA16412.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr4	Plasmodium yoelii yoelii
80	1.52	1.52	16.8	pfa3D7predicted|chr11|chr11.	coding) 28% identity to 45% of EAA22581.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr11	Plasmodium yoelii yoelii
81	1.51	1.51	34.5	pfa3D7predicted|chr5|chr5.	coding) 49% identity to 67% of EAA22286.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr5	Plasmodium yoelii yoelii
82	1.47	1.47	57.4	pfa3D7predicted|chr13|chr13	coding) 26% identity to 45% of EAA17051.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr13	Plasmodium yoelii yoelii
83	1.46	1.46	33	pfa3D7predicted|chr14|chr14.	coding) 25% identity to 44% of EAA17366.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr14	Plasmodium yoelii yoelii
84	1.4	1.41	38.3	pfa3D7predicted|chr3|chr3	coding) 34% identity to 52% of EAA21337.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr3	Plasmodium yoelii yoelii
85	1.39	1.4	37.5	pfa3D7predicted|chr3|chr3	coding) 29% identity to 47% of EAA21938.1: putative protein kinase [Plasmodium yoelii yoelii] Location= chr3	Plasmodium yoelii yoelii
86	1.37	1.39	33.2	pfa3D7predicted|chr13|chr13.	coding) 29% identity to 48% of EAA22695.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr13	Plasmodium yoelii yoelii
87	1.33	1.35	39.2	pfa3D7predicted|chr10|chr10	coding) 49% identity to 68% of EAA16713.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr10	Plasmodium yoelii yoelii

88	1.31	1.31	15.5	pfa3D7predicted|chr14|chr14.	coding) 42% identity to 59% of EAA17764.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr14	Plasmodium yoelii yoelii
89	4.13	4.13	38.9	pfa3D7predicted|chr7|chr7.	coding) 29% identity to 51% of BAA97048.1: cytoplasmic dynein heavy chain [Rattus norvegicus] Location= chr7	Rattus norvegicus
90	1.72	1.72	27.1	pfa3D7predicted|chr9|chr9.	coding) 33% identity to 54% of XP_220603.2: similar to 1-beta dynein [Rattus norvegicus] Location= chr9	Rattus norvegicus
91	2.88	2.92	75.8	pfa3D7predicted|chr8|chr8.	coding) 81% identity to 90% of AAC72001.1: heat shock protein 70 [Toxoplasma gondii] Location= chr8	Toxoplasma gondii

Table 4: Summary of proteins identified by trypsin in-gel digestion (6hr drug-treated) 1D RP-HPLC

N	Unused	Total	% Cov	Accession #	Name	Species
1	2.13	2.13	41.3	pfa3D7predicted|chr10|chr10.	coding) 100% identity to 100% of P14643: Tubulin beta chain (Beta tubulin) Location= chr10	**102|FullPhat|Plasmodium_falciparum_TIGR|(protein**
2	1.62	1.62	50.3	pfa3D7predicted|chr14|chr14.	coding) 99% identity to 100% of AAC47090.1: p82 Location= chr14	**103|FullPhat|Plasmodium_falciparum_TIGR|(protein**
3	1.7	1.7	44.2	pfa3D7predicted|chr12|chr12	coding) null Location= chr12 complement(428489..432874)	**109|FullPhat|Plasmodium_falciparum_Sanger|(protein**
4	1.7	1.7	54.5	pfa3D7predicted|chr7|chr7.	coding) 73% identity to 86% of P24724: Heat shock protein 90 (HSP90) Location= chr7	**112|FullPhat|Plasmodium_falciparum_Sanger|(protein**
5	5.23	5.23	50.9	pfa3D7predicted|chr9|chr9	coding) 46% identity to 60% of P04933: Merozoite surface protein 1 precursor (Merozoite surface antigens) (PMMSA) (P195) Location= chr9	**155f|Genefinder|Plasmodium_falciparum (protein**
6	1.43	1.43	25	pfa3D7predicted|chr9|chr9.	coding) 62% identity to 79% of T48023: ATP-dependent RNA helicase-like protein - Arabidopsis thaliana Location= chr9	**170|FullPhat|Plasmodium_falciparum_Sanger|(protein**
7	9.82	9.82	73.9	pfa3D7predicted|chr9|chr9.	coding) 100% identity to 100% of AAA93010.1: PBGRP Location= chr9	**173|FullPhat|Plasmodium_falciparum_Sanger|(protein**
8	5.21	5.21	53.7	pfa3D7predicted|chr11|chr11	coding) 100% identity to 100% of P38545: GTP-binding nuclear protein Ran (GTPase Ran) (Ras-like protein TC4) Location= chr11	**196|FullPhat|Plasmodium_falciparum_TIGR|(protein**
9	3.4	3.41	40.2	pfa3D7predicted|chr6|chr6.	coding) 34% identity to 54% of 2116222A: variant surface protein Location= chr6	**2|FullPhat|Plasmodium_falciparum_Sanger|(protein**
10	3.01	3.13	40.4	pfa3D7predicted|chr4|chr4	coding) 48% identity to 60% of 2116446C: ORF Location= chr4	**20|FullPhat|Plasmodium_falciparum_Sanger|(protein**
11	2.79	3.74	40	pfa3D7predicted|chr8|chr8.	coding) 37% identity to 53% of 2116222A: variant surface protein Location= chr8	**23|FullPhat|Plasmodium_falciparum_Sanger|(protein**
12	6.5	6.5	60.4	pfa3D7predicted|chr13|chr13	coding) 100% identity to 100% of 1T26.A: Chain A, Plasmodium Falciparum Lactate Dehydrogenase Complexed With Nadh And 4-Hydroxy-1,2,5-Thiadiazole-3-Carboxylic Acid Location= chr13	**270|FullPhat|Plasmodium_falciparum_Sanger|(protein**

13	1.33	1.33	36.6	pfa3D7predicted|chr5|chr5.	coding) 99% identity to 99% of P08116: Processed variable antigen Location= chr5	**31|FullPhat|Plasmodium_falciparum_Sanger|(protein**
14	1.35	2.46	35	pfa3D7predicted|chr8|chr8.	coding) 46% identity to 57% of 2116446C: ORF Location= chr8	**332|FullPhat|Plasmodium_falciparum_Sanger|(protein**
15	1.4	1.4	39.5	pfa3D7predicted|chr6|chr6.	coding) 100% identity to 100% of Q07805: Ornithine aminotransferase (Ornithine--oxo-acid aminotransferase) Location= chr6	**42f|Genefinder|Plasmodium_falciparum_Sanger**
16	2.4	4.54	29.7	pfa3D7predicted|chr4|chr4	coding) 43% identity to 56% of 2116446C: ORF Location= chr4	**68r|Genefinder|Plasmodium_falciparum_Sanger**
17	3.91	3.92	49.7	pfa3D7predicted|chr5|chr5.	coding) 35% identity to 53% of 2116222A: variant surface protein Location= chr5	**881|GlimmerM|Plasmodium_falciparum_Sanger**
18	2.54	2.54	28.2	pfa3D7predicted|chr14|chr14.	coding) 33% identity to 55% of XP_396228.1: similar to dynein, axonemal, heavy chain 8; dynein, axon, heavy chain 8 [Apis mellifera] Location= chr14	Apis mellifera
19	1.6	1.6	70.8	pfa3D7predicted|chr13|chr13	coding) 41% identity to 62% of AAP83582.1: phosphoethanolamine N-methyltransferase [Brassica napus] Location= chr13	Brassica napus
20	1.7	1.7	73.2	pfa3D7predicted|chr6|chr6	coding) 30% identity to 36% of CAE75525.1: Hypothetical protein CBG23547 [Caenorhabditis briggsae] Location= chr6	Caenorhabditis briggsae
21	7.27	7.27	34.7	pfa3D7predicted|pfal_chr2	coding) 100% identity to 100% of AAA29714.1: parasitophorous vacuole antigen Location= pfal_chr2	**chr2|pfal_chr2.genefinder Genefinder|Plasmodium_ falciparum**

22	1.67	1.67	35.3	pfa3D7predicted|pfal_chr2	coding) 48% identity to 68% of AAS48373.1: RNA polymerase II [Cochliobolus heterostrophus] Location= pfal_chr2	Cochliobolus heterostrophus
23	2.11	2.11	40.4	pfa3D7predicted|chr14|chr14	coding) 33% identity to 51% of AAH78240.1: Zgc:100819 [Danio rerio] Location= chr14	Danio rerio
24	3.53	3.53	22.4	pfa3D7predicted|chr13|chr13.	coding) 47% identity to 65% of AAO51219.1: similar to Homo sapiens (Human). Polymerase (RNA) III (DNA directed) (155kD) [Dictyostelium discoideum] Location= chr13	Dictyostelium discoideum
25	1.8	1.8	29.3	pfa3D7predicted|chr3|chr3.	coding) 31% identity to 45% of AAO52259.1: similar to Oryza sativa (Rice). Putative ATP-dependent RNA helicase [Dictyostelium discoideum] Location= chr3	Dictyostelium discoideum
26	1.46	1.46	33.4	pfa3D7predicted|chr6|chr6.	coding) 68% identity to 83% of AAB40928.2: cell division cycle protein 48 [Dictyostelium discoideum] Location= chr6	Dictyostelium discoideum
27	1.99	1.99	46.8	pfa3D7predicted|chr8|chr8.	coding) 26% identity to 49% of AAF48863.1: CG15040-PA [Drosophila melanogaster] Location= chr8	Drosophila melanogaster
28	1.78	1.78	72.4	pfa3D7predicted|pfal_chr2	coding) 28% identity to 34% of NP_727774.2: CG32602-PA [Drosophila melanogaster]	Drosophila melanogaster
29	1.64	1.64	26.3	pfa3D7predicted|chr10|chr10	coding) 40% identity to 59% of AAS64934.1: CG15804-PB, isoform B [Drosophila melanogaster] Location= chr10	Drosophila melanogaster
30	2.23	2.23	18.2	pfa3D7predicted|chr14|chr14.	coding) 37% identity to 60% of AAG45474.1: ASC-1 complex subunit P200 [Homo sapiens] Location= chr14	Homo sapiens
31	2.69	2.69	20.1	pfa3D7predicted|chr14|chr14	coding) 46% identity to 66% of YP_116302.1: putative glutamate synthase large subunit [Nocardia farcinica IFM 10152] Location= chr14	Nocardia farcinica IFM 10152

32	10.93	10.93	36.7	pfa3D7predicted|chr6|chr6.	coding) 48% identity to 63% of CAI04669.1: hypothetical protein PB105705.00.0 [Plasmodium berghei] Location= chr6	**Plasmodium berghei**
33	7.65	7.65	40.2	pfa3D7predicted|chr13|chr13	coding) 85% identity to 93% of CAH98910.1: hypothetical protein PB001524.02.0 [Plasmodium berghei] Location= chr13	**Plasmodium berghei**
34	6.72	6.72	77.4	pfa3D7predicted|chr14|chr14	coding) 84% identity to 95% of CAH99235.1: glyceraldehyde-3-phosphate dehydrogenase, putative [Plasmodium berghei] Location= chr14	**Plasmodium berghei**
35	4.27	4.27	22.9	pfa3D7predicted|chr8|chr8.	coding) 33% identity to 51% of CAH96228.1: hypothetical protein PB000644.01.0 [Plasmodium berghei] Location= chr8	**Plasmodium berghei**
36	4.23	4.23	78.1	pfa3D7predicted|chr5|chr5	coding) 97% identity to 97% of CAH97256.1: 40S ribosomal subunit protein S14, putative [Plasmodium berghei] Location= chr5	**Plasmodium berghei**
37	4.05	4.05	32.4	pfa3D7predicted|chr5|chr5	coding) 73% identity to 84% of CAH96435.1: hypothetical protein PB000785.01.0 [Plasmodium berghei] Location= chr5	**Plasmodium berghei**
38	3.89	3.89	54	pfa3D7predicted|chr9|chr9	coding) 80% identity to 92% of CAH95224.1: conserved hypothetical protein [Plasmodium berghei] Location= chr9	**Plasmodium berghei**
39	3.29	3.29	25.8	pfa3D7predicted|chr14|chr14.	coding) 37% identity to 54% of CAI00610.1: hypothetical protein PB001061.03.0 [Plasmodium berghei] Location= chr14	**Plasmodium berghei**
40	2.65	2.65	87	pfa3D7predicted|chr11|chr11	coding) 96% identity to 98% of AAF27979.1: GTP binding protein; Rab6 [Plasmodium berghei] Location= chr11	**Plasmodium berghei**
41	2.62	2.7	22.5	pfa3D7predicted|chr14|chr14	coding) 57% identity to 73% of CAH98145.1: SEL-1 protein, putative [Plasmodium berghei] Location= chr14	**Plasmodium berghei**
42	2.36	2.36	17.8	pfa3D7predicted|chr14|chr14	coding) 55% identity to 75% of CAH99010.1: exopolyphosphatase, putative [Plasmodium berghei] Location= chr14	**Plasmodium berghei**
43	2.26	2.26	47.3	pfa3D7predicted|chr9|chr9.	coding) 91% identity to 97% of CAH99282.1: s-adenosylmethionine synthetase, putative [Plasmodium berghei] Location= chr9	**Plasmodium berghei**
44	2.17	2.17	17.6	pfa3D7predicted|chr5|chr5.	coding) 53% identity to 67% of CAH98584.1: phosphatidylinositol 4-kinase, putative [Plasmodium berghei] Location= chr5	**Plasmodium berghei**
45	1.72	1.72	23.3	pfa3D7predicted|chr3|chr3.	coding) 33% identity to 52% of CAH99945.1: conserved hypothetical protein [Plasmodium berghei] Location= chr3	**Plasmodium berghei**
46	1.63	1.63	27.9	pfa3D7predicted|chr7|chr7	coding) 37% identity to 52% of CAH99354.1: hypothetical protein PB000201.03.0 [Plasmodium berghei] Location= chr7	**Plasmodium berghei**
47	1.6	1.6	30.3	pfa3D7predicted|chr14|chr14	coding) 86% identity to 96% of CAH99131.1: conserved hypothetical protein [Plasmodium berghei] Location= chr14	**Plasmodium berghei**
48	1.59	1.59	20.1	pfa3D7predicted|chr6|chr6.	coding) 26% identity to 47% of CAH93643.1: myosin-like protein, putative [Plasmodium berghei] Location= chr6	**Plasmodium berghei**
49	1.52	1.53	22.9	pfa3D7predicted|pfal_chr2|pfal_chr2	coding) 37% identity to 57% of CAH98970.1: DNA repair endonuclease, putative [Plasmodium berghei] Location= pfal_chr2	**Plasmodium berghei**
50	1.5	1.5	31.9	pfa3D7predicted|chr14|chr14	coding) 34% identity to 54% of CAH99755.1: metacaspase-like protein, putative [Plasmodium berghei] Location= chr14	**Plasmodium berghei**
51	1.44	1.44	22.1	pfa3D7predicted|chr5|chr5	coding) 54% identity to 71% of CAI00633.1: conserved hypothetical protein	**Plasmodium berghei**
52	1.41	1.41	28.9	pfa3D7predicted|chr10|chr10.	coding) 48% identity to 66% of CAH98446.1: conserved hypothetical protein [Plasmodium berghei] Location= chr10	**Plasmodium berghei**

53	1.41	1.41	30.7	pfa3D7predicted|chr8|chr8.	coding) 43% identity to 62% of CAH95160.1: conserved hypothetical protein [Plasmodium berghei] Location= chr8	**Plasmodium berghei**
54	1.36	1.36	69.1	pfa3D7predicted|chr13|chr13.	coding) 97% identity to 99% of CAH95167.1: 26S proteasome regulatory subunit 7, putative [Plasmodium berghei] Location= chr13	**Plasmodium berghei**
55	1.36	1.36	14.1	pfa3D7predicted|chr13|chr13.	coding) 64% identity to 78% of CAI03160.1: conserved hypothetical protein [Plasmodium berghei] Location= chr13	**Plasmodium berghei**
56	1.33	1.33	16.9	pfa3D7predicted|chr8|chr8	coding) 36% identity to 57% of CAH98657.1: conserved hypothetical protein [Plasmodium berghei] Location= chr8	**Plasmodium berghei**
57	1.32	1.32	26.4	pfa3D7predicted|chr5|chr5	coding) 43% identity to 61% of CAH96070.1: asparagine--tRNA ligase, putative [Plasmodium berghei] Location= chr5	**Plasmodium berghei**
58	7.14	7.16	39.4	pfa3D7predicted|chr5|chr5.	coding) 46% identity to 62% of CAH79456.1: conserved hypothetical protein [Plasmodium chabaudi] Location= chr5	**Plasmodium chabaudi**
59	3.46	3.47	34	pfa3D7predicted|chr11|chr11	coding) 53% identity to 65% of CAH76892.1: conserved hypothetical protein [Plasmodium chabaudi] Location= chr11	**Plasmodium chabaudi**
60	2.6	2.6	25.5	pfa3D7predicted|chr14|chr14.	coding) 63% identity to 77% of CAH75119.1: ferlin, putative [Plasmodium chabaudi] Location= chr14	**Plasmodium chabaudi**
61	2.5	2.5	28.4	pfa3D7predicted|chr3|chr3.	coding) 58% identity to 72% of CAH74986.1: hypothetical protein PC000452.00.0 [Plasmodium chabaudi] Location= chr3	**Plasmodium chabaudi**
62	2.39	2.4	33.5	pfa3D7predicted|chr7|chr7	coding) 48% identity to 62% of CAH77899.1: conserved hypothetical protein [Plasmodium chabaudi] Location= chr7	**Plasmodium chabaudi**
63	2.15	2.15	33.5	pfa3D7predicted|chr6|chr6.	coding) 60% identity to 69% of CAH78500.1: iswi protein homologue, putative [Plasmodium chabaudi] Location= chr6	**Plasmodium chabaudi**
64	1.74	1.74	29.9	pfa3D7predicted|chr5|chr5	coding) 91% identity to 99% of CAH75921.1: 60S ribosomal protein L12, putative [Plasmodium chabaudi] Location= chr5	**Plasmodium chabaudi**
65	1.74	1.74	56.7	pfa3D7predicted|chr14|chr14.	coding) 99% identity to 100% of CAH80423.1: ribosomal protein S28e,	**Plasmodium chabaudi**
66	1.47	1.47	21.3	pfa3D7predicted|chr9|chr9	coding) 39% identity to 57% of CAH82370.1: conserved hypothetical protein [Plasmodium chabaudi] Location= chr9 join	**Plasmodium chabaudi**
67	1.46	1.47	30.8	pfa3D7predicted|chr13|chr13	coding) 58% identity to 75% of CAH87010.1: conserved hypothetical protein [Plasmodium chabaudi] Location= chr13 complement	**Plasmodium chabaudi**
68	1.42	1.42	26.3	pfa3D7predicted|chr5|chr5	coding) 57% identity to 73% of CAH80362.1: RNA polymerase I, putative [Plasmodium chabaudi] Location= chr5 complement	**Plasmodium chabaudi**
69	1.42	1.42	34.7	pfa3D7predicted|chr11|chr11	coding) 86% identity to 93% of CAH80715.1: conserved hypothetical protein [Plasmodium chabaudi] Location= chr11	**Plasmodium chabaudi**
70	1.38	1.38	24.6	pfa3D7predicted|chr6|chr6.	coding) 67% identity to 82% of CAH78485.1: glyoxalase I, putative [Plasmodium chabaudi] Location= chr6 complement	**Plasmodium chabaudi**
71	1.31	1.31	26.7	pfa3D7predicted|chr6|chr6	coding) 52% identity to 72% of CAH84266.1: hypothetical protein PC300949.00.0 [Plasmodium chabaudi] Location= chr6	**Plasmodium chabaudi**
72	1.43	1.43	32.1	pfa3D7predicted|chr8|chr8.	coding) 84% identity to 92% of AAV36000.1: protein disulfide isomerase [Plasmodium chabaudi chabaudi] Location= chr8	**Plasmodium chabaudi chabaudi**
73	1.49	1.49	37.4	pfa3D7predicted|chr5|chr5.	coding) 40% identity to 58% of AAP93201.1: MB2 [Plasmodium gallinaceum] Location= chr5	**Plasmodium gallinaceum**
74	6.27	6.27	84	pfa3D7predicted|chr8|chr8.	coding) 99% identity to 100% of AAC17515.1: 14-3-3 protein [Plasmodium	**Plasmodium knowlesi**

75	1.64	1.64	36.6	pfa3D7predicted|chr4|chr4.	coding) 23% identity to 44% of AAO38039.1: reticulocyte binding-like protein 2b [Plasmodium reichenowi] Location= chr4	**Plasmodium reichenowi**
76	2.45	2.45	36.7	pfa3D7predicted|chr1|chr1.	coding) 29% identity to 50% of CAB96701.1: Pvstp1 [Plasmodium vivax] Location= chr1	**Plasmodium vivax**
77	1.66	1.66	36.9	pfa3D7predicted|chr9|chr9.	coding) 40% identity to 63% of BAC43744.1: PyRhopH2 [Plasmodium yoelii] Location= chr9	**Plasmodium yoelii**
78	1.43	1.43	34.6	pfa3D7predicted|chr13|chr13.	coding) 25% identity to 46% of AAB41263.3: rhoptry protein [Plasmodium yoelii] Location= chr13	**Plasmodium yoelii**
79	13.12	13.12	95	pfa3D7predicted|chr13|chr13.	coding) 100% identity to 100% of EAA15302.1: translation elongation factor EF-1, subunit alpha [Plasmodium yoelii yoelii] Location= chr13	**Plasmodium yoelii yoelii**
80	7.04	7.04	74.1	pfa3D7predicted|chr7|chr7	coding) 51% identity to 65% of EAA20598.1: Drosophila melanogaster LD15209p [Plasmodium yoelii yoelii] Location= chr7	**Plasmodium yoelii yoelii**
81	6.7	6.7	36.7	pfa3D7predicted|chr6|chr6.	coding) 28% identity to 45% of EAA17840.1: Bromodomain, putative [Plasmodium yoelii yoelii] Location= chr6	**Plasmodium yoelii yoelii**
82	5.87	5.87	36	pfa3D7predicted|chr8|chr8	coding) 28% identity to 46% of EAA22073.1: amine oxidase, flavin-containing, putative [Plasmodium yoelii yoelii] Location= chr8	**Plasmodium yoelii yoelii**
83	5.55	5.56	42.8	pfa3D7predicted|chr10|chr10.	coding) 49% identity to 68% of EAA16713.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr10	**Plasmodium yoelii yoelii**
84	5.42	5.42	51.2	pfa3D7predicted|chr13|chr13	coding) 29% identity to 47% of EAA21778.1: chloroquine resistance marker protein [Plasmodium yoelii yoelii] Location= chr13	**Plasmodium yoelii yoelii**
85	4.79	4.8	49.5	pfa3D7predicted|chr14|chr14.	coding) 75% identity to 77% of EAA16792.1: ookinete protein-related [Plasmodium yoelii yoelii] Location= chr14	**Plasmodium yoelii yoelii**
86	4.61	4.61	29.4	pfa3D7predicted|chr5|chr5.	coding) 49% identity to 67% of EAA22286.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr5	**Plasmodium yoelii yoelii**
87	4.54	4.54	36.9	pfa3D7predicted|chr14|chr14	coding) 23% identity to 41% of EAA17472.1: unknown protein-related [Plasmodium yoelii yoelii] Location= chr14	**Plasmodium yoelii yoelii**
88	4.47	4.47	26.2	pfa3D7predicted|chr4|chr4.	coding) 33% identity to 53% of EAA22868.1: hypothetical protein	**Plasmodium yoelii yoelii**
89	3.85	3.85	22.2	pfa3D7predicted|chr14|chr14	coding) 58% identity to 75% of EAA21034.1: rhoptry protein [Plasmodium yoelii yoelii] Location= chr14	**Plasmodium yoelii yoelii**
90	3.77	3.78	38.2	pfa3D7predicted|chr11|chr11.	coding) 26% identity to 44% of EAA16998.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr11	**Plasmodium yoelii yoelii**
91	3.64	3.66	37.3	pfa3D7predicted|chr3|chr3	coding) 22% identity to 40% of EAA17514.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr3	**Plasmodium yoelii yoelii**
92	3.53	3.53	40.4	pfa3D7predicted|chr3|chr3	coding) 37% identity to 57% of EAA17323.1: PWI domain, putative [Plasmodium yoelii yoelii] Location= chr3	**Plasmodium yoelii yoelii**
93	3.48	3.48	21.2	pfa3D7predicted|chr7|chr7	coding) 23% identity to 41% of EAA22829.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr7	**Plasmodium yoelii yoelii**
94	3.32	3.32	25.6	pfa3D7predicted|chr14|chr14	coding) 34% identity to 51% of EAA15702.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr14	**Plasmodium yoelii yoelii**
95	2.96	2.96	29	pfa3D7predicted|chr10|chr10	coding) 25% identity to 40% of EAA19983.1: Drosophila melanogaster CG12781 gene product [Plasmodium yoelii yoelii] Location= chr10	**Plasmodium yoelii yoelii**
96	2.9	2.9	28.8	pfa3D7predicted|chr8|chr8	coding) 56% identity to 68% of EAA22891.1: Protein kinase domain	**Plasmodium yoelii yoelii**

97	2.81	2.81	34.1	pfa3D7predicted|chr8|chr8	coding) 24% identity to 42% of EAA18637.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr8	**Plasmodium yoelii yoelii**
98	2.67	2.68	20.7	pfa3D7predicted|chr14|chr14.	coding) 68% identity to 79% of EAA17417.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr14	**Plasmodium yoelii yoelii**
99	2.58	2.58	33.9	pfa3D7predicted|chr10|chr10.	coding) 39% identity to 53% of EAA16731.1: RNA recognition motif, putative [Plasmodium yoelii yoelii] Location= chr10	**Plasmodium yoelii yoelii**
100	2.43	2.43	20.8	pfa3D7predicted|chr13|chr13	coding) 28% identity to 46% of EAA16405.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr13	**Plasmodium yoelii yoelii**
101	2.4	2.4	32.5	pfa3D7predicted|pfal_chr2|pfal_chr2	coding) 90% identity to 96% of EAA22741.1: DEAD/DEAH box helicase, putative [Plasmodium yoelii yoelii] Location= pfal_chr2	**Plasmodium yoelii yoelii**
102	2.34	2.34	26.5	pfa3D7predicted|chr7|chr7	coding) 74% identity to 86% of EAA20733.1: putative 26S proteosome regulatory subunit [Plasmodium yoelii yoelii] Location= chr7	**Plasmodium yoelii yoelii**
103	2.3	2.3	36.1	pfa3D7predicted|chr11|chr11	coding) 26% identity to 44% of EAA21325.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr11	**Plasmodium yoelii yoelii**
104	2.28	2.28	35.8	pfa3D7predicted|chr11|chr11.	coding) 44% identity to 60% of EAA15380.1: suppressor of NosA [Plasmodium yoelii yoelii] Location= chr11	**Plasmodium yoelii yoelii**
106	2.23	2.23	24.4	pfa3D7predicted|chr5|chr5.	coding) 26% identity to 43% of EAA16133.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr5	**Plasmodium yoelii yoelii**
107	2.22	2.22	41.1	pfa3D7predicted|chr13|chr13.	coding) 49% identity to 64% of EAA19445.1: ABC transporter [Plasmodium yoelii yoelii] Location= chr13	**Plasmodium yoelii yoelii**
108	2.22	2.22	33.2	pfa3D7predicted|chr11|chr11	coding) 67% identity to 83% of EAA17014.1: membrane-associated calcum-binding protein [Plasmodium yoelii yoelii] Location= chr11	**Plasmodium yoelii yoelii**
109	2.19	2.19	69.3	pfa3D7predicted|chr7|chr7	coding) 22% identity to 43% of EAA22916.1: erythrocyte membrane-associated giant protein antigen 332 [Plasmodium yoelii yoelii] Location= chr7	**Plasmodium yoelii yoelii**
110	2.19	2.19	42.1	pfa3D7predicted|chr13|chr13	coding) 26% identity to 45% of EAA17051.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr13	**Plasmodium yoelii yoelii**
111	2.18	2.18	23.6	pfa3D7predicted|pfal_chr2|pfal_chr2.	coding) 46% identity to 62% of EAA22515.1: hypothetical protein [Plasmodium yoelii yoelii] Location= pfal_chr2	**Plasmodium yoelii yoelii**
112	2.11	2.11	24.6	pfa3D7predicted|chr5|chr5	coding) 22% identity to 41% of EAA16943.1: 250-270 copies of a 13 AA repeat, NSSTPITSSSIL [Plasmodium yoelii yoelii] Location= chr5	**Plasmodium yoelii yoelii**
113	2.08	2.08	39.4	pfa3D7predicted|chr14|chr14	coding) 36% identity to 52% of EAA16501.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr14	**Plasmodium yoelii yoelii**
114	2.05	2.05	25	pfa3D7predicted|chr7|chr7	coding) 24% identity to 43% of EAA21354.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr7	**Plasmodium yoelii yoelii**
115	2.03	2.03	18.3	pfa3D7predicted|chr14|chr14.	coding) 42% identity to 60% of EAA16069.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr14	**Plasmodium yoelii yoelii**
117	1.93	1.93	43	pfa3D7predicted|chr13|chr13.	coding) 86% identity to 92% of EAA18291.1: translation elongation factor Tu [Plasmodium yoelii yoelii] Location= chr13	**Plasmodium yoelii yoelii**
118	1.88	1.88	27.5	pfa3D7predicted|chr13|chr13.	coding) 39% identity to 55% of EAA19997.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr13	**Plasmodium yoelii yoelii**

119	1.87	1.87	33.5	pfa3D7predicted|chr4|chr4	coding) 29% identity to 48% of EAA16876.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr4	**Plasmodium yoelii yoelii**
120	1.84	1.84	66.2	pfa3D7predicted|chr5|chr5	coding) 95% identity to 99% of EAA16191.1: 60S ribosomal protein L8 [Plasmodium yoelii yoelii] Location= chr5	**Plasmodium yoelii yoelii**
121	1.84	1.84	32.6	pfa3D7predicted|chr11|chr11	coding) 62% identity to 74% of EAA16316.1: guanylyl cyclase-related [Plasmodium yoelii yoelii] Location= chr11	**Plasmodium yoelii yoelii**
122	1.83	1.83	21.3	pfa3D7predicted|chr8|chr8.	coding) 26% identity to 45% of EAA18589.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr8	**Plasmodium yoelii yoelii**
123	1.83	1.83	32.6	pfa3D7predicted|chr14|chr14	coding) 25% identity to 45% of EAA16943.1: 250-270 copies of a 13 AA repeat, NSSTPITSSSIL [Plasmodium yoelii yoelii] Location= chr14	**Plasmodium yoelii yoelii**
124	1.83	1.83	52.4	pfa3D7predicted|chr8|chr8.	coding) 38% identity to 55% of EAA21161.1: putative peptidyl prolyl cis-trans isomerase with RNA binding region [Plasmodium yoelii yoelii] Location= chr8	**Plasmodium yoelii yoelii**
125	1.82	1.84	23.4	pfa3D7predicted|chr5|chr5.	coding) 38% identity to 54% of EAA16515.1: CPSF A subunit region, putative [Plasmodium yoelii yoelii] Location= chr5	**Plasmodium yoelii yoelii**
126	1.8	1.8	34.4	pfa3D7predicted|chr5|chr5.	coding) 64% identity to 77% of EAA22456.1: G/T mismatch binding protein-related [Plasmodium yoelii yoelii] Location= chr5	**Plasmodium yoelii yoelii**
127	1.77	1.77	34.4	pfa3D7predicted|chr14|chr14	coding) 60% identity to 76% of EAA21606.1: mitogen-activated protein kinase [Plasmodium yoelii yoelii] Location= chr14	**Plasmodium yoelii yoelii**
128	1.72	1.72	18	pfa3D7predicted|chr10|chr10.	coding) 36% identity to 55% of EAA17865.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr10	**Plasmodium yoelii yoelii**
129	1.66	1.66	30.6	pfa3D7predicted|chr8|chr8	coding) 50% identity to 72% of EAA18166.1: S1 RNA binding domain, putative [Plasmodium yoelii yoelii] Location= chr8	**Plasmodium yoelii yoelii**
130	1.64	1.64	25.5	pfa3D7predicted|chr4|chr4.	coding) 58% identity to 69% of EAA15209.1: adi-related [Plasmodium yoelii yoelii] Location= chr4	**Plasmodium yoelii yoelii**
131	1.63	1.63	23.1	pfa3D7predicted|chr1|chr1	coding) 41% identity to 57% of EAA20533.1: Ubiquitin carboxyl-terminal hydrolase family 2, putative [Plasmodium yoelii yoelii] Location= chr1	**Plasmodium yoelii yoelii**
132	1.62	1.62	10.1	pfa3D7predicted|chr13|chr13.	coding) 45% identity to 61% of EAA21291.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr13	**Plasmodium yoelii yoelii**
133	1.61	1.61	13.5	pfa3D7predicted|chr11|chr11.	coding) 27% identity to 44% of EAA22829.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr11	**Plasmodium yoelii yoelii**
134	1.6	1.6	17.5	pfa3D7predicted|chr14|chr14.	coding) 78% identity to 89% of EAA18905.1: DNA repair helicase, putative [Plasmodium yoelii yoelii] Location= chr14	**Plasmodium yoelii yoelii**
135	1.58	1.58	24.1	pfa3D7predicted|chr10|chr10.	coding) 36% identity to 54% of EAA15923.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr10	**Plasmodium yoelii yoelii**
136	1.52	1.52	27	pfa3D7predicted|chr5|chr5.	coding) 27% identity to 44% of EAA18442.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr5	**Plasmodium yoelii yoelii**
137	1.51	1.51	23.2	pfa3D7predicted|chr14|chr14.	coding) 69% identity to 82% of EAA18012.1: NAD(P) transhydrogenase beta subunit, putative [Plasmodium yoelii yoelii] Location= chr14	**Plasmodium yoelii yoelii**

138	1.5	1.51	24.8	pfa3D7predicted|chr5|chr5.	coding) 54% identity to 66% of EAA20683.1: ATP-dependent helicase ddx1 [Plasmodium yoelii yoelii] Location= chr5	**Plasmodium yoelii yoelii**
139	1.5	1.5	31.6	pfa3D7predicted|chr11|chr11.	coding) 48% identity to 66% of EAA18200.1: ERYTHROCYTE MEMBRANE PROTEIN PFEMP3 [Plasmodium yoelii yoelii] Location= chr11	**Plasmodium yoelii yoelii**
140	1.49	1.49	44	pfa3D7predicted|chr13|chr13.	coding) 51% identity to 68% of EAA16510.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr13	**Plasmodium yoelii yoelii**
141	1.48	1.48	30.8	pfa3D7predicted|chr6|chr6	coding) 76% identity to 87% of EAA18236.1: Unknown protein [Plasmodium yoelii yoelii] Location= chr6	**Plasmodium yoelii yoelii**
142	1.45	1.47	22.5	pfa3D7predicted|chr13|chr13	coding) 23% identity to 44% of EAA16160.1: rhoptry protein, putative [Plasmodium yoelii yoelii] Location= chr13	**Plasmodium yoelii yoelii**
143	1.43	1.44	26.2	pfa3D7predicted|chr3|chr3	coding) 30% identity to 47% of EAA18270.1: hypothetical protein [Plasmodium yoelii yoelii] Location= chr3	**Plasmodium yoelii yoelii**
144	1.39	1.4	4.8	pfa3D7predicted|chr10|chr10.	coding) 25% identity to 45% of BAB64297.1: I-connectin [Procambarus clarkii] Location= chr10	Procambarus clarkii
145	1.39	1.39	27	pfa3D7predicted|chr7|chr7.	coding) 29% identity to 51% of BAA97048.1: cytoplasmic dynein heavy chain [Rattus norvegicus] Location= chr7	Rattus norvegicus
146	1.34	1.34	29.4	pfa3D7predicted|chr9|chr9.	coding) 33% identity to 54% of XP_220603.2: similar to 1-beta dynein [Rattus norvegicus] Location= chr9	Rattus norvegicus
147	1.32	1.32	62.4	pfa3D7predicted|chr11|chr11.	coding) 73% identity to 85% of AAQ63186.1: heat shock protein 70 [Theileria annulata] Location= chr11	Theileria annulata
148	1.56	1.56	79.6	pfa3D7predicted|chr8|chr8	coding) 81% identity to 90% of AAC72001.1: heat shock protein 70 [Toxoplasma gondii] Location= chr8	Toxoplasma gondii
149	1.59	1.59	61.4	pfa3D7predicted|chr1|chr1	coding) 28% identity to 54% of ZP_00327118.1: COG5295: Autotransporter adhesin [Trichodesmium erythraeum IMS101] Location= chr1	Trichodesmium erythraeum IMS101
150	1.57	1.57	16.3	pfa3D7predicted|chr11|chr11.	coding) 22% identity to 41% of CAD53080.1: hypothetical protein	Trypanosoma brucei

Table 5: Summary of proteins identified by trypsin in-gel digestion (12hr contl) (1D RP-HPLC)

N	Unused	Total	%Cov(95	Species	Sequence	Modifications
1	7.59	7.59	31.624	Plasmodium_falciparum_TIGR|(protein	QVHPDTGISR	Phospho(S)@9
2	13.85	13.9	29.97	|Plasmodium_falciparum_TIGR|	VPIGTVSVVDLVCR	Oxidation(D)@10; Carbamidomethyl(C)@13; Oxidation(R)@14
3	9.62	9.62	27.426	Plasmodium_falciparum_Sanger	ATDIAENELPSTHPI	
4	14.83	14.8	27.394	Plasmodium_falciparum_Sanger	SVFPSIVGRPK	Phospho(S)@1; Oxidation(F)@3; Ser->Glu@5
5	6.28	6.28	24.859	|Plasmodium_falciparum_Sanger|(proteinnnnnnnn	AEQFTEDIGVVNKR	Protein Terminal Acetyl@N-term
6	20.3	20.3	23.928	Plasmodium_falciparum_Sanger 569	FEKESAEMGK	Oxidation(F)@1; Dethiomethyl(M)@8
7	1.45	1.45	22.772	Plasmodium_falciparum_TIGR|(protein	ENTKAAGNLDVNNENK	Deamidated(N)@8
8	6.27	6.27	22.656	Plasmodium_falciparum_Sanger|(protein	MQIFVKTLTGKTITL	Oxidation(M)@1; Phospho(T)@9; Oxidation(K)@11; Phospho(T)@14
9	2.02	2.02	21.429	Plasmodium_falciparum_Sanger|(protein	LQNIGGGVAAAPAGAAAVETAEAK	Phospho(T)@20; Glu->His@22
10	7.8	7.8	18.692	Plasmodium_falciparum_TIGR|	LSNQPNLVFVGEHAK	
11	5.9	5.9	17.424	|Plasmodium_falciparum_Sanger|(protein	AKGKTGRKKASK	Dioxidation(K)@2; Oxidation(K)@8; Phospho(S)@11
12	5.39	5.39	16.827	Plasmodium_falciparum_Sanger|(protein	IEGFPTLLYFK	
13	9.48	9.48	16.772	Plasmodium_falciparum_Sanger|	HASPYVAPAAAI	Oxidation(H)@1; Oxidation(P)@8
14	23.2	23.2	16.411	|Plasmodium_falciparum_Sanger 501	AKFEELNDDLFR	
15	2.71	2.71	16.346	Plasmodium_falciparum_TIGR|(protein	ENITSMPTFK	Phospho(T)@8
16	8.19	8.19	14.35	|Plasmodium_falciparum_TIGR	NINEIIAPK	
17	3.37	3.37	14.286	Plasmodium_falciparum_Sanger|(protein	IFPGLACRCTK	Carbamidomethyl(C)@7; Carbamidomethyl(C)@9; Phospho(T)@10
18	2.94	2.94	12.409	Plasmodium_falciparum_Sanger|(protein	AEASKEQSK	Phospho(S)@8
19	2.5	2.5	12.295	Plasmodium_falciparum_Sanger|(protein	ESSNSRDR	Phospho(S)@2; Oxidation(R)@8

20	5.6	5.6	12.264	Plasmodium_falciparum_TIGR|(protein	VFLENVIK	
21	14.61	14.6	11.965	Plasmodium_falciparum_Sanger 642	AKGSKPNLPESNI	Phospho(S)@4; Deamidated(N)@12
22	1.77	1.77	11.321	plasmodium_falciparum_TIGR|(protein	GDNKKGTPGAK	Deamidated(N)@3; Oxidation(K)@4; Phospho(T)@7
23	7.49	7.49	10.841	Plasmodium_falciparum_TIGR|(protein	KDLSIGSVDPVVVELKNQNK	Phospho(S)@7; Oxidation(N)@17
24	3.79	3.79	10.811	plasmodium_falciparum_TIGR|(protein	DINTPQNNNKK	Phospho(T)@4
25	12.5	13.2	10.201	Plasmodium_falciparum_Sanger|	ADADKSDKTVK	Dehydrated(D)@4; Oxidation(K)@5; Phospho(S)@6
26	3.57	3.57	9.9338	Plasmodium_falciparum_Sanger|(protein	ETLVRITGGMKVK	Phospho(T)@2
27	3.38	3.38	9.8765	Plasmodium_falciparum_TIGR|(protein	LATSVLAGLLGVV	
28	3.34	3.34	9.7403	plasmodium_falciparum_Sanger|(protein	KVGDDIAK	Oxidation(K)@1
29	2.39	2.39	8.8398	Plasmodium_falciparum_TIGR|(protein	NPFDEVIITGLGNATK	
30	13.98	14	8.82	Plasmodium_falciparum_Sanger|(protein	ALIDVISDTLK	Oxidation(D)@4; Phospho(T)@9; Oxidation(K)@11
31	2.04	2.04	8	Plasmodium_falciparum_Sanger|(protein	IGSRGGDITNGNGSGGESIYGR	Phospho(S)@3; Oxidation(D)@7; Oxidation(N)@10
32	7.24	7.24	7.888	Plasmodium_falciparum_TIGR|(protein	QLAENTVLDESIQK	Oxidation(N)@5; Phospho(T)@6; Phospho(S)@11
33	2.24	2.24	7.8818	Plasmodium_falciparum_Sanger|(protein	EINKPAK	Deamidated(N)@3; Oxidation(P)@5; Oxidation(K)@7
34	4.46	4.46	7.75	Plasmodium_falciparum_Sanger|(protein	NKLSEINNIISGDFLSTLK	Oxidation(N)@7; Oxidation(N)@8; Oxidation(D)@13; Phospho(T)@17
35	2.56	2.56	7.483	Plasmodium_falciparum_Sanger|(protein	GVDLDKLLDLSQDELIK	Leu->Val@8; Phospho(S)@11; Deamidated(Q)@12
36	1.9	1.9	7.2727	Plasmodium_falciparum_TIGR|(protein	LCLIEYGPYAGK	Carbamidomethyl(C)@2; Oxidation(P)@8; Phospho(Y)@9
37	2.09	2.09	7.0896	Plasmodium_falciparum_TIGR|(protein	MLNKMGGQYAPK	Oxidation(M)@1; Deamidated(Q)@8; Oxidation(P)@11
38	1.73	11.1	7.0093	Plasmodium_falciparum_Sanger|(protein	QATKDAGAIAGLNVLR	Phospho(T)@3; Oxidation(D)@5; Methyl(R)@16
39	2.98	2.98	6.8807	Plasmodium_falciparum_TIGR|(protein	LGSRQVHVVRGR	Oxidation(R)@4
40	2.16	2.16	6.8807	Plasmodium_falciparum_Sanger|(protein	QKKQATKNDDNLSIQPRGK	Oxidation(K)@3; Phospho(T)@6; Deamidated(Q)@15
41	5.48	5.48	6.8433	Plasmodium_falciparum_Sanger|(protein	DVNAAVATIKTKR	Oxidation(N)@3; Phospho(T)@11; Deamidated(R)@13
42	4.13	4.13	6.8323	Plasmodium_falciparum_Sanger|(protein	TDEKKVEYDEK	Phospho(T)@1; Oxidation(D)@2; Oxidation(Y)@8; Oxidation(K)@11

43	2.04	2.04	6.7633	Plasmodium_falciparum_TIGR|(protein	DSAAAIVVYDITNR	
44	2.63	2.63	6.4356	|Plasmodium_falciparum_TIGR|(protein	GGIGNIQHTLISDITK	Oxidation(N)@5; Oxidation(H)@8; Phospho(S)@12; Phospho(T)@15
45	3.8	3.8	6.3559	Plasmodium_falciparum_Sanger|(protein	RNYISSGGLEATK	Carbamyl(R)@1; Phospho(S)@5
46	2.28	3.28	6.3291	Plasmodium_falciparum_Sanger|(protein	VGSTAAVYAAAILEYLTAEVLELAGNATKDLKVKR	Phospho(T)@4; Oxidation(D)@30; Oxidation(R)@35
47	2.04	2.04	6.2718	Plasmodium_falciparum_TIGR|(protein	AATSALTTVI	Phospho(T)@8
48	8.67	8.67	5.7009	Plasmodium_falciparum_Sanger|	NKSFLK	Phospho(S)@3
49	2.2	2.2	5	Plasmodium_falciparum_Sanger|(protein	ARAMVGVVGAGGRIDK	Deamidated(R)@2; Arg->Gln@13
50	2.36	2.36	4.4983	Plasmodium_falciparum_TIGR|(protein	ILAEAKSK	Phospho(S)@7
51	3.55	3.55	4.386	Plasmodium_falciparum_Sanger|(protein	TAEIKVSI	
52	3.79	3.79	4.3732	Plasmodium_falciparum_TIGR|(protein	QVQAEMGQIDSDK	Deamidated(Q)@1; Phospho(S)@11
53	2.08	2.08	4.3614	Plasmodium_falciparum_TIGR|(protein	MTHVPMTVSK	Oxidation(P)@5; Oxidation(M)@6; Phospho(S)@9; Oxidation(K)@10
54	2.04	2.04	4.2308	Plasmodium_falciparum_Sanger|(protein	INNAFNLDILR	Deamidated(N)@3; Deamidated(N)@6; Oxidation(D)@8
55	2.03	2.03	4.0404	Plasmodium_falciparum_Sanger|(protein	DTKGQILNAKYFKQFIKNER	Phospho(T)@2; Oxidation(F)@15; Oxidation(K)@17
56	1.82	1.82	3.9344	Plasmodium_falciparum_Sanger|(protein	NLVLQTIK	Deamidated(Q)@5
57	4.18	4.18	3.8095	Plasmodium_falciparum_Sanger|(protein	LGAPFLQNLK	
58	1.38	1.38	3.4582	Plasmodium_falciparum_TIGR|(protein	LNRNGNTGNGNK	Oxidation(R)@3; Oxidation(N)@9; Deamidated(N)@11; Oxidation(K)@12
59	2.05	2.05	3.2698	Plasmodium_falciparum_TIGR|(protein	VSESQELIDLVK	Phospho(S)@4
60	3.39	3.39	3.2663	Plasmodium_falciparum_Sanger|(protein	SNPYFIVGSR	
61	6.81	6.81	3.1969	Plasmodium_falciparum_TIGR|(protein	TEVSKKTFSGIGFNLTEKEAK	Phospho(T)@7; Oxidation(N)@14; Oxidation(K)@18; Oxidation(K)@21
62	1.81	1.81	3.1707	Plasmodium_falciparum_Sanger|(protein	VIKTYTK	Phospho(T)@4
63	1.61	1.61	2.9954	plasmodium_falciparum_Sanger|(protein	YSFAVVTVLGENK	
64	1.8	1.8	2.9748	Plasmodium_falciparum_Sanger|(protein	VPISAADVAR	Oxidation(P)@2; Oxidation(D)@7; Deamidated(R)@10
65	9.22	9.22	2.7477	plasmodium_falciparum_Sanger|	ENSVILLENLR	

66	2.29	2.29	2.5937	Plasmodium_falciparum_Sanger|(protein	IGTPNLPEFWLR	
67	3.04	3.04	2.5899	Plasmodium_falciparum_TIGR|(protein	RPTSYKSSLSLKVDNIPVR	Phospho(S)@4; Oxidation(P)@17; Oxidation(R)@19
68	2.61	2.61	2.544	Plasmodium_falciparum_TIGR|(protein	ESNNSIKKK	Glu->pyro-Glu@N-term; Oxidation(K)@7; Oxidation(K)@9
69	1.75	1.75	2.4336	Plasmodium_falciparum_TIGR|(protein	EIESDKQVQK	
70	3.14	3.14	2.4	Plasmodium_falciparum_Sanger|(protein	DPSLRKSGTGNIFVK	Oxidation(P)@2; Phospho(T)@9; Oxidation(K)@15
71	2.29	2.29	2.2491	Plasmodium_falciparum_TIGR|(protein	NTPSSSGLVK	
72	6.08	6.08	2.2262	|Plasmodium_falciparum_Sanger|(protein	ALTAVSELIESAR	
73	3.53	3.53	2.1635	Plasmodium_falciparum_TIGR|(protein	AGIISSKNAGDAR	Phospho(S)@6; Deamidated(N)@8
74	1.83	1.83	2.0534	Plasmodium_falciparum_TIGR|(protein	SKNFRINTIYPLLK	Deamidated(N)@3; Phospho(T)@8
75	1.84	1.85	1.8328	Plasmodium_falciparum_Sanger|(protein	SDNTAVALDYGMYRMK	Carbamyl(M)@12; Deamidated(R)@14; Oxidation(M)@15
76	2.25	2.25	1.7544	Plasmodium_falciparum_Sanger|(protein	PIILSLHKFR	Phospho(S)@5; Oxidation(R)@10
77	6.81	6.81	1.7519	Plasmodium_falciparum_Sanger|(protein	NNDQLTFLETQVAK	Oxidation(N)@1; Deamidated(N)@2; Deamidated(Q)@4
78	2.58	2.58	1.7391	Plasmodium_falciparum_TIGR|(protein	KKSEIDK	
79	2.16	2.16	1.6169	Plasmodium_falciparum_TIGR|(protein	ADFVGF	Oxidation(D)@2
80	1.35	1.35	1.5429	Plasmodium_falciparum_Sanger|(protein	KSKIININSIININTSEK	Phospho(S)@2; Deamidated(N)@12; Dioxidation(K)@18
81	1.94	1.94	1.5353	Plasmodium_falciparum_TIGR|(protein	VSEQNLESLIR	
82	2.72	2.72	1.4095	Plasmodium_falciparum_Sanger|(protein	NNSTKVSNSSKK	Phospho(T)@4; Oxidation(K)@5; Deamidated(N)@8
83	1.58	1.58	1.4094	Plasmodium_falciparum_Sanger|(protein	SNIDVRDDGGIR	Deamidated(R)@6; Oxidation(D)@7
84	3.52	3.52	1.3233	Plasmodium_falciparum_Sanger|(protein	KIFTLGKSGR	Oxidation(K)@1; Oxidation(F)@3; Phospho(S)@8; Oxidation(R)@10
85	5.29	5.29	1.2141	Plasmodium_falciparum_TIGR|(protein	VSKKKYNKLIK	Phospho(S)@2; Dioxidation(K)@4
86	2.11	2.11	1.1357	Plasmodium_falciparum_Sanger|(protein	DIYGDVIIIKRMFSSHTSK	Oxidation(D)@5; Deamidated(R)@11; Phospho(T)@17
87	6.62	6.62	1.1142	Plasmodium_falciparum_Sanger|(protein	KNSIPPR	Deamidated(N)@2; Oxidation(P)@6; Deamidated(R)@7
88	2.92	2.92	1.0536	Plasmodium_falciparum_TIGR|(protein	KANKNNTTEGNEKNKGSNNK	Phospho(T)@7; Deamidated(N)@14; Oxidation(K)@20
89	3.18	3.18	1.0492	Plasmodium_falciparum_Sanger|(protein	NITKINTLNSNTK	Phospho(T)@3; Deamidated(N)@11; Phospho(T)@12

90	3.88	3.88	0.9884	Plasmodium_falciparum_Sanger|(protein	ANELDVLK	
91	4.57	4.57	0.9873	Plasmodium_falciparum_Sanger|(protein	RYLVDLNSPLFNVLKEVR	Oxidation(D)@5; Deamidated(N)@7; Oxidation(P)@9; Oxidation(N)@12
92		3.11	0.9761	Plasmodium_falciparum_Sanger|(protein	SISSSVKFLSSKERYNNNQKRK	Phospho(S)@4; Oxidation(F)@8; Oxidation(N)@16; Deamidated(N)@17
93	2.48	2.48	0.8607	Plasmodium_falciparum_Sanger|(protein	DDIYKEQKQENNKNAKKIKTFNSEPYWK	Oxidation(K)@16; Oxidation(K)@17; Dioxidation(K)@19; 22
94	1.72	1.72	0.8587	Plasmodium_falciparum_Sanger|(protein	GTFFQDVKVLTPR	Deamidated(Q)@5; Phospho(T)@11; Deamidated(R)@13
95	2.53	2.53	0.8513	Plasmodium_falciparum_Sanger|(protein	MGIKRMYQKIPATILVLK	Dioxidation(P)@11; Phospho(T)@13
96	4.41	4.41	0.8171	Plasmodium_falciparum_Sanger|(protein	VSNGATGKK	Phospho(S)@2; Oxidation(K)@8
97	7.13	7.13	0.724	Plasmodium_falciparum_TIGR|(protein	QPLLRRHSTAILNHNISNLKTKISNVKDKNDK	Phospho(S)@8; Oxidation(H)@14; Deamidated(N)@15
98	2.36	2.36	0.702	Plasmodium_falciparum_TIGR|(protein	LDSDIESPR	Phospho(S)@3
99	3	3	0.6891	Plasmodium_falciparum_TIGR|(protein	NKNNKKNKKNMKNIKNK	Deamidated(N)@13; Asn->Ser@16
100	3.51	3.51	0.6449	Plasmodium_falciparum_TIGR|(protein	ENLNEGKK	Deamidated(N)@2; Deamidated(N)@4; Oxidation(K)@8
101	1.47	1.48	0.6366	Plasmodium_falciparum_TIGR|(protein	SHIKNIGANLISSFK	Phospho(S)@13
102	3.43	3.43	0.5658	Plasmodium_falciparum_Sanger|(protein	LQMNNSTPSITSNGNKK	Deamidated(Q)@2; Oxidation(M)@3
103	3.85	3.85	0.5428	Plasmodium_falciparum_TIGR|(protein	LITLQYNVLNYF	Deamidated(Q)@5
104	2.43	2.43	0.5232	Plasmodium_falciparum_Sanger|(protein	DLSSTNNNIKK	Deamidated(N)@8
105	1.99	1.99	0.5069	Plasmodium_falciparum_Sanger|(protein	MNKSISNNKQNLVDNEK	
106	2.24	2.24	0.506	Plasmodium_falciparum_TIGR|(protein	AAHIMVASLASSLALATCK	Oxidation(M)@5; Phospho(T)@17; Carbamidomethyl(C)@18
107	2.12	2.12	0.4622	Plasmodium_falciparum_Sanger|(protein	IVNSSDCK	Phospho(S)@5; Carbamidomethyl(C)@7
108	6.31	6.31	0.458	|Plasmodium_falciparum_Sanger|(protein	KEKIDNQHVWK	Oxidation(K)@3; Deamidated(N)@6; Deamidated(Q)@7
109	3.12	3.12	0.4461	Plasmodium_falciparum_TIGR|(protein	EIKSNEYYENVESNEELDFLFKDMRKNL	Glu->pyro-Glu@N-term; Phospho(S)@4; Oxidation(M)@24
110	6.55	6.55	0.4124	Plasmodium_falciparum_Sanger|(protein	LINQEKELENIKKK	Deamidated(Q)@4; Dioxidation(K)@6; Formyl(K)@14
111	4.38	4.39	0.4039	Plasmodium_falciparum_TIGR|(protein	KKTKLNSK	Deamidated(N)@6; Phospho(S)@7; Oxidation(K)@8

112	2.23	2.23	0.3755	Plasmodium_falciparum_Sanger|(protein	ENIIASSKINKNKK	Carbamidomethyl@N-term; Oxidation(N)@2; Deamidated(N)@10
113	2.45	2.45	0.3572	Plasmodium_falciparum_Sanger|(protein	MKHADASK	Oxidation(H)@3; Phospho(S)@7; Oxidation(K)@8
114	2.32	2.32	0.3291	plasmodium_falciparum_Sanger|(protein	ITYLIDIVLKIKSNTVNK	Phospho(T)@2; Phospho(T)@15; Deamidated(N)@17
115	2.87	2.87	0.3092	Plasmodium_falciparum_Sanger|(protein	GRKIFNDFLCSNILKYNLK	Oxidation(F)@8; Carbamidomethyl(C)@10; Phospho(S)@11
116	4.18	4.18	0.2689	Plasmodium_falciparum_Sanger|(protein	INNSKINKGRKGINKK	Deamidated(N)@3; Phospho(S)@4; Oxidation(K)@11
117	6.96	6.96	0.1942	Plasmodium_falciparum_TIGR|(protein	LNTNLLNNK	Deamidated(N)@7; Deamidated(N)@8
118	4.64	4.64	0.1449	Plasmodium_falciparum_Sanger|(protein	FGKSVLSGILEGINR	Phospho(S)@7
119	7.48	7.48	0.1361	Plasmodium_falciparum_Sanger|(protein	VTSNLLASYSNER	Phospho(S)@8; Deamidated(N)@11

Table 6: Summary of proteins identified by trypsin in-gel digestion (12hr drug treated) (1D RP-HPLC)

N	Unused	Total	% Cov	Species	Sequence	Modification
1	30.17	30.17	38.374719	Plasmodium_falciparum_Sanger|(protein	EHALLAFTLGVK	
2	24.14	24.14	35.904256	plasmodium_falciparum_Sanger|(protein	SYELPDGNIITVGNER	
3	1.4	1.43	34.666666	|Plasmodium_falciparum_Sanger|(protein	INGNERINGNER	Deamidated(N)@4
4	7.33	7.33	30.18868	Plasmodium_falciparum_TIGR	SGRGKGGKGLGKGGAK	Phospho(S)@1; Deamidated(R)@3; Formyl(K)@12
5	9.06	9.06	30.000001	Plasmodium_falciparum_TIGR|(protein	TTYTLVLLR	Protein Terminal Acetyl@N-term
6	13.83	13.83	28.481013	Plasmodium_falciparum_Sanger|(protein	LISDAELEAIFDR	
7	9.67	9.67	28.037384	Plasmodium_falciparum_TIGR|(protein	ILVGDGGVGK	Oxidation(D)@5
8	2.01	2.01	26.271185	Plasmodium_falciparum_TIGR|(protein	MSITSDNILK	Phospho(S)@2
9	19.28	19.28	26.112759	Plasmodium_falciparum_TIGR|(protein	SKGGKDWRAGRCALSNIIPASTGAAKAVGK	Phospho(S)@1; Oxidation(K)@2; Carbamidomethyl(C)@12
10	14.15	14.15	21.74888	Plasmodium_falciparum_TIGR|(protein	LTAAIGKDVQIVGDDLLVTNPTR	Phospho(D)@15; Phospho(T)@19
11	7.58	7.58	21.559633	Plasmodium_falciparum_TIGR|(protein	IIDVVYNASNNELVRTK	Deamidated(N)@7; Phospho(S)@9; Deamidated(N)@11
12	3.53	3.53	20.997375	Plasmodium_falciparum_Sanger|(protein	TITLDVEPSDTIENVK	Methyl(D)@5
13	6.97	6.97	19.409283	Plasmodium_falciparum_Sanger|(protein	ATDIAENELPSTHPIR	
14	4.97	4.97	19.354838	Plasmodium_falciparum_Sanger|(protein	KKSGRRGRR	Deamidated(R)@6

15	2.25	3.14	17.424242	Plasmodium_falciparum_Sanger|(protein	AGLQFPVGR	Oxidation(P)@6; Oxidation(R)@9
16	4.47	4.47	17.333333	Plasmodium_falciparum_Sanger|(protein	GGDITNGNGSGGESIYGR	Oxidation(D)@3; Oxidation(Y)@16
17	4.18	4.18	17.094018	Plasmodium_falciparum_TIGR|(protein	QVHPDTGISR	Gln->pyro-Glu@N-term; Carbamidomethyl(H)@3
18	23.52	23.52	16.564417	Plasmodium_falciparum_Sanger|(protein	ITPSYVSFVDGERKVGEAAK	Phospho(S)@4; Oxidation(F)@8; Phospho(K)@20
19	3.93	3.93	15.254237	Plasmodium_falciparum_Sanger|(protein	LLEPVPFVK	
20	6.78	6.79	14.112903	Plasmodium_falciparum_Sanger|(protein	GGNRGGSRSGFRGGRGGFRGGR	Oxidation(R)@8; Phospho(S)@9; Oxidation(F)@11; Oxidation(R)@19
21	10.03	10.03	14.04762	|Plasmodium_falciparum_Sanger|(protein	YNVLFVADEVQTGLGR	
22	3.74	3.74	12.781955	Plasmodium_falciparum_Sanger|(protein	ELANQLK	Deamidated(N)@4
23	22.27	23.4	12.703101	Plasmodium_falciparum_TIGR|(protein	NRGKDLSK	Oxidation(K)@4; Oxidation(D)@5; Phospho(S)@7
24	2.2	2.21	12.295082	Plasmodium_falciparum_Sanger|(protein	KIEGVNVLTSVIESAQDVAD	Carbamyl(K)@1; Phospho(T)@9
25	2.02	2.02	11.956522	Plasmodium_falciparum_Sanger|(protein	LAEIFSSGK	Phospho(S)@7; Oxidation(K)@9
26	2.3	2.3	11.538462	Plasmodium_falciparum_TIGR|(protein	TYTKMVFIKVDVDEVSEVTEK	Phospho(T)@1; Phospho(T)@19
27	4.43	4.43	11.504425	Plasmodium_falciparum_Sanger|(protein	SNLLSRFTR	Phospho(S)@1; Oxidation(N)@2; Oxidation(R)@6; Oxidation(F)@7
28	5.19	5.22	10.593221	Plasmodium_falciparum_Sanger|(protein	IKDSKRKMQR	Phospho(S)@4
29	3.63	3.63	9.6774191	Plasmodium_falciparum_TIGR|(protein	TIEVITK	Phospho(T)@6
30	3.46	3.46	9.6551724	Plasmodium_falciparum_Sanger|(protein	VIILGDSGVGK	Phospho(S)@7; Phospho(K)@11
31	5.89	5.89	9.4999999	Plasmodium_falciparum_Sanger|(protein	DLSLSSILR	Phospho(S)@3
32	12.8	12.8	9.0579711	Plasmodium_falciparum_Sanger|(protein	DPRGATLKR	Oxidation(R)@3; Oxidation(K)@8
33	5.13	5.13	8.8607594	Plasmodium_falciparum_Sanger|(protein	VLGLGKGGKGKTGSGKTKKAPLSRASR	Deamidated(R)@24; Phospho(S)@26; Oxidation(R)@27
34	6.19	6.19	8.2914576	Plasmodium_falciparum_TIGR|(protein	VVLALGDYLK	
35	3.65	11.3	8.2848839	plasmodium_falciparum_Sanger|(protein	AMTKDNNLLGK	Phospho(T)@3; Deamidated(N)@7
36	3.77	3.77	8.130081	Plasmodium_falciparum_Sanger|(protein	TAGKTLGPRHK	Oxidation(P)@8; Oxidation(H)@10; Oxidation(K)@11
37	2.91	2.91	8.130081	Plasmodium_falciparum_Sanger|(protein	NPSQSGPYR	Deamidated(N)@1; Phospho(S)@5; Oxidation(P)@7; Deamidated(R)@9
38	2.06	2.06	7.8014188	Plasmodium_falciparum_Sanger|(protein	AVFDNVTAIQK	Phospho(T)@7; Deamidated(Q)@10
39	1.73	1.74	7.3260076	Plasmodium_falciparum_Sanger|(protein	HVVALTGSGTSAESNIPSFR	

40	3.32	3.33	7.0895523	Plasmodium_falciparum_TIGR|(protein	SIPYIHPDVKVNDTVR	Oxidation(P)@7; Deamidated(N)@12; Oxidation(D)@13; Phospho(T)@14
41	1.91	1.91	6.9565214	Plasmodium_falciparum_Sanger|(protein	LRLIHVMVNKARPGR	Deamidated(R)@2; Oxidation(H)@5
42	2.89	2.9	6.9124423	Plasmodium_falciparum_Sanger|(protein	SIEPMIIMSK	Oxidation(P)@4; Oxidation(M)@5
43	11.95	11.95	6.8456374	Plasmodium_falciparum_Sanger|(protein	IPKR	Oxidation(K)@3
44	2.84	2.84	6.8322979	Plasmodium_falciparum_Sanger|(protein	NGHVMLK	Deamidated(N)@1
45	2.15	2.15	6.666667	Plasmodium_falciparum_TIGR|(protein	AFVLIDK	
46	7.7	7.7	6.4788729	Plasmodium_falciparum_TIGR|(protein	ATILMGKNTR	Carbamidomethyl@N-term; Oxidation(K)@7
47	2.07	2.07	6.4220183	Plasmodium_falciparum_Sanger|(protein	LGANTFTTVSTKFSK	Oxidation(N)@4; Oxidation(F)@6; Phospho(T)@11
48	3.15	3.15	6.2091503	Plasmodium_falciparum_Sanger|(protein	KSSQVGK	Phospho(S)@3; Oxidation(K)@7
49	5.53	5.53	6.1281338	Plasmodium_falciparum_Sanger|(protein	VPNSNVIK	
50	1.46	1.46	5.9405942	Plasmodium_falciparum_TIGR|(protein	TNTNPKKGPLHLR	Phospho(T)@3; Oxidation(N)@4
51	1.85	1.88	5.7971016	Plasmodium_falciparum_TIGR|(protein	GLNK	Oxidation(N)@3
52	5.18	5.18	5.5276383	Plasmodium_falciparum_Sanger|(protein	TKMLNSHK	Oxidation(H)@7; Oxidation(K)@8
53	2.98	2.98	5.0179213	Plasmodium_falciparum_Sanger|(protein	QAIESLR	Gln->pyro-Glu@N-term
54	2.73	2.73	5.0000001	Plasmodium_falciparum_Sanger|(protein	TKLVGKSEE	
55	4.1	4.16	4.9689442	Plasmodium_falciparum_Sanger|(protein	SEPIPEDDKNAPVK	
56	2.09	2.09	4.954955	Plasmodium_falciparum_TIGR|(protein	LSIR	
57	3.1	3.1	4.9429659	Plasmodium_falciparum_TIGR|(protein	WTPGMLTNQIIQKFTEPR	Phospho(T)@2; Phospho(T)@7; Phospho(T)@15
58	3.23	3.24	4.9140047	Plasmodium_falciparum_Sanger|(protein	SNNNSTHSKK	Phospho(T)@6
59	12.75	12.76	4.8445407	Plasmodium_falciparum_Sanger|(protein	GLLGEEVLFLNDCVGK	Carbamidomethyl(C)@13
60	1.68	1.68	4.8275862	Plasmodium_falciparum_TIGR|(protein	SKQRRNEALR	Phospho(S)@1; Oxidation(K)@2; Oxidation(N)@6
61	3.48	3.48	4.8214287	plasmodium_falciparum_Sanger|(protein	SASTASTASAASAASTTRSASAASTTR	Phospho(S)@6; Deamidated(R)@18; Dehydrated(S)@21
62	2.11	2.11	4.8148148	Plasmodium_falciparum_TIGR|(protein	IIKGDSMTR	Phospho(S)@6; Carbamyl(M)@7
63	3.32	3.32	4.8076924	Plasmodium_falciparum_Sanger|(protein	SGASKVAKK	Phospho(S)@1

64	2.22	2.22	4.7619049	Plasmodium_falciparum_TIGR|(protein	TNKTNK	Phospho(T)@1; Oxidation(N)@2; Oxidation(N)@5
65	4.44	4.45	4.587156	Plasmodium_falciparum_TIGR|(protein	EASTSKGATK	Phospho(S)@5; Phospho(T)@9
66	4.14	4.14	4.4217687	Plasmodium_falciparum_TIGR|(protein	DVGITRTTTGNR	Phospho(T)@5; Deamidated(R)@6
67	3.48	3.48	4.3052837	Plasmodium_falciparum_Sanger|(protein	VGSFQGTDIVIR	Oxidation(F)@4; Oxidation(D)@8
68	2.14	2.14	4.2307694	Plasmodium_falciparum_Sanger|(protein	SLRNEQESNK	Deamidated(N)@4
69	1.91	1.91	4.2071197	Plasmodium_falciparum_TIGR|(protein	GRGGMNRGTYGR	
70	3.45	3.45	4.1522492	plasmodium_falciparum_TIGR|(protein	LLNKPSLDLLK	Deamidated(N)@3; Oxidation(P)@5; Oxidation(K)@11
71	1.55	1.57	4.0160641	Plasmodium_falciparum_Sanger|(protein	DVDNYAR	
72	4.12	4.13	3.8199183	plasmodium_falciparum_TIGR|(protein	GNNNYNNNLER	Deamidated(N)@2; Asn->His@7; Oxidation(N)@8
73	5.38	5.42	3.8167939	plasmodium_falciparum_TIGR|(protein	SSTSTQK	Phospho(T)@5
74	7.01	7.01	3.7406486	plasmodium_falciparum_TIGR|(protein	GKPTDLSIHETAWGLAR	
75	1.83	1.84	3.5230353	Plasmodium_falciparum_TIGR|(protein	NIITTNIFANFKQK	Deamidated(N)@6; Oxidation(K)@12; Deamidated(Q)@13
76	2.59	2.59	3.4055728	Plasmodium_falciparum_Sanger|(protein	TIVSASR	Phospho(S)@6; Oxidation(R)@7
77	2.28	2.65	3.3259425	Plasmodium_falciparum_TIGR|(protein	LTSKAGTISGIFSK	Phospho(T)@7; Phospho(S)@13
78	3.42	3.43	3.318584	Plasmodium_falciparum_TIGR|(protein	LPTLEFR	
79	2.94	3.19	3.3112582	Plasmodium_falciparum_TIGR|(protein	ILKTIKTHK	Oxidation(K)@3; Phospho(T)@4; Phospho(T)@7
80	2.19	2.19	3.2697547	Plasmodium_falciparum_TIGR|(protein	LTDIYIDYTVVEDLAKHAVFNK	Phospho(T)@9; Oxidation(N)@21; Oxidation(K)@22
81	2.34	2.34	3.1976745	Plasmodium_falciparum_TIGR|(protein	AGAAAAAEAGK	
82	1.56	1.58	3.1746034	Plasmodium_falciparum_TIGR|(protein	LNNIIKYKTNK	Oxidation(K)@8; Phospho(T)@9; Oxidation(K)@11
83	2.23	2.23	3.164557	plasmodium_falciparum_TIGR|(protein	SNQAAEAAVAAGKAAETAEK	Phospho(S)@1; Deamidated(N)@2; Oxidation(K)@13; Oxidation(K)@20
84	7.59	7.59	3.088803	Plasmodium_falciparum_TIGR|(protein	KNKNESSSDVLSKHSSAYR	Phospho(K)@3; Oxidation(N)@4; Phospho(S)@6; Oxidation(H)@14
85	1.35	1.38	3.0456852	Plasmodium_falciparum_Sanger|(protein	KDTLK	
86	2.38	2.38	2.9748283	Plasmodium_falciparum_Sanger|(protein	VPVDNLEAQLIGLDYFTK	
87	1.57	1.57	2.9629629	plasmodium_falciparum_Sanger|(protein	LNTNTQPR	Deamidated(N)@2; Deamidated(N)@4

88	2.45	2.45	2.9411765	Plasmodium_falciparum_TIGR|(protein	LTNGQIRLTLSSIDGTEK	Phospho(T)@2; Oxidation(R)@7
89	1.94	1.94	2.9126214	plasmodium_falciparum_Sanger|(protein	SLFLDDFNR	
90	3.7	3.7	2.8606964	Plasmodium_falciparum_TIGR|(protein	NSRTKLAIVYSPMHGIGRK	Oxidation(N)@1; Phospho(S)@2; Phospho(S)@11; Oxidation(P)@12
91	2.53	2.54	2.8481012	Plasmodium_falciparum_Sanger|(protein	PTLSTVRK	Oxidation(K)@8
92	2.03	2.03	2.7923211	Plasmodium_falciparum_Sanger|(protein	NKNMYR	Oxidation(M)@4
93	7.23	7.26	2.5928522	Plasmodium_falciparum_Sanger|(protein	KCHNVIGNIR	Carbamidomethyl(C)@2
94	6.96	6.97	2.5386313	Plasmodium_falciparum_TIGR|(protein	TSGTSYRGEFETRMK	Phospho(T)@4; Oxidation(F)@10; Dioxidation(R)@13; Oxidation(M)@14
95	7.97	7.97	2.3364486	Plasmodium_falciparum_Sanger|(protein	LSSIMER	
96	2.15	2.15	2.2491349	Plasmodium_falciparum_TIGR|(protein	NTPSSSGLVK	Phospho(T)@2; Oxidation(K)@10
97	2.06	2.09	2.247191	Plasmodium_falciparum_TIGR|(protein	LAVNLIPFPR	
98	2.4	2.4	2.209131	Plasmodium_falciparum_TIGR|(protein	VPDTPLDNNAK	
99	3.7	3.7	2.1929825	Plasmodium_falciparum_Sanger|(protein	TQITIEYK	Phospho(T)@4; Oxidation(Y)@7
100	3.5	3.5	2.106319	Plasmodium_falciparum_Sanger|(protein	NSSSGNGK	Phospho(S)@2; Deamidated(N)@6
101	1.94	1.95	2.0408163	Plasmodium_falciparum_TIGR|(protein	TLTNFALLQNR	Phospho(T)@1; Deamidated(N)@4; Oxidation(R)@11
102	2.66	2.69	2.0036429	Plasmodium_falciparum_TIGR|(protein	IQKKNIWSLEK	Oxidation(K)@3; Oxidation(N)@5; Phospho(S)@8; Oxidation(K)@11
103	1.45	1.47	1.8867925	plasmodium_TIGR|(protein	IIRR	Oxidation(R)@3
104	2.17	2.18	1.8610422	Plasmodium_falciparum_Sanger|(protein	LKSTNIYFIK	Oxidation(K)@2; Deamidated(N)@5; Oxidation(Y)@7
105	4.36	4.36	1.8181818	Plasmodium_falciparum_TIGR|(protein	TIEVGNTDAEGRLTLADALVYAEK	Phospho(T)@1; Oxidation(N)@6
106	1.78	1.78	1.7886179	Plasmodium_falciparum_Sanger|(protein	PPPPPPLY	Oxidation(P)@4; Oxidation(Y)@8
107	3.95	3.98	1.7306246	Plasmodium_falciparum_TIGR|(protein	GDNK	
108	2.05	2.07	1.7171716	Plasmodium_falciparum_Sanger|(protein	LLNQ	Deamidated(N)@3
109	3.76	3.77	1.6491754	Plasmodium_falciparum_TIGR|(protein	TDKNK	
110	3.7	3.79	1.6442452	Plasmodium_falciparum_Sanger|(protein	YDFMNETNELKVGRNVINYK	Deamidated(N)@5; Phospho(T)@7; Oxidation(N)@8; Deamidated(N)@18
111	2.02	2.03	1.5873017	plasmodium_falciparum_Sanger|(protein	AGSELTRK	Phospho(S)@3

112	4.01	5.17	1.5228426	Plasmodium_falciparum_Sanger|(protein	EGAKNGINK	Deamidated(N)@8
113	1.79	1.8	1.4844804	Plasmodium_falciparum_TIGR|(protein	DTLMADFKKGISK	Phospho(S)@12
114	2.08	2.08	1.4285714	Plasmodium_falciparum_Sanger|(protein	KTIDANISR	Phospho(S)@8
115	1.59	1.61	1.3552069	Plasmodium_falciparum_Sanger|(protein	ELFTSLKR	Phospho(S)@5
116	2.36	2.36	1.3539651	Plasmodium_falciparum_Sanger|(protein	SSSIGLKLTK	Oxidation(K)@7; Phospho(T)@9; Oxidation(K)@10
117	2.46	2.46	1.3221154	Plasmodium_falciparum_TIGR|(protein	NKVSDKDDPK	Oxidation(K)@2; Oxidation(D)@7
118	2.24	2.26	1.270648	Plasmodium_falciparum_Sanger|(protein	YSNTSSSIGSFSK	Oxidation(Y)@1; Phospho(S)@2; Oxidation(F)@11
119	3.12	3.13	1.2571429	Plasmodium_falciparum_Sanger|(protein	SGTGNIFVKNLDK	Deamidated(N)@10
120	5.47	5.48	1.2320329	plasmodium_falciparum_Sanger|(protein	VAMKKPK	
121	1.71	1.77	1.1711125	Plasmodium_falciparum_TIGR|(protein	EEVGELSQK	Glu->pyro-Glu@N-term; Deamidated(Q)@8
122	1.58	1.6	1.1243386	Plasmodium_falciparum_Sanger|(protein	KGNSSKLR	Phospho(S)@5
123	1.86	3.68	1.1142061	Plasmodium_falciparum_TIGR|(protein	LSKRIESLR	Phospho(S)@2
124	2.84	2.93	1.1070111	Plasmodium_falciparum_Sanger|(protein	NGNMNKR	Deamidated(N)@3
125	3.74	3.74	1.0685664	Plasmodium_falciparum_Sanger|(protein	QAKKLNNILNPNR	Gln->pyro-Glu@N-term; Oxidation(K)@3
126	3.61	3.74	1.0025063	Plasmodium_falciparum_TIGR|(protein	GNNNINNNNK	Deamidated(N)@2; Deamidated(N)@3; Deamidated(N)@4; Deamidated(N)@7

Table 7: Summary of proteins identified by trypsin in-gel digestion (18hr contl) (1D RP-HPLC)

N	Unused	Total	% Cov	Accession #	Name	Species
1	13.91	13.91	70.5	Pfa3D7predicted|chr12|chr12.	coding) null Location= chr12 complement	**101r|Genefinder|Plasmodium_falciparum_Sange**
2	9.22	9.22	63.4	Pfa3D7predicted|chr10|chr10.	coding) 100% identity to 100% of P14643: Tubulin beta chain (Beta tubulin)	**102|FullPhat|Plasmodium_falciparum_TIGR|(protein**
3	28.74	28.74	87.7	Pfa3D7predicted|chr14|chr14.	coding) 99% identity to 100% of AAC47090.1: p82 Location= chr14 420442..422790	**103|FullPhat|Plasmodium_falciparum_TIGR|(protein**

4	3.93	3.93	54.7	Pfa3D7predicted|chr12|chr12	coding) null Location= chr12 complement(428489..432874)	**109|FullPhat|Plasmodium_falciparum_Sanger|(protein**
5	39.81	39.81	88.3	Pfa3D7predicted|chr7|chr7	coding) 73% identity to 86% of P24724: Heat shock protein 90 (HSP90)	**112|FullPhat|Plasmodium_falciparum_Sanger|(protein**
6	7.17	7.17	86.6	Pfa3D7predicted|chr3|chr3	coding) 100% identity to 100% of O00806: 60S acidic ribosomal protein P2 Location= chr3 404654..404992	**118|FullPhat|Plasmodium_falciparum_Sanger|(protein**
7	2.88	10.35	79.3	Pfa3D7predicted|chr14|chr14	coding) 100% identity to 100% of P14883: ACTIN II Location= chr14 join(507360..507807, 508186..508868)	**124|FullPhat|Plasmodium_falciparum_TIGR|(protein**
8	1.48	1.48	26	Pfa3D7predicted|chr6|chr6.	coding) 100% identity to 100% of P19259: Membrane protein PF12 precursor	**126|FullPhat|Plasmodium_falciparum_Sanger|(protein**
9	8.53	8.53	76.6	Pfa3D7predicted|chr12|chr12	coding) null Location= chr12	**132f|Genefinder|Plasmodium_falciparum_Sanger|(protein**
10	6.93	6.93	68.6	Pfa3D7predicted|chr14|chr14.	coding) 100% identity to 100% of 1A5C.B: Chain B, Fructose-1,6-Bisphosphate Aldolase	**1335|GlimmerM|Plasmodium_falciparum_TIGR|(protein**
11	1.42	1.42	30.9	Pfa3D7predicted|chr4|chr4.	coding) 40% identity to 54% of 2116446C: ORF Location= chr4 complement	**135r|Genefinder|Plasmodium_falciparum_Sanger|(protein**
12	31.81	31.81	70.3	Pfa3D7predicted|chr9|chr9.	coding) 46% identity to 60% of P04933: Merozoite surface protein 1 precursor (Merozoite surface antigens)	**155f|Genefinder|Plasmodium_falciparum_Sanger|(protein**
13	4.95	4.95	70.4	Pfa3D7predicted|chr11|chr11.	coding) 96% identity to 98% of Q94660: 60S acidic ribosomal protein P0	**157f|Genefinder|Plasmodium_falciparum_TIGR|(protein**
14	4.12	4.12	88	Pfa3D7predicted|chr10|chr10.	coding) 97% identity to 99% of Q03400: S-antigen protein precursor	**160f|Genefinder|Plasmodium_falciparum_TIGR|(protein**
15	2.17	2.19	37	Pfa3D7predicted|chr10|chr10	coding) 30% identity to 56% of T17451: fimbriae-associated protein Fap1 - Streptococcus parasanguinis	**166f|Genefinder|Plasmodium_falciparum_TIGR|(protein**
16	3.52	3.52	52	Pfa3D7predicted|chr6|chr6.	coding) 39% identity to 54% of 2116446C: ORF Location= chr6 complement(join	**169|FullPhat|Plasmodium_falciparum_Sanger|(protein**
17	61.49	61.49	93.9	Pfa3D7predicted|chr9|chr9	coding) 100% identity to 100% of AAA93010.1: PBGRP	**173|FullPhat|Plasmodium_falciparum_Sanger|(protein**
18	22.07	22.07	91.3	Pfa3D7predicted|chr10|chr10.	coding) 100% identity to 100% of Q8IJN7: Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)	**173|FullPhat|Plasmodium_falciparum_TIGR|(protein**
19	5.69	5.69	47.8	Pfa3D7predicted|chr12|chr12.	coding) null Location= chr12 join(1610351..1611416, 1611465..1612729)	**179f|Genefinder|Plasmodium_falciparum_Sanger|(protein**

20	1.68	1.68	24.8	Pfa3D7predicted|chr12|chr12.	coding) null Location= chr12 complement(join	**18r|Genefinder|Plasmodium_falciparum_Sanger|(protein**
21	6.31	6.31	93	Pfa3D7predicted|chr11|chr11.	coding) 100% identity to 100% of P38545: GTP-binding nuclear protein Ran (GTPase Ran) (Ras-like protein TC4)	**196|FullPhat|Plasmodium_falciparum_TIGR|(protein**
22	3.66	3.66	44.5	Pfa3D7predicted|chr12|chr12	coding) null Location= chr12 join(757642..763610, 763814..763917, 764421..764941, 764987..765172)	**201|FullPhat|Plasmodium_falciparum_Sanger|(protein**
23	28.82	28.82	77.2	Pfa3D7predicted|chr9|chr9.	coding) 100% identity to 100% of P27362: Phosphoglycerate kinase	**218|FullPhat|Plasmodium_falciparum_Sanger|(protein**
24	1.54	1.54	26.8	Pfa3D7predicted|chr4|chr4.	coding) 40% identity to 57% of AAQ74128.1: A4tres CIDR1 [synthetic construct	**219|FullPhat|Plasmodium_falciparum_Sanger|(protein**
25	4.02	4.02	49.5	Pfa3D7predicted|chr5|chr5.	coding) 100% identity to 100% of 1V8B.D: Chain D, Crystal Structure Of A Hydrolase	**227|FullPhat|Plasmodium_falciparum_Sanger|(protein**
26	1.9	1.9	22.3	Pfa3D7predicted|chr10|chr10	coding) 36% identity to 49% of 2116446C: ORF Location= chr10 join(28491..33893, 34843..36165)	**23|FullPhat|Plasmodium_falciparum_TIGR|(protein**
27	4.33	4.33	62.1	Pfa3D7predicted|chr6|chr6.	coding) 100% identity to 100% of Q02155: HEXOKINASE	**231|FullPhat|Plasmodium_falciparum_Sanger|(protein**
28	4.83	4.83	76.9	Pfa3D7predicted|chr12|chr12.	coding) null Location= chr12 complement(join(929026..929330, 929963..929982, 927816..928816))	**241|FullPhat|Plasmodium_falciparum_Sanger|(protein**
29	1.85	3.99	46.8	Pfa3D7predicted|chr11|chr11.	coding) 73% identity to 81% of P13830: Ring-infected erythrocyte surface antigen precursor	**242f|Genefinder|Plasmodium_falciparum_TIGR|(protein**
30	3.32	3.32	39.1	Pfa3D7predicted|chr12|chr12	coding) null Location= chr12 join(1045985..1046008, 1046269..1049395, 1049550..1049821)	**268|FullPhat|Plasmodium_falciparum_Sanger|(protein**
31	15.72	15.72	73.4	Pfa3D7predicted|chr13|chr13.	coding) 100% identity to 100% of 1T26.A: Chain A, Lactate Dehydrogenase Complexed With Nadh And 4-Hydroxy-1,2,5-Thiadiazole-3-Carboxylic Acid	**270|FullPhat|Plasmodium_falciparum_Sanger|(protein**
32	33.45	33.45	86.3	Pfa3D7predicted|chr5|chr5	coding) 99% identity to 99% of P08116: Processed variable antigen	**31|FullPhat|Plasmodium_falciparum_Sanger|(protein**
33	8.93	8.93	63.4	Pfa3D7predicted|chr12|chr12	coding) null Location= chr12 complement(join(79399..79402, 76846..78713))	**32|GlimmerM|Plasmodium_falciparum_Sanger|(protein**
34	7.5	7.5	67	pfa3D7predicted|chr11|chr11.	coding) 93% identity to 96% of EAA17669.1: 26s protease regulatory subunit 6a (tat-binding protein homolog 1) (tbp-1). [baker's yeast	**321|FullPhat|Plasmodium_falciparum_TIGR|(protein**

35	1.97	1.97	36.5	Pfa3D7predicted|chr13|chr13.	coding) 44% identity to 61% of 2116222A: variant surface protein	**345r|Genefinder|Plasmodium_falciparum_Sanger|(protein**
36	2.25	2.25	33.3	Pfa3D7predicted|chr12|chr12.	coding) null Location= chr12 join	**34f|Genefinder|Plasmodium_falciparum_Sanger|(protein**
37	4.66	4.66	57.9	Pfa3D7predicted|chr12|chr12	coding) null Location= chr12 join(1482951..1482995, 1484414..1484515, 1484675..1485898)	**360|FullPhat|Plasmodium_falciparum_Sanger|(protein**
38	1.38	1.38	59.6	Pfa3D7predicted|chr12|chr12.	coding) null Location= chr12	**361|FullPhat|Plasmodium_falciparum_Sanger|(protein**
39	2.02	2.02	36.9	Pfa3D7predicted|chr4|chr4.	coding) 27% identity to 49% of P13830: Ring-infected erythrocyte surface antigen precursor	**38|FullPhat|Plasmodium_falciparum_Sanger|(protein**
40	1.84	1.84	35.3	Pfa3D7predicted|chr12|chr12	coding) null Location= chr12 complement(join(590201..592517, 589888..589901))	**397|GlimmerM|Plasmodium_falciparum_Sanger|(protein**
41	1.59	1.59	16.1	Pfa3D7predicted|chr8|chr8.	coding) 32% identity to 46% of AAO52354.1: similar to Dictyostelium discoideum (Slime mold).	**41|FullPhat|Plasmodium_falciparum_Sanger|(protein**
42	12.97	12.97	48.7	Pfa3D7predicted|chr1|chr1.	coding) 93% identity to 94% of Q26005: Ring-infected erythrocyte surface antigen	**42|FullPhat|Plasmodium_falciparum_Sanger|(protein**
43	11.45	11.45	69.3	Pfa3D7predicted|chr9|chr9.	coding) 100% identity to 100% of P14642: TUBULIN ALPHA CHAIN	**42|FullPhat|Plasmodium_falciparum_Sanger|(protein**
44	1.96	1.96	86.6	Pfa3D7predicted|chr13|chr13.	coding) null Location= chr13 complement(1653242..1654162)	**424|FullPhat|Plasmodium_falciparum_Sanger|(protein**
45	2.01	2.01	42.7	Pfa3D7predicted|chr12|chr12.	coding) null Location= chr12 complement(join	**44r|Genefinder|Plasmodium_falciparum_Sanger|(protein**
46	9.92	22.49	95.2	Pfa3D7predicted|chr7|chr7.	coding) 82% identity to 91% of Q05746: HEAT SHOCK 70 KD PROTEIN (HSP70) (CYTOPLASMIC ANTIGEN) (74.6 KD PROTEIN)	**45|FullPhat|Plasmodium_falciparum_Sanger|(protein**
47	1.96	1.96	47	Pfa3D7predicted|chr12|chr12	coding) null Location= chr12 complement(1900238..1905055)	**456|FullPhat|Plasmodium_falciparum_Sanger|(protein**
48	25.35	25.35	94.9	Pfa3D7predicted|chr12|chr12	coding) null Location= chr12 1920770..1921900	**460|FullPhat|Plasmodium_falciparum_Sanger|(protein**
49	1.59	1.59	48.4	Pfa3D7predicted|chr12|chr12.	coding) null Location= chr12 complement(join	**47r|Genefinder|Plasmodium_falciparum_Sanger|(protein**
50	1.75	1.75	30.1	Pfa3D7predicted|chr9|chr9.	coding) 91% identity to 92% of P13825: Aspartic acid-rich protein precursor	**533|GlimmerM|Plasmodium_falciparum_Sanger|(protein**
51	1.65	1.65	59.1	Pfa3D7predicted|chr7|chr7.	coding) 22% identity to 48% of AAA29651.1: mature-parasite-infected erythrocyte surface antigen	**54|FullPhat|Plasmodium_falciparum_Sanger|(protein**
52	1.55	1.55	55	Pfa3D7predicted|chr13|chr13.	coding) 100% identity to 100% of Ligated Adenylosuccinate Synthetase	**546|FullPhat|Plasmodium_falciparum_Sanger|(protein**

53	51.19	51.19	93.2	Pfa3D7predicted|chr12|chr12	coding) null Location= chr12 complement	**598|GlimmerM|Plasmodium_falciparum_Sanger|(protein**
54	1.88	2.02	30.6	Pfa3D7predicted|chr9|chr9.	coding) 31% identity to 49% of 2116446C: ORF Location= chr9 join(20080..25533, 26527..27885)	**6|FullPhat|Plasmodium_falciparum_Sanger|(protein**
55	2.57	2.57	51.1	Pfa3D7predicted|chr13|chr13	coding) null Location= chr13 complement(2478805..2479629)	**618|FullPhat|Plasmodium_falciparum_Sanger|(protein**
56	4.48	4.48	66.5	Pfa3D7predicted|chr13|chr13	coding) null Location= chr13 complement(2486719..2488170)	**620|FullPhat|Plasmodium_falciparum_Sanger|(protein**
57	1.35	1.35	28.3	Pfa3D7predicted|chr12|chr12.	coding) null Location= chr12 complement	**633|GlimmerM|Plasmodium_falciparum_Sanger|(protein**
58	1.6	1.6	31.9	Pfa3D7predicted|chr12|chr12	coding) null Location= chr12 complement(1093533..1095761)	**733|GlimmerM|Plasmodium_falciparum_Sanger|(protein**
59	5.47	6.65	53.8	Pfa3D7predicted|chr14|chr14.	coding) 100% identity to 100% of P39898: Plasmepsin 1 precursor (Aspartic hemoglobinase I) (PFAPG)	**76|FullPhat|Plasmodium_falciparum_TIGR|(protein**
60	3.46	6.17	57.4	Pfa3D7predicted|chr14|chr14.	coding) 100% identity to 100% of P46925: Plasmepsin 2 precursor (Aspartic hemoglobinase II) (PFAPD)	**77|FullPhat|Plasmodium_falciparum_TIGR|(protein**
61	2.04	2.04	59.9	Pfa3D7predicted|chr14|chr14.	coding) 61% identity to 79% of P39898: Plasmepsin 1 precursor (Aspartic hemoglobinase I) (PFAPG)	**78|FullPhat|Plasmodium_falciparum_TIGR|(protein**
62	1.78	1.78	32	Pfa3D7predicted|chr12|chr12.	coding) null Location= chr12 join	**78f|Genefinder|Plasmodium_falciparum_Sanger|(protein**
63	7.12	7.12	64.4	Pfa3D7predicted|chr4|chr4.	coding) 100% identity to 100% of Q25691: Vacuolar ATP synthase subunit B (V-ATPase B subunit) (Vacuolar proton pump B subunit)	**80|FullPhat|Plasmodium_falciparum_Sanger|(protein**
64	19.4	19.4	82.4	Pfa3D7predicted|chr6|chr6.	coding) 100% identity to 100% of Q07805: Ornithine aminotransferase (Ornithine--oxo-acid aminotransferase)	**90|FullPhat|Plasmodium_falciparum_Sanger|(protein**
65	6.86	6.95	86.8	Pfa3D7predicted|chr13|chr13.	coding) 97% identity to 99% of EAA22057.1: 26s protease regulatory subunit s10b (p44) (conserved atpase domain protein 44)	**90|FullPhat|Plasmodium_falciparum_Sanger|(protein**
66	2.54	2.54	65.4	Pfa3D7predicted|chr8|chr8.	coding) 61% identity to 81% of ZP_00159396.2: COG0542: ATPases with chaperone activity, ATP-binding subunit	Anabaena variabilis ATCC 29413
67	7.45	7.45	41.7	Pfa3D7predicted|chr14|chr14.	coding) 33% identity to 55% of XP_396228.1: similar to dynein, axonemal, heavy chain 8; dynein, axon, heavy chain 8 [Apis mellifera]	Apis mellifera

68	5.84	5.84	55.4	Pfa3D7predicted|chr5|chr5.	coding) 38% identity to 58% of NP_178539.2: cation efflux family protein	Arabidopsis thaliana
69	9.51	9.51	82.2	Pfa3D7predicted|chr13|chr13	coding) 41% identity to 62% of AAP83582.1: phosphoethanolamine N-methyltransferase [Brassica napus]	Brassica napus
70	2.09	2.09	55.8	Pfa3D7predicted|chr1|chr1.	coding) 27% identity to 54% of CAE74824.1: Hypothetical protein CBG22662	Caenorhabditis briggsae
71	4.51	4.51	33.4	Pfa3D7predicted|pfal_chr2	coding) 100% identity to 100% of AAA29714.1: parasitophorous vacuole antigen	chr2|pfal_chr2.genefinder_74r|Genefinder|Plasmodium_ falciparum_TIGR|(protein
72	2.71	2.71	45.3	Pfa3D7predicted|pfal_chr2|	coding) 100% identity to 100% of P50498: Merozoite surface antigen 2 precursor (MSA-2) (45 kDa merozoite surface antigen)	chr2|pfal_chr2.genefinder_77r|Genefinder|Plasmodium_ falciparum_TIGR|(protein
73	12.06	12.06	58.5	Pfa3D7predicted|chr5|chr5.	coding) 32% identity to 53% of EAL38034.1: karyopherin beta	Cryptosporidium hominis
74	2.01	2.01	53	Pfa3D7predicted|chr5|chr5.	coding) 57% identity to 68% of EAL37070.1: protein kinase	Cryptosporidium hominis
75	13.83	13.83	63.3	Pfa3D7predicted|chr13|chr13.	coding) 28% identity to 52% of CAD98262.1: hypothetical predicted Armadillo/beta-catenin-like repeat protein, unknown function	Cryptosporidium parvum
76	23.44	23.44	67.6	Pfa3D7predicted|chr6|chr6.	coding) 68% identity to 83% of AAB40928.2: cell division cycle protein 48	Dictyostelium discoideum
77	9.15	9.15	96.2	Pfa3D7predicted|pfal_chr2	coding) 28% identity to 34% of NP_727774.2: CG32602-PA [Drosophila melanogaster]	Drosophila melanogaster
78	4.82	4.82	43.2	Pfa3D7predicted|chr14|chr14	coding) 41% identity to 60% of AAN71353.1: RE29621p	Drosophila melanogaster
79	23.07	23.07	84.7	Pfa3D7predicted|chr14|chr14.	coding) 65% identity to 79% of EAL32818.1: GA15316-PA	Drosophila pseudoobscura
80	2.53	2.53	19.1	Pfa3D7predicted|chr10|chr10.	coding) 29% identity to 51% of XP_419006.1: PREDICTED: similar to axonemal dynein heavy chain 5, partial	Gallus gallus
81	1.5	1.5	67.4	Pfa3D7predicted|chr10|chr10.	coding) 31% identity to 51% of XP_487575.1: similar to hypothetical protein	Mus musculus
82	3.42	3.42	83.6	Pfa3D7predicted|chr13|chr13.	coding) 93% identity to 95% of BAA88568.1: ubiquitin	Oncorhynchus mykiss

83	31.42	31.42	91.4	Pfa3D7predicted|chr6|chr6.	coding) 91% identity to 97% of CAH97765.1: pyruvate kinase, putative	**Plasmodium berghei**
84	27.98	27.98	87.8	Pfa3D7predicted|chr14|chr14.	coding) 84% identity to 95% of CAH99235.1: glyceraldehyde-3-phosphate dehydrogenase, putative	**Plasmodium berghei**
85	18.15	18.15	97.6	Pfa3D7predicted|chr10|chr10	coding) 95% identity to 97% of CAH96568.1: hsp60, putative	**Plasmodium berghei**
86	17.46	17.46	92	Pfa3D7predicted|chr9|chr9.	coding) 91% identity to 97% of CAH99282.1: s-adenosylmethionine synthetase, putative	**Plasmodium berghei**
87	16.54	16.54	90.7	Pfa3D7predicted|chr11|chr11.	coding) 78% identity to 89% of CAI01680.1: hypothetical protein PB300335.00.0	**Plasmodium berghei**
88	15.91	15.91	83.1	Pfa3D7predicted|chr13|chr13.	coding) 80% identity to 88% of CAH93761.1: phosphoribosylpyrophosphate synthetase, putative	**Plasmodium berghei**
89	14.82	14.82	79.2	Pfa3D7predicted|chr5|chr5.	coding) 33% identity to 50% of CAI03992.1: rhoptry-associated protein, putative	**Plasmodium berghei**
90	12.78	12.78	67.6	Pfa3D7predicted|chr13|chr13	coding) 96% identity to 98% of CAH98192.1: vacuolar ATP synthase catalytic subunit a, putative	**Plasmodium berghei**
91	7.66	7.66	81.6	Pfa3D7predicted|chr9|chr9.	coding) 80% identity to 92% of CAH95224.1: conserved hypothetical protein	**Plasmodium berghei**
92	6.89	6.89	77.8	Pfa3D7predicted|chr11|chr11.	coding) 94% identity to 99% of CAI00576.1: t-complex protein 1, alpha subunit, putative	**Plasmodium berghei**
93	6.45	6.45	81.1	Pfa3D7predicted|chr14|chr14.	coding) 97% identity to 99% of CAI05484.1: eukaryotic translation initiation factor 2 gamma subunit, putative	**Plasmodium berghei**
94	6.18	6.18	64.4	Pfa3D7predicted|chr7|chr7.	coding) 92% identity to 96% of CAH94563.1: conserved GTP-binding protein, putative	**Plasmodium berghei**
95	5.23	5.23	52.9	Pfa3D7predicted|chr14|chr14.	coding) 69% identity to 85% of CAI05016.1: leucine aminopeptidase, putative	**Plasmodium berghei**
96	4.97	4.97	80.8	Pfa3D7predicted|chr6|chr6.	coding) 81% identity to 89% of CAH99760.1: conserved hypothetical protein	**Plasmodium berghei**
97	4.93	4.93	71.8	Pfa3D7predicted|chr8|chr8.	coding) 84% identity to 90% of CAH94808.1: conserved hypothetical protein	**Plasmodium berghei**
98	4.16	4.16	54	Pfa3D7predicted|chr3|chr3.	coding) 94% identity to 98% of CAI04191.1: T-complex protein 1 epsilon subunit, putative	**Plasmodium berghei**

99	3.85	3.85	51.8	Pfa3D7predicted|chr9|chr9.	coding) 81% identity to 90% of CAH98134.1: RNA-binding protein, putative	**Plasmodium berghei**
100	3.55	3.55	75.6	Pfa3D7predicted|chr14|chr14	coding) 96% identity to 98% of CAH98785.1: ribosomal protein S2, putative	**Plasmodium berghei**
101	3.51	3.51	40.5	Pfa3D7predicted|chr13|chr13	coding) 46% identity to 64% of CAH96693.1: hypothetical protein PB103910.00.0	**Plasmodium berghei**
102	3.51	3.51	55.4	Pfa3D7predicted|chr13|chr13.	coding) 89% identity to 96% of CAH96222.1: conserved hypothetical protein	**Plasmodium berghei**
103	3.16	3.16	31.6	Pfa3D7predicted|chr6|chr6.	coding) 48% identity to 63% of CAI04669.1: hypothetical protein PB105705.00.0	**Plasmodium berghei**
104	3.16	3.16	49.6	Pfa3D7predicted|chr11|chr11.	coding) 74% identity to 85% of CAH99527.1: protein disulfide isomerase related protein, putative	**Plasmodium berghei**
105	3.05	3.05	38.5	Pfa3D7predicted|chr11|chr11.	coding) 26% identity to 55% of CAH94962.1: conserved hypothetical protein	**Plasmodium berghei**
106	2.57	2.57	63.1	Pfa3D7predicted|chr5|chr5.	coding) 87% identity to 94% of CAH94712.1: actin depolymerizing factor, putative [Plasmodium berghei]	**Plasmodium berghei**
107	2.56	2.56	43.4	Pfa3D7predicted|chr11|chr11.	coding) 84% identity to 92% of CAH94531.1: translation elongation factor EF-1, subunit alpha, putative	**Plasmodium berghei**
108	2.45	2.45	78.5	Pfa3D7predicted|chr14|chr14.	coding) 34% identity to 52% of CAH93814.1: hypothetical protein PB100384.00.0	**Plasmodium berghei**
109	2.35	2.35	54.9	Pfa3D7predicted|chr6|chr6	coding) 76% identity to 88% of CAH94470.1: malate:quinone oxidoreductase, putative	**Plasmodium berghei**
110	2.27	2.27	60.6	Pfa3D7predicted|chr14|chr14.	coding) 78% identity to 92% of CAI00286.1: conserved hypothetical protein	**Plasmodium berghei**
111	2.21	2.21	34.9	Pfa3D7predicted|chr11|chr11	coding) 87% identity to 95% of CAH99201.1: spermidine synthase, putative	**Plasmodium berghei**
112	2.13	2.13	58.3	Pfa3D7predicted|chr11|chr11.	coding) 81% identity to 89% of CAH97383.1: conserved hypothetical protein	**Plasmodium berghei**
113	2.12	2.12	90.7	Pfa3D7predicted|chr13|chr13.	coding) 87% identity to 96% of CAH99325.1: 40S ribosomal protein S7 homologue, putative	**Plasmodium berghei**
114	2.07	2.07	56.2	Pfa3D7predicted|chr14|chr14.	coding) 98% identity to 100% of CAI00161.1: ribosomal protein L10, putative	**Plasmodium berghei**

115	2.04	2.04	40.6	Pfa3D7predicted|chr13|chr13.	coding) 75% identity to 87% of CAH98010.1: proteasome regulatory component, putative	**Plasmodium berghei**
116	2.02	2.02	40.1	Pfa3D7predicted|chr4|chr4.	coding) 88% identity to 92% of CAH97914.1: conserved hypothetical protein	**Plasmodium berghei**
117	1.67	1.67	60.1	Pfa3D7predicted|chr13|chr13	coding) 29% identity to 48% of CAH99838.1: conserved hypothetical protein	**Plasmodium berghei**
118	1.63	1.63	29.6	Pfa3D7predicted|chr3|chr3	coding) 33% identity to 52% of CAH99945.1: conserved hypothetical protein	**Plasmodium berghei**
119	1.59	1.59	21.6	Pfa3D7predicted|chr8|chr8.	coding) 33% identity to 51% of CAH96228.1: hypothetical protein PB000644.01.0	**Plasmodium berghei**
120	1.57	1.59	41.4	Pfa3D7predicted|chr14|chr14.	coding) 75% identity to 84% of CAH99091.1: conserved hypothetical protein	**Plasmodium berghei**
121	1.57	1.57	54	Pfa3D7predicted|chr11|chr11.	coding) 76% identity to 89% of CAI05080.1: conserved hypothetical protein	**Plasmodium berghei**
122	1.51	1.61	19.8	Pfa3D7predicted|chr14|chr14.	coding) 37% identity to 52% of CAH97021.1: conserved hypothetical protein	**Plasmodium berghei**
123	1.45	1.47	18.3	Pfa3D7predicted|chr13|chr13.	coding) 29% identity to 47% of CAH99222.1: conserved hypothetical protein	**Plasmodium berghei**
124	1.39	1.39	30	Pfa3D7predicted|chr11|chr11.	coding) 37% identity to 52% of CAH95643.1: conserved hypothetical protein	**Plasmodium berghei**
125	1.35	1.35	19.2	Pfa3D7predicted|chr14|chr14.	coding) 54% identity to 67% of CAH93595.1: conserved hypothetical protein	**Plasmodium berghei**
126	7.84	7.84	55.9	Pfa3D7predicted|chr9|chr9.	coding) 80% identity to 89% of CAH84421.1: hypothetical protein PC301031.00.0	**Plasmodium chabaudi**
127	6.3	6.3	64.1	Pfa3D7predicted|chr13|chr13.	coding) 71% identity to 82% of CAH77822.1: elongation factor 1-gamma, putative	**Plasmodium chabaudi**
128	5.61	5.61	53.3	Pfa3D7predicted|chr5|chr5.	coding) 34% identity to 57% of CAH74690.1: rhoptry-associated protein, putative	**Plasmodium chabaudi**
129	4.3	4.3	45.5	Pfa3D7predicted|chr7|chr7.	coding) 70% identity to 84% of CAH84832.1: Cg4 protein, putative	**Plasmodium chabaudi**
130	3.95	3.95	49	Pfa3D7predicted|chr10|chr10	coding) 70% identity to 84% of CAH87109.1: methionine--tRNA ligase, putative	**Plasmodium chabaudi**
131	3.9	3.9	62.6	Pfa3D7predicted|pfal_chr2|	coding) 83% identity to 91% of CAH76801.1: proteasome 26S regulatory subunit, putative	**Plasmodium chabaudi**
132	3.53	3.53	53.4	Pfa3D7predicted|chr11|chr11.	coding) 65% identity to 75% of CAH75082.1: ethanolamine kinase, putative	**Plasmodium chabaudi**

133	3.22	3.22	75.7	Pfa3D7predicted|chr10|chr10	coding) 94% identity to 100% of CAH74575.1: conserved hypothetical protein	**Plasmodium chabaudi**
134	2.88	2.9	31.9	Pfa3D7predicted|chr13|chr13.	coding) 28% identity to 46% of CAH77112.1: conserved hypothetical protein	**Plasmodium chabaudi**
135	2.76	2.76	41.5	Pfa3D7predicted|chr3|chr3.	coding) 58% identity to 72% of CAH74986.1: hypothetical protein PC000452.00.0	**Plasmodium chabaudi**
136	2.68	2.68	55.4	Pfa3D7predicted|chr8|chr8.	coding) 92% identity to 97% of CAH77317.1: guanine nucleotide-binding protein, putative	**Plasmodium chabaudi**
137	2.31	2.31	50.2	Pfa3D7predicted|pfal_chr2	coding) 33% identity to 59% of CAH75228.1: conserved hypothetical protein	**Plasmodium chabaudi**
138	2.25	2.25	29	Pfa3D7predicted|chr5|chr5.	coding) 48% identity to 66% of CAH82363.1: hypothetical protein PC000350.05.0	**Plasmodium chabaudi**
139	2.11	2.13	27.7	Pfa3D7predicted|chr5|chr5.	coding) 46% identity to 62% of CAH79456.1: conserved hypothetical protein	**Plasmodium chabaudi**
140	2.09	2.09	39.3	Pfa3D7predicted|chr3|chr3.	coding) 62% identity to 80% of CAH81834.1: dihydrolipoamide acyltransferase, putative	**Plasmodium chabaudi**
141	2.03	2.03	21.8	Pfa3D7predicted|chr13|chr13	coding) 25% identity to 42% of CAH80283.1: conserved hypothetical protein	**Plasmodium chabaudi**
142	2.01	2.01	81.3	Pfa3D7predicted|chr11|chr11	coding) 93% identity to 98% of CAH81099.1: ribosomal protein S4, putative	**Plasmodium chabaudi**
143	2.01	2.01	66.7	pfa3D7predicted|chr10|chr10	coding) 98% identity to 99% of CAH82248.1: hypothetical protein PC000267.05.0	**Plasmodium chabaudi**
144	1.99	4.01	52	pfa3D7predicted|chr7|chr7.	coding) 73% identity to 83% of CAH74321.1: cell division cycle ATPase, putative	**Plasmodium chabaudi**
145	1.81	1.83	30.1	pfa3D7predicted|chr7|chr7.	coding) 48% identity to 62% of CAH77899.1: conserved hypothetical protein	**Plasmodium chabaudi**
146	1.55	1.55	32.4	pfa3D7predicted|chr1|chr1.	coding) 47% identity to 54% of CAH82299.1: conserved hypothetical protein	**Plasmodium chabaudi**
147	1.41	1.41	41.2	pfa3D7predicted|chr11|chr11.	coding) 73% identity to 82% of CAH81206.1: conserved hypothetical protein	**Plasmodium chabaudi**
148	1.39	1.39	30.9	pfa3D7predicted|chr14|chr14.	coding) 48% identity to 63% of CAH78879.1: conserved hypothetical protein	**Plasmodium chabaudi**
149	1.36	1.36	45.5	pfa3D7predicted|chr11|chr11	coding) 71% identity to 82% of CAH89188.1: heat shock protein 90, putative	**Plasmodium chabaudi**
150	17.32	17.32	84.5	pfa3D7predicted|chr8|chr8	coding) 84% identity to 92% of AAV36000.1: protein disulfide isomerase	**Plasmodium chabaudi chabaudi**

151	13.94	13.94	73.1	pfa3D7predicted|chr14|chr14.	coding) 99% identity to 100% of CAB51741.1: RNA helicase-1	**Plasmodium cynomolgi**
152	16.41	16.41	90.7	pfa3D7predicted|chr8|chr8.	coding) 100% identity to 100% of AAC17515.1: 14-3-3 protein	**Plasmodium knowlesi**
153	7.08	7.08	57.5	pfa3D7predicted|chr14|chr14.	coding) 76% identity to 89% of AAC15794.1: plasmepsin	**Plasmodium malariae**
154	3.5	3.5	34.4	pfa3D7predicted|chr4|chr4.	coding) 23% identity to 45% of AAO38039.1: reticulocyte binding-like protein 2b	**Plasmodium reichenowi**
155	2.12	2.12	29.4	pfa3D7predicted|chr4|chr4.	coding) 29% identity to 53% of CAB96701.1: Pvstp1	**Plasmodium vivax**
156	18.51	18.51	83.9	pfa3D7predicted|chr9|chr9.	coding) 42% identity to 65% of BAC43744.1: PyRhopH2	**Plasmodium yoelii**
157	2.73	2.73	65.3	pfa3D7predicted|chr9|chr9.	coding) 44% identity to 65% of BAB19269.1: high molecular weight rhoptry protein 3	**Plasmodium yoelii**
158	35.78	35.78	98.9	pfa3D7predicted|chr13|chr13.	coding) 100% identity to 100% of EAA15302.1: translation elongation factor EF-1,	**Plasmodium yoelii yoelii**
159	16.89	16.89	86.3	pfa3D7predicted|chr11|chr11	coding) 67% identity to 83% of EAA17014.1: membrane-associated calcum-binding protein	**Plasmodium yoelii yoelii**
160	12.04	12.04	79.6	pfa3D7predicted|chr14|chr14	coding) 84% identity to 93% of EAA22670.1: stress-induced protein sti1-like protein	**Plasmodium yoelii yoelii**
161	10.92	10.92	85.3	pfa3D7predicted|chr3|chr3.	coding) 91% identity to 98% of EAA19132.1: putative T-complex protein beta subunit	**Plasmodium yoelii yoelii**
162	8.79	8.79	73.5	pfa3D7predicted|pfal_chr2	coding) 90% identity to 96% of EAA22741.1: DEAD/DEAH box helicase, putative	**Plasmodium yoelii yoelii**
163	8.49	8.49	45.9	pfa3D7predicted|chr14|chr14.	coding) 33% identity to 53% of EAA21738.1: hypothetical protein	**Plasmodium yoelii yoelii**
164	8.25	8.25	64.5	pfa3D7predicted|chr6|chr6.	coding) 86% identity to 94% of EAA21693.1: putative chaperonin	**Plasmodium yoelii yoelii**
165	8.08	8.08	59.7	pfa3D7predicted|chr8|chr8.	coding) 65% identity to 82% of EAA16104.1: hypothetical protein	**Plasmodium yoelii yoelii**
166	7.45	7.45	88.8	pfa3D7predicted|chr4|chr4.	coding) 97% identity to 100% of EAA16768.1: 26S proteasome ATPase	**Plasmodium yoelii yoelii**
167	7.4	7.4	75.8	pfa3D7predicted|chr9|chr9.	coding) 83% identity to 92% of EAA15347.1: inosine-5'-monophosphate dehydrogenase	**Plasmodium yoelii yoelii**

168	6.29	6.29	65.9	pfa3D7predicted|chr10|chr10.	coding) 51% identity to 67% of EAA15245.1: KH domain, putative	**Plasmodium yoelii yoelii**
169	5.95	5.95	60.1	pfa3D7predicted|chr3|chr3.	coding) 92% identity to 97% of EAA21335.1: chaperonin, 60 kDa	**Plasmodium yoelii yoelii**
170	5.6	5.71	89.3	pfa3D7predicted|chr10|chr10.	coding) 96% identity to 98% of EAA18347.1: 26S proteasome subunit 4-like protein [Plasmodium yoelii yoelii]	**Plasmodium yoelii yoelii**
171	4.78	4.78	68.3	pfa3D7predicted|chr13|chr13.	coding) 80% identity to 89% of EAA20629.1: lysyl-tRNA synthetase	**Plasmodium yoelii yoelii**
172	4.62	4.62	51.1	pfa3D7predicted|chr14|chr14.	coding) 83% identity to 94% of EAA18974.1: 6-phosphogluconate dehydrogenase, decarboxylating	**Plasmodium yoelii yoelii**
173	4.52	4.52	73.5	pfa3D7predicted|chr13|chr13.	coding) 94% identity to 98% of EAA22457.1: chaperonin containing TCP-1 delta subunit	**Plasmodium yoelii yoelii**
174	4.24	4.24	64.2	pfa3D7predicted|chr10|chr10.	coding) 25% identity to 40% of EAA19983.1: Drosophila melanogaster CG12781 gene product	**Plasmodium yoelii yoelii**
175	4.21	4.21	41.1	pfa3D7predicted|chr3|chr3.	coding) 90% identity to 94% of EAA20950.1: Plasmodium vivax PV1H14065_P-related	**Plasmodium yoelii yoelii**
176	4.15	4.15	34.6	pfa3D7predicted|chr14|chr14.	coding) 92% identity to 97% of EAA16260.1: ATP synthase subunit	**Plasmodium yoelii yoelii**
177	4.14	4.14	76.8	pfa3D7predicted|chr6|chr6.	coding) 72% identity to 86% of EAA15273.1: DnaJ homolog, putative	**Plasmodium yoelii yoelii**
178	4.02	4.02	76.1	pfa3D7predicted|chr6|chr6.	coding) 77% identity to 90% of EAA20799.1: Egd2p, putative	**Plasmodium yoelii yoelii**
179	3.93	3.93	57.8	pfa3D7predicted|chr14|chr14.	coding) 92% identity to 97% of EAA21924.1: DnaJ homolog	**Plasmodium yoelii yoelii**
180	3.84	3.84	43.5	pfa3D7predicted|chr8|chr8	coding) 96% identity to 99% of EAA21162.1: putative impotin alpha 1b	**Plasmodium yoelii yoelii**
181	3.76	3.76	57.4	pfa3D7predicted|chr10|chr10	coding) 93% identity to 96% of EAA18207.1: ribosomal protein S2, putative	**Plasmodium yoelii yoelii**
182	3.74	3.74	43	pfa3D7predicted|chr6|chr6.	coding) 81% identity to 90% of EAA17228.1: probable mitochondrial import receptor subunit tom40 homolog	**Plasmodium yoelii yoelii**
183	3.32	3.32	49.7	pfa3D7predicted|chr10|chr10.	coding) 80% identity to 91% of EAA22115.1: hypothetical protein	**Plasmodium yoelii yoelii**

184	3.28	3.28	60.6	pfa3D7predicted|chr14|chr14.	coding) 67% identity to 82% of EAA17993.1: Exp-2	**Plasmodium yoelii yoelii**
185	3.25	3.25	25.5	pfa3D7predicted|chr3|chr3.	coding) 30% identity to 50% of EAA17831.1: hypothetical protein	**Plasmodium yoelii yoelii**
186	3.02	3.02	56.9	pfa3D7predicted|chr14|chr14	coding) 73% identity to 89% of EAA19135.1: similar to RIKEN cDNA	**Plasmodium yoelii yoelii**
187	3	3	61.4	pfa3D7predicted|pfal_chr2|	coding) 75% identity to 88% of EAA15720.1: T-complex protein 1	**Plasmodium yoelii yoelii**
188	2.98	2.98	63.8	pfa3D7predicted|chr6|chr6.	coding) 87% identity to 97% of EAA16340.1: ethylene-inducible protein hever	**Plasmodium yoelii yoelii**
189	2.92	2.92	40.4	pfa3D7predicted|chr5|chr5.	coding) 79% identity to 89% of EAA15582.1: 58 kda phosphoprotein (heat shock-related protein) (hrp).	**Plasmodium yoelii yoelii**
190	2.77	2.77	38.4	pfa3D7predicted|chr10|chr10.	coding) 64% identity to 81% of EAA21498.1: adenosine deaminase	**Plasmodium yoelii yoelii**
191	2.63	2.63	25.8	pfa3D7predicted|chr5|chr5.	coding) 49% identity to 67% of EAA22286.1: hypothetical protein	**Plasmodium yoelii yoelii**
192	2.44	2.44	31.5	pfa3D7predicted|chr13|chr13	coding) 32% identity to 51% of EAA18561.1: hypothetical protein	**Plasmodium yoelii yoelii**
193	2.43	2.43	33.6	pfa3D7predicted|chr5|chr5.	coding) 53% identity to 70% of EAA23004.1: unconventional myosin PfM-B-related	**Plasmodium yoelii yoelii**
194	2.4	2.4	45.4	pfa3D7predicted|chr14|chr14.	coding) 37% identity to 53% of EAA16617.1: hypothetical protein	**Plasmodium yoelii yoelii**
195	2.4	2.4	54.3	pfa3D7predicted|chr13|chr13	coding) 62% identity to 79% of EAA17424.1: putative HSP protein	**Plasmodium yoelii yoelii**
196	2.36	2.36	19.6	pfa3D7predicted|chr10|chr10.	coding) 36% identity to 55% of EAA17865.1: hypothetical protein	**Plasmodium yoelii yoelii**
197	2.32	2.32	43.4	pfa3D7predicted|chr11|chr11	coding) 26% identity to 46% of EAA19159.1: hypothetical protein	**Plasmodium yoelii yoelii**
198	2.3	2.3	25.3	pfa3D7predicted|chr11|chr11.	coding) 33% identity to 52% of EAA19052.1: hypothetical protein	**Plasmodium yoelii yoelii**
199	2.29	2.29	31	pfa3D7predicted|chr14|chr14.	coding) 26% identity to 47% of EAA17782.1: PR7 protein, putative	**Plasmodium yoelii yoelii**
200	2.25	2.25	18.8	pfa3D7predicted|chr14|chr14.	coding) 48% identity to 63% of EAA15464.1: histidyl-tRNA synthetase, putative	**Plasmodium yoelii yoelii**
201	2.23	2.23	36.9	pfa3D7predicted|chr10|chr10.	coding) 31% identity to 47% of EAA18343.1: chloroquine resistance marker protein, putative	**Plasmodium yoelii yoelii**

202	2.21	2.21	26.1	pfa3D7predicted|chr14|chr14	coding) 26% identity to 43% of EAA17484.1: hypothetical protein	**Plasmodium yoelii yoelii**
203	2.16	2.16	27.9	pfa3D7predicted|chr5|chr5.	coding) 27% identity to 44% of EAA18442.1: hypothetical protein	**Plasmodium yoelii yoelii**
204	2.15	2.15	31.6	pfa3D7predicted|chr14|chr14.	coding) 23% identity to 41% of EAA17472.1: unknown protein-related	**Plasmodium yoelii yoelii**
205	2.11	2.11	33	pfa3D7predicted|chr10|chr10	coding) 53% identity to 71% of EAA22689.1: hypothetical protein	**Plasmodium yoelii yoelii**
206	2.1	2.12	34.6	pfa3D7predicted|chr14|chr14	coding) 57% identity to 75% of EAA18971.1: Arabidopsis thaliana At3g05350/T12H1_32	**Plasmodium yoelii yoelii**
207	2.05	2.05	42.5	pfa3D7predicted|chr13|chr13.	coding) 29% identity to 48% of EAA21778.1: chloroquine resistance marker protein	**Plasmodium yoelii yoelii**
208	2.03	2.03	34	pfa3D7predicted|chr5|chr5.	coding) 22% identity to 41% of EAA16943.1: 250-270 copies of a 13 AA repeat, NSSTPITSSSIL	**Plasmodium yoelii yoelii**
209	2.02	2.02	29.7	pfa3D7predicted|chr7|chr7	coding) 28% identity to 49% of EAA16587.1: R27-2 protein [Plasmodium yoelii yoelii]	**Plasmodium yoelii yoelii**
210	1.88	1.88	43.5	pfa3D7predicted|chr14|chr14.	coding) 36% identity to 52% of EAA16501.1: hypothetical protein	**Plasmodium yoelii yoelii**
211	1.85	1.87	25	pfa3D7predicted|chr3|chr3.	coding) 26% identity to 45% of EAA18284.1: hypothetical protein	**Plasmodium yoelii yoelii**
212	1.8	1.8	26.9	pfa3D7predicted|chr3|chr3	coding) 34% identity to 52% of EAA21337.1: hypothetical protein	**Plasmodium yoelii yoelii**
213	1.66	1.66	48.5	pfa3D7predicted|chr11|chr11.	coding) 75% identity to 84% of EAA15858.1: ubiquitin-like protein dsk2	**Plasmodium yoelii yoelii**
214	1.65	1.65	36.5	pfa3D7predicted|chr7|chr7.	coding) 27% identity to 45% of EAA21352.1: hypothetical protein	**Plasmodium yoelii yoelii**
215	1.55	1.55	48.9	pfa3D7predicted|chr9|chr9.	coding) 80% identity to 87% of EAA18321.1: translation elongation factor 1 beta-related	**Plasmodium yoelii yoelii**
216	1.46	1.46	53.2	pfa3D7predicted|pfal_chr2	coding) 89% identity to 94% of EAA18103.1: ATP synthase F1, alpha subunit	**Plasmodium yoelii yoelii**
217	1.45	1.47	30.4	pfa3D7predicted|chr14|chr14.	coding) 34% identity to 51% of EAA15702.1: hypothetical protein	**Plasmodium yoelii yoelii**
218	1.45	1.45	14.7	pfa3D7predicted|chr14|chr14.	coding) 42% identity to 60% of EAA16069.1: hypothetical protein	**Plasmodium yoelii yoelii**

219	1.44	1.44	43.8	pfa3D7predicted|chr13|chr13	coding) 77% identity to 88% of EAA19931.1: AMP deaminase homolog	**Plasmodium yoelii yoelii**
220	1.41	1.41	29.8	pfa3D7predicted|chr10|chr10.	coding) 76% identity to 91% of EAA16668.1: 26S proteasome subunit P40.5, putative	**Plasmodium yoelii yoelii**
221	1.34	1.34	20.8	pfa3D7predicted|chr14|chr14.	coding) 32% identity to 49% of EAA19220.1: hypothetical protein	**Plasmodium yoelii yoelii**
222	1.32	1.32	45.7	pfa3D7predicted|chr13|chr13.	coding) 96% identity to 98% of EAA22608.1: Mov34/MPN/PAD-1 family, putative	**Plasmodium yoelii yoelii**
223	1.46	1.46	18.8	pfa3D7predicted|chr7|chr7.	coding) 29% identity to 51% of BAA97048.1: cytoplasmic dynein heavy chain	Rattus norvegicus
224	29.74	29.87	97.9	pfa3D7predicted|chr11|chr11	coding) 73% identity to 85% of AAQ63186.1: heat shock protein 70	Theileria annulata
225	36.29	38.65	96.2	pfa3D7predicted|chr8|chr8.	coding) 81% identity to 90% of AAC72001.1: heat shock protein 70	Toxoplasma gondii
226	2	2	30.3	pfa3D7predicted|chr5|chr5.	coding) 37% identity to 52% of NP_800965.1: hypothetical protein VPA1455	Vibrio parahaemolyticus RIMD 2210633

Table 8: Summary of proteins identified by trypsin in-gel digestion (18hr drug treated) (1D RP-HPLC)

N	**Unused**	**Total**	**% Cov**	**Accession #**	**Name**	**Species**
1	5.7	5.7	81.6	pfa3D7predicted|chr12|chr12	coding) null Location= chr12 complement	**101r|Genefinder|Plasmodium_falciparum_Sanger|(protein**
2	3.41	3.41	69.7	pfa3D7predicted|chr10|chr10.	coding) 100% identity to 100% of P14643: Tubulin beta chain (Beta tubulin)	**102|FullPhat|Plasmodium_falciparum_TIGR|(protein**
3	15.61	15.61	93.9	pfa3D7predicted|chr14|chr14	coding) 99% identity to 100% of AAC47090.1: p82	**103|FullPhat|Plasmodium_falciparum_TIGR|(protein**
4	21.32	21.34	94.2	pfa3D7predicted|chr7|chr7	coding) 73% identity to 86% of P24724: Heat shock protein 90 (HSP90)	**112|FullPhat|Plasmodium_falciparum_Sanger|(protein**
5	6	6	86.6	pfa3D7predicted|chr3|chr3	coding) 100% identity to 100% of O00806: 60S acidic ribosomal protein P2	**118|FullPhat|Plasmodium_falciparum_Sanger|(protein**
6	1.5	1.5	61.1	pfa3D7predicted|chr11|chr11	coding) 26% identity to 52% of Q9MBF8: Dynein 1-beta heavy chain, flagellar inner arm I1 complex (1-beta DHC) (Dynein 1,	**118f|Genefinder|Plasmodium_falciparum_TIGR|(protein**
7	14.8	14.8	80.9	pfa3D7predicted|chr9|chr9.	coding) 46% identity to 60% of P04933: Merozoite surface protein 1 precursor (Merozoite surface antigens)	**155f|Genefinder|Plasmodium_falciparum_Sanger|(protein**
8	2.78	2.78	87.6	pfa3D7predicted|chr11|chr11	coding) 96% identity to 98% of Q94660: 60S acidic ribosomal protein P0	**157f|Genefinder|Plasmodium_falciparum_TIGR|(protein**
9	40.16	40.16	99.4	pfa3D7predicted|chr9|chr9	coding) 100% identity to 100% of AAA93010.1: PBGRP	**173|FullPhat|Plasmodium_falciparum_Sanger|(protein**
10	4.1	4.1	93	pfa3D7predicted|chr10|chr10	coding) 100% identity to 100% of Q8IJN7: Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)	**173|FullPhat|Plasmodium_falciparum_TIGR|(protein**

11	2.37	10.71	95.2	pfa3D7predicted|chr7|chr7	coding) 81% identity to 91% of Q05746: HEAT SHOCK 70 KD PROTEIN (HSP70) (CYTOPLASMIC ANTIGEN) (74.6 KD PROTEIN)	**17f|Genefinder|Plasmodium_falciparum_Sanger|(protein**
12	2.14	2.14	57.6	pfa3D7predicted|chr9|chr9.	coding) 99% identity to 100% of P13825: Aspartic acid-rich protein precursor	**183|FullPhat|Plasmodium_falciparum_Sanger|(protein**
13	2.72	2.72	58.7	pfa3D7predicted|chr12|chr12.	coding) null Location= chr12 complement	**18r|Genefinder|Plasmodium_falciparum_Sanger|(protein**
14	3	3	59.1	pfa3D7predicted|chr14|chr14.	coding) null Location= chr14 2709354..2712680	**1901|GlimmerM|Plasmodium_falciparum_TIGR|(protein**
15	6.63	6.63	99.1	pfa3D7predicted|chr11|chr11.	coding) 100% identity to 100% of P38545: GTP-binding nuclear protein Ran (GTPase Ran) (Ras-like protein TC4)	**196|FullPhat|Plasmodium_falciparum_TIGR|(protein**
16	2.1	2.1	36.4	pfa3D7predicted|chr14|chr14	coding) 45% identity to 66% of AAO53165.1: similar to midasin, a large protein with an N-terminal domain, a central AAA domain	**196r|Genefinder|Plasmodium_falciparum_TIGR|(protein**
17	1.91	1.91	58.4	pfa3D7predicted|chr12|chr12.	coding) null Location= chr12 join	**201|FullPhat|Plasmodium_falciparum_Sanger|(protein**
18	1.56	1.66	50.3	pfa3D7predicted|chr12|chr12	coding) null Location= chr12 complement	**202|FullPhat|Plasmodium_falciparum_Sanger|(protein**
19	15.14	15.14	94.1	pfa3D7predicted|chr9|chr9	coding) 100% identity to 100% of P27362: Phosphoglycerate kinase	**218|FullPhat|Plasmodium_falciparum_Sanger|(protein**
20	1.43	1.43	62	pfa3D7predicted|chr5|chr5	coding) 100% identity to 100% of 1V8B.D: Chain D, Crystal Structure Of A Hydrolase	**227|FullPhat|Plasmodium_falciparum_Sanger|(protein**
21	19.92	19.92	94.9	pfa3D7predicted|chr13|chr13	coding) 100% identity to 100% of 1T26.A: Chain A,Lactate Dehydrogenase Complexed With Nadh And 4-Hydroxy-1,2,5-Thiadiazole-3-Carboxylic Acid	**270|FullPhat|Plasmodium_falciparum_Sanger|(protein**
22	2.93	2.93	78.8	pfa3D7predicted|chr12|chr12.	coding) null Location= chr12 complement	**31|GlimmerM|Plasmodium_falciparum_Sanger|(protein**
23	3.44	4.91	73.2	pfa3D7predicted|chr14|chr14	coding) 100% identity to 100% of P46925: Plasmepsin 2 precursor (Aspartic hemoglobinase II) (PFAPD)	**35f|Genefinder|Plasmodium_falciparum_TIGR|(protein**
24	1.66	1.66	74.4	pfa3D7predicted|chr12|chr12.	coding) null Location= chr12 complement	**382|GlimmerM|Plasmodium_falciparum_Sanger|(protein**
25	3.23	3.23	40.9	pfa3D7predicted|chr12|chr12	coding) null Location= chr12 join	**411|FullPhat|Plasmodium_falciparum_Sanger|(protein**
26	6.6	6.6	86.3	pfa3D7predicted|chr9|chr9	coding) 100% identity to 100% of P14642: TUBULIN ALPHA CHAIN	**42|FullPhat|Plasmodium_falciparum_Sanger|(protein**
27	21.79	21.79	98.7	pfa3D7predicted|chr12|chr12.	coding) null Location= chr12 1920770..1921900	**460|FullPhat|Plasmodium_falciparum_Sanger|(protein**
28	1.54	1.54	31.9	pfa3D7predicted|chr12|chr12	coding) null Location= chr12 1931956..1932570	**462|FullPhat|Plasmodium_falciparum_Sanger|(protein**
29	4.04	4.04	62.8	pfa3D7predicted|chr1|chr1.	coding) 93% identity to 94% of Q26005: Ring-infected erythrocyte surface antigen	**52|GlimmerM|Plasmodium_falciparum_Sanger|(protein**

30	2.37	2.37	56.3	pfa3D7predicted|chr12|chr12.	coding) null Location= chr12 complement	**55|FullPhat|Plasmodium_falciparum_Sanger|(protein**
31	25.28	25.28	98.2	pfa3D7predicted|chr12|chr12.	coding) null Location= chr12 complement	**596|GlimmerM|Plasmodium_falciparum_Sanger|(protein**
32	14.58	14.58	91.1	pfa3D7predicted|chr6|chr6	coding) 100% identity to 100% of Q07805: Ornithine aminotransferase (Ornithine--oxo-acid aminotransferase)	**90|FullPhat|Plasmodium_falciparum_Sanger|(protein**
33	2.9	2.9	96.7	pfa3D7predicted|chr13|chr13.	coding) 97% identity to 99% of EAA22057.1: 26s protease regulatory subunit s10b (p44) (conserved atpase domain protein 44)	**90|FullPhat|Plasmodium_falciparum_Sanger|(protein**
34	5.05	5.05	71.3	pfa3D7predicted|chr14|chr14.	coding) 33% identity to 55% of XP_396228.1: similar to dynein, axonemal, heavy chain 8; dynein, axon, heavy chain 8	Apis mellifera
35	7.8	7.8	95.1	pfa3D7predicted|chr13|chr13.	coding) 41% identity to 62% of AAP83582.1: phosphoethanolamine N-methyltransferase [Brassica napus]	Brassica napus
36	2.26	2.26	66.7	pfa3D7predicted|pfal_chr2	coding) 100% identity to 100% of P50498: Merozoite surface antigen 2 precursor (MSA-2) (45 kDa merozoite surface antigen)	**chr2|pfal_chr2.genefinder_77r|Genefinder|Plasmodium_falciparum_ TIGR|(protein**
37	1.65	1.65	45.8	pfa3D7predicted|pfal_chr2	coding) 46% identity to 61% of 2116446C: ORF Location= pfal_chr2 complement	**chr2|pfal_chr2.phat_239|FullPhat|Plasmodium_falciparum_ TIGR|(protein**
38	11.25	11.25	86.7	pfa3D7predicted|chr5|chr5	coding) 32% identity to 53% of EAL38034.1: karyopherin beta	Cryptosporidium hominis
39	2.12	2.12	73.5	pfa3D7predicted|chr14|chr14	coding) 41% identity to 68% of EAL36447.1: nuclear DNA-binding	Cryptosporidium hominis
40	4.93	4.93	76.4	pfa3D7predicted|chr13|chr13	coding) 28% identity to 52% of CAD98262.1: hypothetical predicted Armadillo/beta-catenin-like repeat protein, unknown function [Cryptosporidium parvum]	Cryptosporidium parvum
41	1.5	1.5	57.3	pfa3D7predicted|chr10|chr10	coding) 67% identity to 80% of EAK88291.1: CHD3 ortholog with 2x chromodomains plus SNF2 ATpase	Cryptosporidium parvum
42	13.65	13.65	86.9	pfa3D7predicted|chr6|chr6.	coding) 68% identity to 83% of AAB40928.2: cell division cycle protein 48	Dictyostelium discoideum
43	15.51	15.51	82.9	pfa3D7predicted|chr14|chr14	coding) 65% identity to 79% of EAL32818.1: GA15316-PA	Drosophila pseudoobscura
44	2	2	39.5	pfa3D7predicted|chr5|chr5.	coding) 43% identity to 53% of XP_489181.1: hypothetical protein XP_489181	Mus musculus
45	3.05	3.05	95.3	pfa3D7predicted|chr13|chr13	coding) 93% identity to 95% of BAA88568.1: ubiquitin	Oncorhynchus mykiss
46	24.04	24.04	100	pfa3D7predicted|chr14|chr14.	coding) 84% identity to 95% of CAH99235.1: glyceraldehyde-3-phosphate dehydrogenase, putative	**Plasmodium berghei**
47	9.47	9.47	90.8	pfa3D7predicted|chr9|chr9.	coding) 91% identity to 97% of CAH99282.1: s-adenosylmethionine synthetase,	**Plasmodium berghei**
48	7.79	7.79	73.5	pfa3D7predicted|chr9|chr9	coding) 80% identity to 92% of CAH95224.1: conserved hypothetical protein	**Plasmodium berghei**
49	7.51	7.51	93.1	pfa3D7predicted|chr5|chr5	coding) 33% identity to 50% of CAI03992.1: rhoptry-associated protein, putative	**Plasmodium berghei**
50	6.29	6.29	70.3	pfa3D7predicted|chr6|chr6	coding) 48% identity to 63% of CAI04669.1: hypothetical protein PB105705.00.0	**Plasmodium berghei**
51	4.7	4.7	93.2	pfa3D7predicted|chr11|chr11	coding) 78% identity to 89% of CAI01680.1: hypothetical protein PB300335.00.0	**Plasmodium berghei**
52	4.65	4.65	97.3	pfa3D7predicted|chr6|chr6.	coding) 91% identity to 97% of CAH97765.1: pyruvate kinase, putative	**Plasmodium berghei**
53	4.36	4.36	98.2	pfa3D7predicted|chr13|chr13	coding) 80% identity to 88%: phosphoribosylpyrophosphate synthetase,	**Plasmodium berghei**

54	4.27	4.27	62.5	pfa3D7predicted|chr5|chr5.	coding) 73% identity to 84% of CAH96435.1: hypothetical protein PB000785.01.0	**Plasmodium berghei**
55	3.13	3.13	40.6	pfa3D7predicted|chr13|chr13	coding) 46% identity to 64% of CAH96693.1: hypothetical protein PB103910.00.0	**Plasmodium berghei**
56	2.34	2.34	53.1	pfa3D7predicted|pfal_chr2	coding) 31% identity to 53% of CAH95160.1: conserved hypothetical protein	**Plasmodium berghei**
57	2.33	2.33	88.5	pfa3D7predicted|chr7|chr7	coding) 92% identity to 96% of CAH94563.1: conserved GTP-binding protein, putative	**Plasmodium berghei**
58	2.17	2.17	75.5	pfa3D7predicted|chr13|chr13	coding) 89% identity to 96% of CAH96222.1: conserved hypothetical protein	**Plasmodium berghei**
59	2.11	2.11	84.4	pfa3D7predicted|chr11|chr11	coding) 74% identity to 85% of CAH99527.1: protein disulfide isomerase related protein, putative	**Plasmodium berghei**
60	2.09	2.09	71.3	pfa3D7predicted|chr9|chr9.	coding) 89% identity to 96% of CAH98869.1: 26S proteasome regulatory subunit, putative	**Plasmodium berghei**
61	2.06	2.06	60.9	pfa3D7predicted|chr4|chr4	coding) 88% identity to 92% of CAH97914.1: conserved hypothetical protein	**Plasmodium berghei**
62	2.03	2.03	62.6	pfa3D7predicted|chr14|chr14	coding) 34% identity to 52% of CAH93814.1: hypothetical protein PB100384.00.0	**Plasmodium berghei**
63	1.89	1.89	90.5	pfa3D7predicted|chr14|chr14	coding) 98% identity to 100% of CAI00161.1: ribosomal protein L10, putative	**Plasmodium berghei**
64	1.7	1.7	79.1	pfa3D7predicted|chr11|chr11	coding) 87% identity to 95% of CAH99201.1: spermidine synthase	**Plasmodium berghei**
65	1.6	1.6	55.9	pfa3D7predicted|chr11|chr11	coding) 31% identity to 49% of CAH97207.1: conserved hypothetical protein	**Plasmodium berghei**
66	1.42	1.42	51.4	pfa3D7predicted|chr7|chr7	coding) 43% identity to 62% of CAH97542.1: hypothetical protein PB000344.02.0	**Plasmodium berghei**
67	1.38	1.38	63.8	pfa3D7predicted|chr3|chr3	coding) 33% identity to 52% of CAH99945.1: conserved hypothetical protein	**Plasmodium berghei**
68	6.64	6.75	89.1	pfa3D7predicted|chr9|chr9	coding) 96% identity to 99% of CAH95223.1: Heat shock protein, putative	**Plasmodium berghei**
69	4.63	4.63	78	pfa3D7predicted|chr8|chr8	coding) 92% identity to 97% of CAH77317.1: guanine nucleotide-binding protein, putative	**Plasmodium chabaudi**
70	3.24	3.24	69.4	pfa3D7predicted|pfal_chr2	coding) 83% identity to 91% of CAH76801.1: proteasome 26S regulatory subunit, putative	**Plasmodium chabaudi**
71	2.55	2.55	54.7	pfa3D7predicted|chr14|chr14	coding) 48% identity to 63% of CAH78879.1: conserved hypothetical protein	**Plasmodium chabaudi**
72	2.54	2.54	76	pfa3D7predicted|chr5|chr5.	coding) 34% identity to 57% of CAH74690.1: rhoptry-associated protein, putative	**Plasmodium chabaudi**
73	2.48	2.51	58.2	pfa3D7predicted|chr6|chr6.	coding) 51% identity to 65% of CAH80265.1: SET-domain protein, putative	**Plasmodium chabaudi**
74	2.12	2.12	66.6	pfa3D7predicted|chr10|chr10.	coding) 70% identity to 84% of CAH87109.1: methionine--tRNA ligase, putative	**Plasmodium chabaudi**
75	1.94	1.94	77.4	pfa3D7predicted|pfal_chr2|	coding) 33% identity to 59% of CAH75228.1: conserved hypothetical protein	**Plasmodium chabaudi**
76	1.8	1.8	56.5	pfa3D7predicted|chr5|chr5.	coding) 46% identity to 62% of CAH79456.1: conserved hypothetical	**Plasmodium chabaudi**

77	1.78	1.78	60.2	pfa3D7predicted|chr9|chr9.	coding) 39% identity to 57% of CAH82370.1: conserved hypothetical protein	**Plasmodium chabaudi**
78	1.75	1.75	80.4	pfa3D7predicted|chr13|chr13.	coding) 71% identity to 82% of CAH77822.1: elongation factor 1-gamma, putative	**Plasmodium chabaudi**
79	1.54	1.54	66.7	pfa3D7predicted|chr9|chr9.	coding) 80% identity to 89% of CAH84421.1: hypothetical protein PC301031.00.0	**Plasmodium chabaudi**
80	7.01	7.01	92.1	pfa3D7predicted|chr8|chr8.	coding) 84% identity to 92% of AAV36000.1: protein disulfide isomerase	**Plasmodium chabaudi chabaudi**
81	14.29	14.29	94.7	pfa3D7predicted|chr14|chr14.	coding) 99% identity to 100% of CAB51741.1: RNA helicase-1	**Plasmodium cynomolgi**
82	13.53	13.53	98.7	pfa3D7predicted|chr8|chr8	coding) 100% identity to 100% of AAC17515.1: 14-3-3 protein	**Plasmodium knowlesi**
83	5.78	5.78	91.5	pfa3D7predicted|chr14|chr14.	coding) 76% identity to 89% of AAC15794.1: plasmepsin	**Plasmodium malariae**
84	2.91	2.91	49	pfa3D7predicted|chr4|chr4	coding) 23% identity to 45% of AAO38039.1: reticulocyte binding-like protein 2b	**Plasmodium reichenowi**
85	1.56	1.56	58.3	pfa3D7predicted|chr8|chr8	coding) 32% identity to 54% of CAB96701.1: Pvstp1	**Plasmodium vivax**
86	8.71	8.71	90.5	pfa3D7predicted|chr9|chr9	coding) 40% identity to 63% of BAC43744.1: PyRhopH2	**Plasmodium yoelii**
87	2.08	2.08	79.6	pfa3D7predicted|chr9|chr9	coding) 44% identity to 65% of BAB19269.1: high molecular weight rhoptry protein 3	**Plasmodium yoelii**
88	16.12	16.12	98.9	pfa3D7predicted|chr13|chr13	coding) 100% identity to 100% of EAA15302.1: translation elongation factor EF-1, subunit alpha	**Plasmodium yoelii yoelii**
89	10.4	10.4	100	pfa3D7predicted|chr11|chr11	coding) 67% identity to 83% of EAA17014.1: membrane-associated calcum-binding protein	**Plasmodium yoelii yoelii**
90	4.4	4.4	51.7	pfa3D7predicted|chr8|chr8.	coding) 65% identity to 82% of EAA16104.1: hypothetical protein	**Plasmodium yoelii yoelii**
91	3.97	3.97	97.7	pfa3D7predicted|chr4|chr4	coding) 97% identity to 100% of EAA16768.1: 26S proteasome ATPase	**Plasmodium yoelii yoelii**
92	3.73	3.73	81.7	pfa3D7predicted|chr13|chr13	coding) 62% identity to 79% of EAA17424.1: putative HSP protein	**Plasmodium yoelii yoelii**
93	3.29	3.29	60.9	pfa3D7predicted|chr14|chr14.	coding) 75% identity to 77% of EAA16792.1: ookinete protein-related	**Plasmodium yoelii yoelii**
94	3.22	3.22	62.7	pfa3D7predicted|chr14|chr14	coding) 37% identity to 53% of EAA16617.1: hypothetical protein	**Plasmodium yoelii yoelii**
95	3.15	3.15	57.8	pfa3D7predicted|chr13|chr13.	coding) 29% identity to 48% of EAA22695.1: hypothetical protein	**Plasmodium yoelii yoelii**
96	2.9	2.9	90.2	pfa3D7predicted|chr6|chr6.	coding) 81% identity to 90% of EAA17228.1: probable mitochondrial import receptor subunit tom40 homolog	**Plasmodium yoelii yoelii**
97	2.85	2.85	66.7	pfa3D7predicted|chr8|chr8.	coding) 29% identity to 46% of EAA16762.1: hypothetical protein	**Plasmodium yoelii yoelii**
98	2.85	2.85	64.7	pfa3D7predicted|pfal_chr2|	coding) 90% identity to 96% of EAA22741.1: DEAD/DEAH box helicase, putative	**Plasmodium yoelii yoelii**
99	2.76	2.76	67.2	pfa3D7predicted|chr10|chr10.	coding) 51% identity to 67% of EAA15245.1: KH domain, putative	**Plasmodium yoelii yoelii**
100	2.69	2.69	66.5	pfa3D7predicted|chr14|chr14.	coding) 73% identity to 89% of EAA19135.1: similar to RIKEN cDNA 2810018A15 gene, putative	**Plasmodium yoelii yoelii**
101	2.64	2.64	40.5	pfa3D7predicted|chr6|chr6.	coding) 29% identity to 46% of EAA21359.1: hypothetical protein	**Plasmodium yoelii yoelii**
102	2.52	2.52	65.3	pfa3D7predicted|chr4|chr4	coding) 49% identity to 67% of EAA16412.1: hypothetical protein	**Plasmodium yoelii yoelii**
103	2.35	2.35	64.9	pfa3D7predicted|chr11|chr11	coding) 65% identity to 75% of EAA17211.1: hMLH1 gene product-related	**Plasmodium yoelii yoelii**
104	2.22	2.22	63.6	pfa3D7predicted|chr6|chr6.	coding) 32% identity to 52% of EAA20836.1: von Willebrand factor type A domain, putative	**Plasmodium yoelii yoelii**
105	2.1	2.1	51.3	pfa3D7predicted|chr13|chr13.	coding) 26% identity to 46% of EAA17097.1: hypothetical protein	**Plasmodium yoelii yoelii**

106	2.06	2.06	56.7	pfa3D7predicted|chr13|chr13.	coding) 29% identity to 48% of EAA21778.1: chloroquine resistance marker protein	**Plasmodium yoelii yoelii**
107	2.04	2.04	79.4	pfa3D7predicted|chr14|chr14	coding) 67% identity to 82% of EAA17993.1: Exp-2	**Plasmodium yoelii yoelii**
108	2.01	2.01	59.5	pfa3D7predicted|chr3|chr3	coding) 82% identity to 91% of EAA17678.1: Plasmodium vivax PV1H14065_P-related	**Plasmodium yoelii yoelii**
109	2	2	24.2	pfa3D7predicted|chr14|chr14.	coding) 67% identity to 83% of EAA17693.1: hypothetical protein	**Plasmodium yoelii yoelii**
110	1.92	1.92	81.4	pfa3D7predicted|chr6|chr6	coding) 87% identity to 97% of EAA16340.1: ethylene-inducible protein hever	**Plasmodium yoelii yoelii**
111	1.85	1.85	41.7	pfa3D7predicted|chr14|chr14	coding) 42% identity to 60% of EAA16069.1: hypothetical protein	**Plasmodium yoelii yoelii**
112	1.83	1.83	70.5	pfa3D7predicted|chr4|chr4.	coding) 43% identity to 60% of EAA17079.1: hypothetical protein	**Plasmodium yoelii yoelii**
113	1.82	1.82	52.4	pfa3D7predicted|chr7|chr7	coding) 28% identity to 49% of EAA16587.1: R27-2 protein	**Plasmodium yoelii yoelii**
114	1.71	1.71	60.1	pfa3D7predicted|chr14|chr14	coding) 39% identity to 57% of EAA18364.1: hypothetical protein	**Plasmodium yoelii yoelii**
115	1.59	1.59	53.6	pfa3D7predicted|chr8|chr8.	coding) 36% identity to 54% of EAA18547.1: CCAAT-box DNA binding protein subunit B, putative	**Plasmodium yoelii yoelii**
116	1.53	1.54	61.6	pfa3D7predicted|chr13|chr13.	coding) 27% identity to 45% of EAA15536.1: chloroquine resistance marker protein	**Plasmodium yoelii yoelii**
117	1.52	1.52	78.1	pfa3D7predicted|chr6|chr6.	coding) 72% identity to 86% of EAA15273.1: DnaJ homolog, putative	**Plasmodium yoelii yoelii**
118	1.5	1.5	46	pfa3D7predicted|chr13|chr13.	coding) 28% identity to 47% of EAA21348.1: hypothetical protein	**Plasmodium yoelii yoelii**
119	1.44	1.44	85.9	pfa3D7predicted|chr14|chr14	coding) 83% identity to 94% of EAA18974.1: 6-phosphogluconate dehydrogenase, decarboxylating	**Plasmodium yoelii yoelii**
120	1.38	1.42	54	pfa3D7predicted|chr5|chr5	coding) 26% identity to 43% of EAA16133.1: hypothetical protein	**Plasmodium yoelii yoelii**
121	1.36	1.36	30.8	pfa3D7predicted|chr8|chr8	coding) 26% identity to 45% of EAA18589.1: hypothetical protein	**Plasmodium yoelii yoelii**
122	1.32	1.32	45.8	pfa3D7predicted|chr1|chr1.	coding) 41% identity to 57% of EAA20533.1: Ubiquitin carboxyl-terminal hydrolase family 2, putative	**Plasmodium yoelii yoelii**
123	1.45	1.45	58.5	pfa3D7predicted|chr9|chr9.	coding) 59% identity to 75% of EAA16564.1: hypothetical protein	**Plasmodium yoelii yoelii**
124	2	2	64	pfa3D7predicted|chr4|chr4	coding) 100% identity to 100% of EAA15878.1: Tubulin/FtsZ family, putative	**Plasmodium yoelii yoelii**
125	2.32	2.32	51.1	pfa3D7predicted|chr8|chr8	coding) 65% identity to 82% of EAA16104.1: hypothetical protein	**Plasmodium yoelii yoelii**
126	12.55	13.85	98.8	pfa3D7predicted|chr11|chr11.	coding) 73% identity to 85% of AAQ63186.1: heat shock protein 70	Theileria annulata
127	21.25	24.01	95.4	pfa3D7predicted|chr8|chr8.	coding) 81% identity to 90% of AAC72001.1: heat shock protein 70	Toxoplasma gondii

Table 9. Differentially expressed *P. falciparum* proteins clustered by treatment with Ref#31

Number	PlasmoDB ID	Annotation	Adj p-value (Treatment)	Adj p-value (Time)	Adj p-value (Interaction)	F-ratio (Treatment)
1	MAL13P1.120	splicing factor, putative	0.0377	0.1242	0.1451	9.002701
2	MAL13P1.13	conserved Plasmodium protein, unknown function	0.0175	0.4261	0.5524	8.001505
3	MAL13P1.214	phosphoethanolamine N-methyltransferase	0.0174	0.0097	0.0164	10811.212
4	MAL13P1.226	conserved Plasmodium protein, unknown function	0.0325	0.115	0.141	9.006587
5	MAL13P1.256	phosphatidylinositol transfer protein, putative	0.0371	0.1265	0.13	9.02E+00
6	MAL13P1.293	conserved Plasmodium protein, unknown function	0.0183	0.0183	0.0183	956046.3
7	MAL13P1.296	conserved Plasmodium protein, unknown function	0.0384	0.5143	0.6092	8.001835
8	MAL13P1.540	heat shock protein 70 hsp70, putative	0.0498	0.0781	0.0899	8.981169
9	MAL7P1.126	conserved Plasmodium protein, unknown function	0.0371	0.1265	0.1424	9.034018
10	MAL7P1.147	ubiquitin carboxyl-terminal hydrolase, putative	0.0366	0.1277	0.1455	9.001615
11	MAL7P1.216	rifin	0.0374	0.1276	0.1462	9.002939
12	MAL8P1.69	14-3-3 protein, putative	0.0043	0.0026	0.0084	9402.952
13	PF07_0020	methyltransferase, putative	0.0375	0.1295	0.1378	9.012922
14	PF07_0029	heat shock protein 86	0.0068	0.0038	0.0099	13323.744
15	PF07_0118	conserved Plasmodium membrane protein, unknown function	2.65E-02	1.13E-01	1.38E-01	9.001968
16	PF08_0002	surface-associated interspersed gene 8.2 SURFIN8.2	0.0091	0.0755	0.1202	9.002246
17	PF08_0054	heat shock 70 kDa protein	0.049	0.0866	0.0945	8.811907
18	PF10_0155	enolase	0.0093	0.0056	0.0114	861661.9
19	PF10_0232	Chromodomain-helicase-DNA-binding protein 1 homolog, putative	0.0185	0.0117	0.0039	1301.2194
20	PF10_0248	conserved Plasmodium membrane protein, unknown function	0.0357	0.1313	0.1338	9.006357
21	PF10_0289	adenosine deaminase, putative	0.0367	0.1202	0.1441	9.0104
22	PF10_0331	Sec1 family protein, putative	0.0276	0.1153	0.1387	9.001239
23	PF11_0008	erythrocyte membrane protein 1, PfEMP1	0.0116	0.006	0.0124	4.76E+07
24	PF11_0061	histone H4	0.0049	7.00E-04	0.0033	11841.873
25	PF11_0062	histone H2B	0.0048	0.011	0.0088	254604.5

26	PF11_0096	casein kinase II, alpha subunit	0.0183	0.0183	0.0183	312984.72
27	PF11_0183	GTP-binding nuclear protein ran/tc4	0.0321	0.0476	0.0853	9.048219
28	PF11_0186	conserved Plasmodium protein, unknown function	0.0198	0.0198	0.0198	2.73E+11
29	PF11_0242	calcium-dependent protein kinase, putative	0.0377	0.1242	0.1451	9.003289
30	PF11_0301	spermidine synthase	0.0119	0.0073	0.0134	49937.76
31	PF11_0302	conserved Plasmodium protein, unknown function	0.0165	0.0165	0.0165	2011196.2
32	PF11_0354	conserved Plasmodium protein, unknown function	0.0055	0.0688	0.1163	9.0041895
33	PF13_0063	26S proteasome regulatory subunit 7, putative	0.0326	0.5045	0.6177	8.000535
34	PF13_0067	conserved Plasmodium protein, unknown function	0.0163	0.0163	0.0163	1556952.8
35	PF14_0007	stevor	0.0216	0.1039	0.1327	9.098504
36	PF14_0059	conserved Plasmodium protein, unknown function	0.0103	0.0859	0.1188	9.001813
37	PF14_0070	pre-mRNA splicing factor, putative	0.0349	0.0443	0.0816	9.017208
38	PF14_0075	plasmepsin IV	0.0382	0.0542	0.0986	8.973502
39	PF14_0102	rhoptry-associated protein 1, RAP1	0.0084	0.0056	0.0117	11577.732
40	PF14_0120	conserved Plasmodium protein, unknown function	0.0384	0.517	0.6255	8.000557
41	PF14_0124	actin II	0.0182	0.0102	0.0041	3619.8813
42	PF14_0179	conserved Plasmodium protein, unknown function	0.0119	0.0254	0.0223	1.19E+08
43	PF14_0185	ATP-dependent RNA Helicase, putative	0.0163	0.0163	0.0163	440222.12
44	PF14_0226	conserved Plasmodium protein, unknown function	0.0384	0.3253	0.6175	8.07E+00
45	PF14_0230	60S ribosomal protein L5, putative	0.001	0	0.0019	554022.1
46	PF14_0232	conserved Plasmodium protein, unknown function	0.0066	0.0041	0.0102	1715.5292
47	PF14_0260	metabolite/drug transporter, putative	0.016	0.008	0.0027	81.23784
48	PF14_0261	proliferation-associated protein 2g4, putative	0.0182	0.0102	0.0041	1135.9166
49	PF14_0278	ATP-dependent DNA helicase, putative	0.0375	0.1295	0.146	9.004232
50	PF14_0379	conserved Plasmodium protein, unknown function	0.0299	0.1145	0.1384	9.01E+00
51	PF14_0425	fructose-bisphosphate aldolase	0.0124	0.5048	0.5751	24.938982
52	PF14_0482	conserved Plasmodium protein, unknown function	0.0048	0.078	0.1159	9.016808
53	PF14_0598	glyceraldehyde-3-phosphate dehydrogenase	4.00E-04	6.00E-04	5.00E-04	18491.457
54	PF14_0655	helicase 45	0.0146	0.0074	0.014	5874.9966

55	PFB0505c	3-oxoacyl-acyl carrier protein synthase III, putative	0.0357	0.1313	0.1468	9.004578
56	PFC0135c	exportin 1, putative	0.022	0.061	0.076	9.008977
57	PFC0335c	conserved Plasmodium protein, unknown function	0.0054	0.0875	0.1165	9.001657
58	PFC0610c	zinc finger protein, putative	0.0165	0.0976	0.1276	9.004351
59	PFC0835c	conserved protein, unknown function	0.004	0.0023	0.0087	17744.775
60	PFD0462w	DNAJ protein	0.0477	0.5499	0.6684	7.996296
61	PFD0670c	lysine decarboxylase-like protein, putative	0.0112	0.029	0.0228	1607583
62	PFE0075c	rhoptry-associated protein 3, RAP3	0.0302	0.0432	0.0956	9.00E+00
63	PFE0080c	rhoptry-associated protein 2, RAP2	0.0075	0.0023	0.0106	51019.152
64	PFE1445c	conserved Plasmodium protein, unknown function	0.0301	0.1014	0.1412	9.005066
65	PFF0435w	ornithine aminotransferase	0.0039	0.0026	0.0036	109827.76
66	PFF0645c	integral membrane protein, putative	0.0173	0.077	0.1247	9.057972
67	PFF0940c	cell division cycle protein 48 homologue, putative	0.0018	8.00E-04	0.0044	1574580.5
68	PFF0945c	acyl-CoA synthetase, PfACS12	0.0021	0.014	0.013	4.55E+07
69	PFF1300w	pyruvate kinase	0.0466	0.3397	0.6116	8.042231
70	PFI0005w	erythrocyte membrane protein 1, PfEMP1	0.0339	0.0525	0.085	9.015148
71	PFI0030c	rifin	0.003	0.0106	0.0081	3.89E+08
72	PFI0345w	GTPase activator, putative	0.0183	1.83E-02	0.0183	4497137.5
73	PFI0645w	elongation factor 1-beta	0.0201	0.0992	0.1283	9.005682
74	PFI0875w	Heat shock protein 70 HSP70 homologue	0.0408	0.0867	0.0905	8.912575
75	PFI0880c	glideosome-associated protein 50	0.0055	0.0031	0.0097	18772.744
76	PFI1090w	S-adenosylmethionine synthetase	0.0046	0.0026	0.0083	5.81E+04
77	PFI1285w	protein kinase, putative	0.0097	0.0974	0.1208	9.002587
78	PFI1445w	High molecular weight rhoptry protein-2	0.0123	0.0069	0.0136	245729.84
79	PFL0115w	dynein heavy chain, putative	0.0061	0.0766	0.1146	9.00401
80	PFL0185c	nucleosome assembly protein 1, putative	0.0274	0.079	0.1356	9.018749
81	PFL0510c	conserved Plasmodium protein, unknown function	0.0334	0.1062	0.1419	9.011538
82	PFL0590c	non-SERCA-type Ca2+ -transporting P-ATPase	0.0357	1.31E-01	0.1468	9.005981
83	PFL1070c	endoplasmin homolog precursor, putative	0.0079	0.0051	0.0115	8316.239

84	PFL1130c	conserved Plasmodium protein, unknown function	0.0299	0.1145	0.1384	9.000337
85	PFL1270w	cof-like hydrolase, had-superfamily, subfamily iib	0.0357	0.101	0.1468	9.002221
86	PFL1980c	conserved Plasmodium protein, unknown function	0.0452	0.5439	0.6678	7.9978304
87	PFL2485c	tryptophanyl-tRNA synthetase, putative	0.0374	0.0202	0.0374	73039.875

Key:

Treatment significant	Time significant	Interaction significant

Table 10: Differentially expressed *P. falciparum* proteins clustered by time

Number	PlasmoDB ID	Annotation	Adj p-value (Treatment)	Adj p-value (Time)	Adj p-value (Interaction)	F-ratio (Time)
1	MAL13P1.102	conserved Plasmodium protein, unknown function	0.2927	0.0359	0.4712	8.990068
2	PFE1195w	karyopherin beta	0.206	0.0236	0.484	8.986577
3	PF14_0185	ATP-dependent RNA Helicase, putative	0.0163	0.0163	0.0163	440222.12
4	MAL8P1.220	erythrocyte membrane protein 1, PfEMP1	0.2641	0.028	0.5165	12.966075
5	PF10_0232	Chromodomain-helicase-DNA-binding protein 1 homolog, putative	0.0185	0.0117	0.0039	2.34E+09
6	PFI0035c	rifin	0.2356	0.0137	0.4609	9.022491
7	PF11_0091	transcription factor with AP2 domains, putative	0.072	0.0152	0.0039	3970604.5
8	PF14_0232	conserved Plasmodium protein, unknown function	0.0066	0.0041	0.0102	4885.453
9	PFL2485c	tryptophanyl-tRNA synthetase, putative	0.0374	0.0202	0.0374	73039.875
10	PF13_0067	conserved Plasmodium protein, unknown function	0.0163	0.0163	0.0163	1556952.8
11	PFC0640w	CSP and TRAP-related protein CTRP	0.5715	0.0304	0.0123	5928730
12	PF11_0313	60S ribosomal protein P0	0.2595	0.0301	0.4666	8.966604
13	PFF0675c	myosin E	0.5709	0.0289	0.0109	4934446
14	PFD1015c	erythrocyte membrane protein 1, PfEMP1	0.0711	0.0129	0.0033	1.75E+07
15	PF14_0598	glyceraldehyde-3-phosphate dehydrogenase	4.00E-04	6.00E-04	5.00E-04	16859.965
16	PF11_0317	structural mainte0ce of chromosome protein, putative	0.5494	0.0128	0.9015	2.45E+08
17	PF11_0008	erythrocyte membrane protein 1, PfEMP1	0.0116	0.006	0.0124	1.43E+08

18	PFF1015w	conserved Plasmodium protein, unknown function	0.3163	0.0474	0.4785	8.988561
19	PFA0175w	conserved Plasmodium protein, unknown function	0.2792	0.0324	0.472	9.002015
20	PFL1685w	conserved Plasmodium protein, unknown function	0.286	0.0356	0.4667	8.99615
21	PFD0680c	ubiquitin carboxyl-terminal hydrolase a, putative	0.2332	0.019	0.4586	9.003376
22	PF14_0487	conserved Plasmodium protein, unknown function	0.2332	0.019	0.4586	9.00254
23	PF14_0179	conserved Plasmodium protein, unknown function	0.0119	0.0254	0.0223	2.98E+07
24	PF10_0115	QF122 antigen	0.3162	0.0493	0.0562	7.006202
25	PF07_0024	inositol phosphatase, putative	0.3175	0.0236	0.4445	12.982472
26	PFF0945c	acyl-CoA synthetase, PfACS12	0.0021	0.014	0.013	1.14E+07
27	PFD0670c	lysine decarboxylase-like protein, putative	0.0112	0.029	0.0228	401895.75
28	MAL13P1.214	phosphoethanolamine N-methyltransferase	0.0174	0.0097	0.0164	32910.85
29	MAL8P1.69	14-3-3 protein, putative	0.0043	0.0026	0.0084	27842.305
30	PF07_0029	heat shock protein 86	0.0068	0.0038	0.0099	38673.2
31	PF11_0062	histone H2B	0.0048	0.011	0.0088	63778.395
32	PF11_0183	GTP-binding nuclear protein ran/tc4	0.0321	0.0476	0.0853	7.034721
33	PF14_0655	helicase 45	0.0146	0.0074	0.014	18021.19
34	PFE0075c	rhoptry-associated protein 3, RAP3	0.0302	0.0432	0.0956	7.0100837
35	PFF0435w	ornithine aminotransferase	0.0039	0.0026	0.0036	323623.1
36	PFF0940c	cell division cycle protein 48 homologue, putative	0.0018	8.00E-04	0.0044	4693108
37	PFI1445w	High molecular weight rhoptry protein-2	0.0123	0.0069	0.0136	740825.8
38	PFL1070c	endoplasmin homolog precursor, putative	0.0079	0.0051	0.0115	24208.705
39	PF11_0061	histone H4	0.0049	7.00E-04	0.0033	37566.18
40	PFE0080c	rhoptry-associated protein 2, RAP2	0.0075	0.0023	0.0106	154750.52
41	MAL8P1.73	conserved Plasmodium protein, unknown function	0.3101	0.0274	0.449	12.958111
42	PFI0180w	alpha tubulin	0.26	0.0148	0.4146	13.0128145
43	PF10_0155	enolase	0.0093	0.0056	0.0114	2588148
44	PFI1090w	S-adenosylmethionine synthetase	0.0046	0.0026	0.0083	170739.16
45	PF11_0301	spermidine synthase	0.0119	0.0073	0.0134	148370.55
46	PF14_0102	rhoptry-associated protein 1, RAP1	0.0084	0.0056	0.0117	34798.426

47	PF10_0084	tubulin beta chain, putative	0.2691	0.0294	0.5192	12.839848
48	PF14_0486	elongation factor 2	0.3008	0.0266	0.4423	12.880881
49	PF14_0368	thioredoxin peroxidase 1	0.2383	0.0173	0.4608	9.020752
50	PF14_0230	60S ribosomal protein L5, putative	0.001	0	0.0019	1698630.2
51	PFI0880c	glideosome-associated protein 50	0.0055	0.0031	0.0097	55106.527
52	PFL1110c	CAMP-dependent protein kinase regulatory subunit, putative	0.2948	0.0109	0.4437	12.99903
53	PF08_0074	DNA/RNA-binding protein Alba, putative	0.3198	0.0333	0.0577	7.0406713
54	PF11_0098	endoplasmic reticulum-resident calcium binding protein	0.2643	0.0286	0.5227	12.866636
55	PFE1150w	multidrug resistance protein	0.3416	0.0417	0.4939	8.997959
56	PFC0835c	conserved protein, unknown function	0.004	0.0023	0.0087	50930.48
57	PF11_0065	40S ribosomal protein S4, putative	0.3053	0.0154	0.4616	12.957173
58	PFB0445c	DEAD box helicase, UAP56	0.3128	0.0266	0.4441	12.8424015
59	PF11_0362	protein phosphatase, putative	0.3416	0.0417	0.4939	8.986228
60	PFA0765c	erythrocyte membrane protein 1, PfEMP1	0.3055	0.0399	0.4834	8.99476
61	PF14_0070	pre-mRNA splicing factor, putative	0.0349	0.0443	0.0816	7.00624
62	MAL13P1.313	conserved Plasmodium protein, unknown function	0.3416	0.0454	0.4939	8.9844
63	PF10_0024	Plasmodium exported protein hyp2, unknown function	0.065	0.0012	0.0257	4.59E+09
64	PF13_0210	conserved Plasmodium protein, unknown function	0.318	0.0399	0.4834	8.994084
65	PF11_0186	conserved Plasmodium protein, unknown function	0.0198	0.0198	0.0198	2.73E+11
66	PF10_0130	conserved Plasmodium protein, unknown function	0.3379	0.0467	0.4902	8.965755
67	PFI1505c	elongation factor Tu family protein-related	0.3379	0.0467	0.4902	8.990484
68	PFF0195c	conserved Plasmodium protein, unknown function	0.7199	0.0254	0.9024	6.00037
69	PF14_0455	multidrug resistance protein 2 heavy metal transport family	0.2462	0.0266	0.5573	12.989088
70	PF11_0437	60S ribosomal protein L28, putative	0.0919	0.0163	0.0051	5543.512
71	PF11_0518	Plasmodium falciparum isolate 3D7	0.3297	0.0467	0.4902	8.953739
72	MAL8P1.112	conserved Plasmodium protein, unknown function	0.3098	0.0399	0.4797	8.979819
73	PFF0295c	conserved Plasmodium protein, unknown function	0.3416	0.0467	0.4939	8.990105
74	PFI0030c	rifin	0.003	0.0106	0.0081	9.72E+07

75	PF14_0261	proliferation-associated protein 2g4, putative	0.0182	0.0102	0.0041	7447248.5
76	PF14_0260	metabolite/drug transporter, putative	0.016	0.008	0.0027	4.56E+07
77	MAL13P1.60	erythrocyte binding antigen-140	0.258	0.0477	0.0451	7.015633
78	PF14_0124	actin II	0.0182	0.0102	0.0041	9.15E+08
79	MAL8P1.95	conserved Plasmodium protein, unknown function	0.2373	0.018	0.455	8.969892
80	PF14_0324	Hsp70/Hsp90 organizing protein, putative	0.3043	0.0391	0.4761	8.944293
81	PF14_0359	HSP40, subfamily A, putative	0.2344	0.0191	0.439	9.013328
82	PFE1250w	acyl-CoA synthetase, PfACS10	0.291	0.0382	0.4752	8.995631
83	PFL0050c	Plasmodium exported protein PHISTb, unknown function	0.291	0.0382	0.4752	8.978572
84	PFL1545c	chaperonin, cpn60	0.5575	0.0045	0.7019	8609340
85	PF13_0033	26S proteasome regulatory subunit, putative	0.2559	0.0269	0.4639	9.003452
86	PFE1050w	adenosylhomocysteinaseS-adenosyl-L-homocystein e hydrolase	0.5634	0.0067	0.5683	2126440
87	MAL13P1.343	proteasome regulatory subunit, putative	0.2833	0.0382	0.4752	8.998989
88	PFL1425w	t-complex protein 1, gamma subunit, putative	0.054	0.0195	0.0345	2214439.2
89	PF10_0159	glycophorin-binding protein 130 precursor	0.0641	0.0028	0.1703	1.35E+07
90	PF11_0302	conserved Plasmodium protein, unknown function	0.0165	0.0165	0.0165	2011196.2
91	PF11_0035	Plasmodium exported protein, unknown function	0.558	0.0039	0.8187	3234.6
92	PF10_0193	microtubule-associated protein 1 light chain 3, putative	0.2432	0.0029	0.4502	9.17951
93	MAL13P1.78	conserved Plasmodium protein, unknown function	0.2097	0.0098	0.4468	9.020384
94	PFF0825c	mitochondrial import receptor subunit tom40	0.0898	0.0195	0.0898	473140.88
95	PFB0630c	conserved Plasmodium protein, unknown function	0.2344	0.0191	0.4561	9.021189
96	PF14_0634	conserved Plasmodium protein, unknown function	0.0898	0.0195	0.0898	8890640
97	PF14_0348	ATP-dependent Clp protease proteolytic subunit, putative	0.3438	0.0393	0.4994	8.987066
98	PF13_0328	proliferating cell nuclear antigen	0.2885	0.0371	0.4741	8.997738
99	MAL13P1.293	conserved Plasmodium protein, unknown function	0.0183	0.0183	0.0183	956046.3
100	PF11_0096	casein kinase II, alpha subunit	0.0183	0.0183	0.0183	312984.72
101	PFI0345w	GTPase activator, putative	0.0183	0.0183	0.0183	4497137.5

Key

Treatment significant	Time significant	Interaction significant

Table 11: Differentially expressed *P. falciparum* proteins clustered by treatment and time interaction

Number	PlasmoDB ID	Annotation	Adj p-value (Treatment)	Adj p-value (Time)	Adj p-value (Interaction)	F-ratio (Interaction)
1	PFD0020c	erythrocyte membrane protein 1, PfEMP1	0.2739	0.4824	0.0253	12.9796
2	PF14_0185	ATP-dependent RNA Helicase, putative	0.0163	0.0163	0.0163	440222.12
3	PF10_0232	Chromodomain-helicase-DNA-binding protein 1 homolog, putative	0.0185	0.0117	0.0039	7.01E+09
4	PFF1365c	HECT-domain ubiquitin-transferase, putative	0.289	0.4592	0.0258	12.99404
5	MAL13P1.206	Na+ -dependent Pi transporter, sodium-dependent phosphate transporter	0.2384	0.1306	0.0339	7.0663986
6	PF11_0091	transcription factor with AP2 domains, putative	0.072	0.0152	0.0039	1.19E+07
7	PF13_0322	falcilysin	0.2384	0.1306	0.038	7.008874
8	PF11_0099	heat shock protein DnaJ homologue Pfj2	0.2384	0.1306	0.038	7.026347
9	PF14_0232	conserved Plasmodium protein, unknown function	0.0066	0.0041	0.0102	1705.5603
10	PFL2485c	tryptophanyl-tRNA synthetase, putative	0.0374	0.0202	0.0374	73039.875
11	PF13_0067	conserved Plasmodium protein, unknown function	0.0163	0.0163	0.0163	1556952.8
12	PFC0640w	CSP and TRAP-related protein CTRP	0.5715	0.0304	0.0123	1.78E+07
13	PFF0675c	myosin E	0.5709	0.0289	0.0109	1.48E+07
14	PF11_0184	DNA mismatch repair protein MLH1, putative	0.2281	0.1102	0.0316	7.0210867
15	PF11_0157	glycerol-3-phosphate dehydrogenase, putative	0.2384	0.1306	0.038	7.0237327
16	PFD1015c	erythrocyte membrane protein 1, PfEMP1	0.0711	0.0129	0.0033	5.26E+07
17	PFI1830c	erythrocyte membrane protein 1, PfEMP1	0.2281	0.0979	0.0316	7.0072083
18	PF14_0598	glyceraldehyde-3-phosphate dehydrogenase	4.00E-04	6.00E-04	5.00E-04	18623.625
19	PFD0985w	transcription factor with AP2 domains, putative	0.2981	0.5197	0.0255	12.990983
20	PF11_0008	erythrocyte membrane protein 1, PfEMP1	0.0116	0.006	0.0124	4.76E+07
21	PF14_0657	conserved Plasmodium protein, unknown function	0.2454	0.1241	0.0277	7.0023046
22	PFL1890c	HD superfamily phosphohydrolase protein	0.2341	0.1124	0.0148	7.004878

23	PFE0570w	RNA pseudouridylate synthase, putative	0.3097	0.4951	0.003	13.006807
24	PFL0925w	formin 2, putative	0.6248	0.7981	0.0405	5.9974346
25	PFL2405c	PFG377 protein	0.2454	0.1279	0.035	7.0006704
26	PF11_0435	conserved Plasmodium membrane protein, unknown function	0.2577	0.4512	0.0051	13.030219
27	PFD0865c	cdc2-related protein kinase 1	0.2454	0.1279	0.031	7.008791
28	PF07_0023	DNA replication licensing factor mcm7 homologue, putative	0.2103	0.0796	0.0146	7.0063086
29	PF14_0544	conserved Plasmodium protein, unknown function	0.234	0.1133	0.0281	7.0051866
30	PF14_0419	conserved Plasmodium protein, unknown function	0.2454	0.1279	0.035	7.00077
31	MAL13P1.380	conserved Plasmodium protein, unknown function	0.3405	0.4915	0.02	12.99251
32	PFB0895c	replication factor C subunit 1, putative	0.2454	0.1279	0.035	7.0119896
33	PFL1930w	conserved Plasmodium protein, unknown function	0.2454	0.1279	0.035	7.0011606
34	PFI1150w	conserved Plasmodium protein, unknown function	0.3218	0.4762	0.0097	13.024725
35	PF14_0448	40S ribosomal protein S2, putative	0.243	0.1272	0.0405	7.0217743
36	PFI1180w	patatin-like phospholipase, putative	0.0516	0.0516	0.0178	5.46E+08
37	PFB0665w	serine/threonine protein kinase, putative	0.3318	0.4591	0.001	13.014323
38	PF14_0179	conserved Plasmodium protein, unknown function	0.0119	0.0254	0.0223	2.98E+07
39	PFI0320w	arginase, putative	0.0584	0.0584	0.0406	1.80E+07
40	PFA0280w	asparagine-rich antigen Pfa35-2	0.2307	0.0849	0.0275	7.002076
41	PFL0625c	eukaryotic translation initiation factor 3 subunit 10, putative	0.3413	0.4815	0.0139	12.994638
42	PF14_0722	cysteine repeat modular protein 4, putative	0.2266	0.1061	0.0295	7.001416
43	PFF0945c	acyl-CoA synthetase, PfACS12	0.0021	0.014	0.013	1.14E+07
44	PFD0670c	lysine decarboxylase-like protein, putative	0.0112	0.029	0.0228	401895.75
45	PF14_0225	conserved Plasmodium membrane protein, unknown function	0.2561	0.1462	0.047	6.9898176
46	PF11_0022	Plasmodium falciparum isolate 3D7	0.0526	0.5163	0.0438	8.96484
47	PFF1415c	DNAJ domain protein, putative	0.2053	0.0938	0.0068	7.022723
48	PFF1155w	hexokinase	0.28	0.5026	0.0232	12.982066
49	MAL13P1.214	phosphoethanolamine N-methyltransferase	0.0174	0.0097	0.0164	10993.473
50	MAL8P1.69	14-3-3 protein, putative	0.0043	0.0026	0.0084	9662.6875

51	PF07_0029	heat shock protein 86	0.0068	0.0038	0.0099	13166.518
52	PF11_0062	histone H2B	0.0048	0.011	0.0088	63778.395
53	PF14_0655	helicase 45	0.0146	0.0074	0.014	6059.1396
54	PFF0435w	ornithine aminotransferase	0.0039	0.0026	0.0036	110060.445
55	PFF0940c	cell division cycle protein 48 homologue, putative	0.0018	8.00E-04	0.0044	1565719.9
56	PFI1445w	High molecular weight rhoptry protein-2	0.0123	0.0069	0.0136	247374.11
57	PFL1070c	endoplasmin homolog precursor, putative	0.0079	0.0051	0.0115	8187.7944
58	PF11_0061	histone H4	0.0049	7.00E-04	0.0033	11884.197
59	PFE0080c	rhoptry-associated protein 2, RAP2	0.0075	0.0023	0.0106	51006.152
60	PF10_0268	merozoite capping protein 1	0.0558	0.0558	0.0373	147606.03
61	PF10_0155	enolase	0.0093	0.0056	0.0114	865223
62	PFI1090w	S-adenosylmethionine synthetase	0.0046	0.0026	0.0083	57857.81
63	PF11_0301	spermidine synthase	0.0119	0.0073	0.0134	49951.715
64	PF14_0102	rhoptry-associated protein 1, RAP1	0.0084	0.0056	0.0117	11946.328
65	PF14_0230	60S ribosomal protein L5, putative	0.001	0	0.0019	557175.44
66	PFI0880c	glideosome-associated protein 50	0.0055	0.0031	0.0097	18422.475
67	PFC0835c	conserved protein, unknown function	0.004	0.0023	0.0087	17025.895
68	PF10_0024	Plasmodium exported protein hyp2, unknown function	0.065	0.0012	0.0257	6.5501328
69	PF11_0186	conserved Plasmodium protein, unknown function	0.0198	0.0198	0.0198	2.73E+11
70	PF11_0437	60S ribosomal protein L28, putative	0.0919	0.0163	0.0051	16626.283
71	PFI0030c	rifin	0.003	0.0106	0.0081	9.72E+07
72	PF14_0261	proliferation-associated protein 2g4, putative	0.0182	0.0102	0.0041	2.23E+07
73	PF10_0057	regulator of nonsense transcripts, putative	0.0558	0.0558	0.0367	1.12E+15
74	MAL7P1.155	Zinc finger, C3HC4 type, putative	0.0558	0.0558	0.0367	1.12E+15
75	PF14_0260	metabolite/drug transporter, putative	0.016	0.008	0.0027	1.37E+08
76	PF14_0166	lysine-tRNA ligase, putative	0.0558	0.0558	0.0367	1.12E+15
77	PFE0175c	unconventional myosin pfm-b	0.0558	0.0558	0.0367	1.12E+15
78	MAL13P1.60	erythrocyte binding antigen-140	0.258	0.0477	0.0451	7.039224
79	PF14_0124	actin II	0.0182	0.0102	0.0041	2.75E+09

80	PFB0585w	Leu/Phe-tRNA protein transferase, putative	0.0558	0.0558	0.0367	1.12E+15
81	PF10_0131	conserved Plasmodium protein, unknown function	0.0558	0.0558	0.0367	1.12E+15
82	MAL8P1.41	RWD domain-containing protein, putative	0.0558	0.0558	0.0367	1.12E+15
83	PFL0670c	bifunctional aminoacyl-tRNA synthetase, putative	0.238	0.1296	0.0364	7.004916
84	PF11_0303	26S proteasome regulatory complex subunit, putative	0.0558	0.0558	0.0367	1.12E+15
85	PFL1425w	t-complex protein 1, gamma subunit, putative	0.054	0.0195	0.0345	2214439.2
86	PF11_0302	conserved Plasmodium protein, unknown function	0.0165	0.0165	0.0165	2011196.2
87	PF14_0363	metacaspase-like protein	0.0898	0.0898	0.0195	1.48E+09
88	PFL1880w	acyl-CoA synthetase, PfACS11	0.0898	0.0898	0.0195	2.40E+07
89	PF14_0493	sortilin, putative	0.054	0.054	0.0165	271689.38
90	MAL13P1.293	conserved Plasmodium protein, unknown function	0.0183	0.0183	0.0183	956046.3
91	PF11_0096	casein kinase II, alpha subunit	0.0183	0.0183	0.0183	312984.72
92	PFI0345w	GTPase activator, putative	0.0183	0.0183	0.0183	4497137.5

Key:

Treatment significant	Time significant	Interaction significant

Table 12: Detected Acetylation sites (an addition of an acetyl group, either at the N-terminus of the protein or at lysine)

Annotation	Sequence	Modifications
6hrs - untreated		
HSP70	ASAKGSKPNLPESNI	Protein Terminal Acetyl@N-term; Phospho(S)@2; Deamidated(N)@9; Deamidated(N)@14
Actin	GEEDVQALVVDNGSGNVK	Protein Terminal Acetyl@N-term
Actin	GEEDVQALVVDNGSGNVK	Protein Terminal Acetyl@N-term; Deamidated(N)@12
Actin	GEEDVQALVVDNGSGNVK	Protein Terminal Acetyl@N-term; Deamidated(N)@12
Parasitophorous vacuole antigen	GATVSHTK	Acetyl@N-term
Parasitophorous vacuole antigen	GATVSHTK	Acetyl@N-term

Parasitophorous vacuole antigen	GATVSHTK	Acetyl@N-term
Parasitophorous vacuole antigen	GATVSHTK	Acetyl@N-term
Parasitophorous vacuole antigen	GATVSHTK	Acetyl@N-term
HSP90	STETFAFNADIR	Protein Terminal Acetyl@N-term
HSP90	STETFAFNADIR	Protein Terminal Acetyl@N-term
HSP90	STETFAFNADIR	Protein Terminal Acetyl@N-term
HSP90	STETFAFNADIR	Protein Terminal Acetyl@N-term
EMP1	MARPSGSAGGGAGGKKEDESAK	Protein Terminal Acetyl@N-term; Oxidation(P)@4; Phospho(S)@5; Phospho(S)@7
EMP1	MARPSGSAGGGAGGKKEDESAK	Protein Terminal Acetyl@N-term; Oxidation(R)@3; Phospho(S)@5
EMP1	ARPSGSAGGGAGGK	Protein Terminal Acetyl@N-term; Deamidated(R)@2; Phospho(S)@4
EMP1	ARPSGSAGGGAGGK	Protein Terminal Acetyl@N-term; Deamidated(R)@2; Phospho(S)@6
EMP1	ARPSGSAGGGAGGK	Protein Terminal Acetyl@N-term; Oxidation(K)@14
Transcription factor with AP2 domain(s) (putative)	KERKKVSK	Protein Terminal Acetyl@N-term; Deamidated(R)@3; Phospho(S)@7; Carbamyl(K)@8
14-3-3 protein	SKANVHNKNVAATYRKK	Protein Terminal Acetyl@N-term; Oxidation(K)@8; Deamidated(N)@9; Phospho(T)@13
PfEMP1	VNQNGGGGGK	Protein Terminal Acetyl@N-term
Histone H2A	MSAKGKTGRK	Protein Terminal Acetyl@N-term; Phospho(S)@2; Oxidation(K)@6; Phospho(T)@7
Histone H2A	MSAKGKTGRKKASKGTSNSAK	Protein Terminal Acetyl@N-term; Phospho(T)@7; Oxidation(K)@14; Phospho(S)@19
Phosphoribosylpyrophosphate synthetase (putative)	MSFFVSK	Protein Terminal Acetyl@N-term; Oxidation(F)@4; Oxidation(K)@7
PfEMP1	MVAAAKGGGSSQDAK	Protein Terminal Acetyl@N-term; Oxidation(K)@6
Hypothetical protein - function unknown	SSIRPELK	Protein Terminal Acetyl@N-term; Phospho(S)@2; Oxidation(K)@8
Tubulin alpha	MFSAVGGGTGSGF	Protein Terminal Acetyl@N-term; Phospho(S)@3; Phospho(S)@11; Oxidation(F)@13
Tubulin alpha	FSAVGGGTGSGFGCLMLERLSVDYGKKSK	Protein Terminal Acetyl@N-term; Phospho(S)@2; Carbamidomethyl(C)@14
Merozoite capping protein 1 (putative)	AQLAENTVLDESIQK	Protein Terminal Acetyl@N-term
HSP90	AQLAENTVLDESIQK	Protein Terminal Acetyl@N-term
Histone H4	MSGRGKGGKGLGKGGAK	Protein Terminal Acetyl@N-term; Phospho(S)@2; Oxidation(K)@13; Carbamyl(K)@17
Histone H4	MSGRGKGGKGLGKGGAK	Protein Terminal Acetyl@N-term; Phospho(S)@2; Oxidation(K)@13; Carbamyl(K)@17
PfEMP1	GTGSSTPSVPK	Protein Terminal Acetyl@N-term; Phospho(T)@2
Metacaspase-like protein (putative)	LSSMDNR	Protein Terminal Acetyl@N-term; Phospho(S)@3; Deamidated(N)@6

6hrs - treated		
Actin	GEEDVQALVVDNGSGNVK	Protein Terminal Acetyl@N-term; Deamidated(N)@12
Actin	GEEDVQALVVDNGSGNVK	Protein Terminal Acetyl@N-term; Deamidated(N)@12
Actin	GEEDVQALVVDNGSGNVK	Protein Terminal Acetyl@N-term; Deamidated(N)@12
Actin	GEEDVQALVVDNGSGNVK	Protein Terminal Acetyl@N-term
Hypothetical protein - function unknown	MSLKNSK	Protein Terminal Acetyl@N-term; Oxidation(N)@5; Phospho(S)@6
Hypothetical protein - function unknown	MSSKSDR	Protein Terminal Acetyl@N-term; Phospho(S)@5; Oxidation(R)@7
14-3-3 protein	ATSEELKQLR	Protein Terminal Acetyl@N-term
Phosphoglycerate kinase	LGNKLSISDLK	Protein Terminal Acetyl@N-term; Oxidation(K)@4; Phospho(S)@8; Oxidation(D)@9
HSP70	ASLNKKNIVK	Protein Terminal Acetyl@N-term; Phospho(S)@2; Deamidated(N)@4; Oxidation(K)@10
PfEMP1	EPHGGSGGGGDVIDHQSAKHLL	Protein Terminal Acetyl@N-term; Oxidation(H)@15; Phospho(S)@17
PfEMP1	MARPSGSAGGGAGGKKEDESAK	Protein Terminal Acetyl@N-term; Phospho(S)@5
Tubulin alpha	KLADNCTGLQGFLMFSAVGGGTGSGFGCLM	Deamidated(N)@5; Carbamidomethyl(C)@6; Oxidation(F)@12; Oxidation(M)@14; Phospho(S)@16; Carbamidomethyl(C)@28
PfEMP1	MARPGSGGGGSSQDAK	Protein Terminal Acetyl@N-term; Deamidated(R)@3; Phospho(S)@12
HSP90	STETFAFNADIR	Protein Terminal Acetyl@N-term
HSP90	MSTETFAFNADIR	Protein Terminal Acetyl@N-term; Oxidation(F)@8; Oxidation(N)@9; Oxidation(R)@13
HSP90	STETFAFNADIR	Protein Terminal Acetyl@N-term
HSP90	STETFAFNADIR	Protein Terminal Acetyl@N-term
12hrs-untreated		
ribosomal protein S19s	AEQFTEDIGVVNKR	Protein Terminal Acetyl@N-term
12hr treated		
phosphoglycerate mutase	TTYTLVLLR	Protein Terminal Acetyl@N-term
18hrs - untreated		

HSP90	IGLKEYVDRMK	Protein Terminal Acetyl@N-term; Deamidated(R)@9
HSP90	STETFAFNADIR	Protein Terminal Acetyl@N-term
HSP90	STETFAFNADIR	Protein Terminal Acetyl@N-term
HSP90	STETFAFNADIR	Protein Terminal Acetyl@N-term; Phospho(T)@2
HSP90	STETFAFNADIR	Protein Terminal Acetyl@N-term
HSP90	STETFAFNADIR	Protein Terminal Acetyl@N-term
HSP90	STETFAFNADIR	Protein Terminal Acetyl@N-term
HSP70	ASAKGSKPNLPESNI	Protein Terminal Acetyl@N-term; Phospho(S)@6
HSP70	MASAKGSKPNLPESNIAIGIDLGTTYSCVGVWR	Protein Terminal Acetyl@N-term; Phospho(S)@3; Dioxidation(Y)@26; Carbamidomethyl(C)@28; Oxidation(W)@32
Phosphoglycerate kinase	KSSVVSLF	Protein Terminal Acetyl@N-term; Phospho(S)@6
Phosphoglycerate kinase	LGNKLSISDLKDIKNK	Protein Terminal Acetyl@N-term; Phospho(S)@6; Phospho(S)@8; Phospho(K)@16
Glyceraldehyde-3-phosphate dehydrogenase, putative	AVTKLGINGFGRIGR	Protein Terminal Acetyl@N-term; Phospho(T)@3; Deamidated(R)@15
Glyceraldehyde-3-phosphate dehydrogenase, putative	AVTKLGINGFGRIGR	Protein Terminal Acetyl@N-term; Phospho(T)@3; Oxidation(K)@4; Dioxidation(R)@12
Glyceraldehyde-3-phosphate dehydrogenase	AVTKLGINGFGR	Protein Terminal Acetyl@N-term; Oxidation(K)@4; Oxidation(F)@10; Oxidation(R)@12
Actin	GEEDVQALVVDNGSGNVK	Protein Terminal Acetyl@N-term; Deamidated(N)@12
Actin	GEEDVQALVVDNGSGNVK	Protein Terminal Acetyl@N-term; Deamidated(N)@12
Actin	GEEDVQALVVDNGSGNVK	Protein Terminal Acetyl@N-term
Actin	GEEDVQALVVDNGSGNVK	Protein Terminal Acetyl@N-term; Deamidated(N)@16
Actin	GEEDVQALVVDNGSGNVK	Protein Terminal Acetyl@N-term; Deamidated(N)@12
Actin	GEEDVQALVVDNGSGNVK	Protein Terminal Acetyl@N-term
Actin	GEEDVQALVVDNGSGNVK	Protein Terminal Acetyl@N-term; Deamidated(N)@12
Actin	GEEDVQALVVDNGSGNVK	Protein Terminal Acetyl@N-term
Cell division cycle protein 48 (putative)	EDNTDKKALVDENNGENK	Protein Terminal Acetyl@N-term; Phospho(T)@4; Deamidated(N)@14; Oxidation(N)@17
Elongation factor 2 (putative)	VNFTVDQVR	Protein Terminal Acetyl@N-term; Oxidation(F)@3
Enolase	AHVITRINAR	Protein Terminal Acetyl@N-term; Phospho(T)@5; Dioxidation(R)@6; Deamidated(N)@8
Enolase	AHVITRINAR	Protein Terminal Acetyl@N-term; Carbamyl(R)@6; Oxidation(N)@8; Oxidation(R)@10
HSP60 (putative)	MVKQVAANTNDK	Protein Terminal Acetyl@N-term; Phospho(T)@9; Carbamyl(K)@12

HSP60 (putative)	MVKQVAANTNDK	Protein Terminal Acetyl@N-term; Oxidation(K)@12
14-3-3 protein	ADAMRTL	Protein Terminal Acetyl@N-term
14-3-3 protein	LIEMADAMR	Protein Terminal Acetyl@N-term; Oxidation(M)@4
HSP70	MYTTPTSINLKTK	Protein Terminal Acetyl@N-term; Phospho(T)@3; Phospho(S)@7; Phospho(T)@12
Phosphoethanolamine N-methyltransferase	NRNYISSGGLEATK	Protein Terminal Acetyl@N-term; Dehydrated(T)@13
Erythrocyte membrane protein 3	ATIKKYHIRGR	Protein Terminal Acetyl@N-term; Phospho(T)@2; Oxidation(K)@4; Oxidation(Y)@6
T-complex protein 1, gamma subunit	MLKNPGTVLVFKPNTK	Protein Terminal Acetyl@N-term; Deamidated(N)@4
T-complex protein 1, gamma subunit	MLKNPGTVLVFKPNTK	Protein Terminal Acetyl@N-term; Deamidated(N)@4
Elongation factor 1-gamma (putative)	ISKNINKTK	Protein Terminal Acetyl@N-term; Phospho(S)@2; Oxidation(N)@4; Phospho(T)@8
Conserved GTP-binding protein (putative)	MGLVGLPNVGK	Protein Terminal Acetyl@N-term; Oxidation(P)@7; Oxidation(K)@11
Chaperonin, 60 kDa	SHLMSLPIVLLK	Protein Terminal Acetyl@N-term
Hypothetical PIESP2 erythrocyte surface protein	GKRSYPKSGHK	Protein Terminal Acetyl@N-term; Carbamyl(K)@7; Phospho(S)@8; Oxidation(H)@10
Lysyl-tRNA synthetase	MRVSASGQKLR	Protein Terminal Acetyl@N-term; Phospho(S)@4; Oxidation(K)@9
Lysyl-tRNA synthetase	MRVSASGQKLR	Protein Terminal Acetyl@N-term; Oxidation(R)@2; Phospho(S)@6; Deamidated(Q)@8
Chaperonin containing TCP-1 delta subunit	AVAHPTAK	Protein Terminal Acetyl@N-term
T-complex protein 1 epsilon subunit (putative)	MNIAIDEYGQPFVILR	Protein Terminal Acetyl@N-term
DnaJ homolog	FFSSGFPFDSMGGQQARR	Protein Terminal Acetyl@N-term; Oxidation(P)@7; Oxidation(M)@11; Deamidated(Q)@15
Proteasome 26S regulatory subunit (putative)	TAEDKKAVSIQVPVKDVDDK	Protein Terminal Acetyl@N-term; Oxidation(K)@6; Phospho(S)@9
Ubiquitin-activating enzyme e1	QNKTPPLKK	Protein Terminal Acetyl@N-term; Phospho(T)@4; Oxidation(P)@6; Oxidation(K)@9
DNA/RNA-binding protein	MTKKPTFYARIGK	Protein Terminal Acetyl@N-term; Phospho(T)@2; Oxidation(K)@3; Oxidation(K)@13
DNA/RNA-binding protein	ASTEEVSQER	Protein Terminal Acetyl@N-term
Ribosomal protein S4 (putative)	GKGIKKHLK	Protein Terminal Acetyl@N-term
Translation elongation factor 1 beta-related	ASNASLLNVK	Protein Terminal Acetyl@N-term
Translation elongation factor 1 beta-related	ASNASLLNVK	Protein Terminal Acetyl@N-term; Phospho(S)@5; Oxidation(N)@8
Translation elongation factor 1 beta-related	ASNASLLNVK	Protein Terminal Acetyl@N-term; Phospho(S)@5
Hypothetical protein	MVTNLGLMVTNLGLK	Protein Terminal Acetyl@N-term; Phospho(T)@10; Deamidated(N)@11
18hrs - treated		

Glyceraldehyde-3-phosphate dehydrogenase	MAVTKLGINGFGR	Protein Terminal Acetyl@N-term; Oxidation(K)@5; Deamidated(R)@13
Actin	GEEDVQALVVDNGSGNVK	Protein Terminal Acetyl@N-term; Deamidated(N)@12
Actin	GEEDVQALVVDNGSGNVK	Protein Terminal Acetyl@N-term; Deamidated(N)@12
Actin	GEEDVQALVVDNGSGNVK	Protein Terminal Acetyl@N-term; Deamidated(N)@12
Actin	GEEDVQALVVDNGSGNVK	Protein Terminal Acetyl@N-term; Deamidated(N)@12
Actin	GEEDVQALVVDNGSGNVK	Protein Terminal Acetyl@N-term; Deamidated(N)@12
Actin	GEEDVQALVVDNGSGNVK	Protein Terminal Acetyl@N-term; Deamidated(N)@12
HSP90	STETFAFNADIR	Protein Terminal Acetyl@N-term
HSP90	STETFAFNADIR	Protein Terminal Acetyl@N-term
HSP90	STETFAFNADIR	Protein Terminal Acetyl@N-term
HSP90	STETFAFNADIR	Protein Terminal Acetyl@N-term
HSP90	MSTETFAFNADIR	Protein Terminal Acetyl@N-term; Oxidation(F)@8; Oxidation(N)@9; Oxidation(R)@13
HSP90	STETFAFNADIR	Protein Terminal Acetyl@N-term
HSP90	STETFAFNADIR	Protein Terminal Acetyl@N-term
HSP90	STETFAFNADIR	Protein Terminal Acetyl@N-term
HSP90	STETFAFNADIR	Protein Terminal Acetyl@N-term
HSP90	STETFAFNADIR	Protein Terminal Acetyl@N-term
RNA helicase-1	MVVGTPGRVYDMIDK	Protein Terminal Acetyl@N-term; Deamidated(R)@8
14-3-3 protein	MSKANVHNKNVAATYRK	Protein Terminal Acetyl@N-term; Oxidation(H)@7; Dioxidation(K)@9; Oxidation(Y)@15
14-3-3 protein	MSKANVHNKNVAATYRK	Protein Terminal Acetyl@N-term; Bromo(Y)@15
Karyopherin beta	DKIVEVIEGLSSSESHIR	Protein Terminal Acetyl@N-term; Oxidation(K)@2; Deamidated(R)@18
Membrane-associated calcum-binding protein	MMKINLYK	Protein Terminal Acetyl@N-term; Oxidation(K)@3; Oxidation(K)@8
Chaperonin cpn60, mitochondrial precursor	SSFDNNYLSLLGSANTLIVKKDR	Protein Terminal Acetyl@N-term; Oxidation(K)@21; Oxidation(D)@22; Deamidated(R)@23
Hypothetical protein	MQHENFKRMLMFGLRSLSDFCNPTSK	Protein Terminal Acetyl@N-term; Oxidation(K)@7; Oxidation(R)@8; Oxidation(M)@9; Carbamidomethyl(C)@21
Tubulin beta	MREIVHIQAGQCGNQIGAKF	Protein Terminal Acetyl@N-term; Dioxidation(R)@2; Carbamidomethyl(C)@12; Deamidated(N)@14; Deamidated(Q)@15
Ookinete protein-related	MSDILYGNSLSNGKK	Protein Terminal Acetyl@N-term; Deamidated(N)@12
Ookinete protein-related	MSDILYGNSLSNGKK	Protein Terminal Acetyl@N-term; Deamidated(N)@8
Proteasome 26S regulatory subunit (putative)	MTAEDKKAVSIQVPVKDVDDK	Oxidation(K)@7; Dioxidation(P)@14; Dioxidation(K)@16; Oxidation(K)@21

Proteasome 26S regulatory subunit (putative)	TAEDKKAVSIQVPVKDVDDKRRKLNNSKIKK	Deamidated(Q)@11; Oxidation(P)@13; Oxidation(K)@30; Dioxidation(K)@31
Proteasome 26S regulatory subunit (putative)	TAEDKKAVSIQVPVKDVDDKRRKLNNSKIKK	Oxidation(K)@5; Oxidation(K)@23; Oxidation(N)@25
Hypothetical protein	LERNNKNIKLLITDDISR	Protein Terminal Acetyl@N-term; Oxidation(N)@4; Oxidation(K)@6; Deamidated(N)@7
Nucleosome assembly protein 1	AANEGNQPIPPEEEKEISSLLESIK	Protein Terminal Acetyl@N-term
Conserved GTP-binding protein, putative	MGLVGLPNVGK	Protein Terminal Acetyl@N-term; Oxidation(P)@7; Oxidation(N)@8
High molecular weight rhoptry protein 3	KFLDKEQR	Protein Terminal Acetyl@N-term; Oxidation(D)@4
CCAAT-box DNA binding protein subunit B, putative	MPLGMIPNLIK	Protein Terminal Acetyl@N-term; Oxidation(P)@2; Deamidated(N)@8; Oxidation(K)@11
Pvstp1	MLMVIEFDDPIK	Protein Terminal Acetyl@N-term
6-phosphofructokinase	DTKSGDKNAANKGGADGLVKTVSVLLRDNK	Protein Terminal Acetyl@N-term; Oxidation(D)@6; Oxidation(N)@11; Oxidation(K)@30

Key	
	Proteins (Set 1) implicated in alpha,beta unsaturated sequiterpene lactone induced cell growth inhibition*
	Set 1 PTMs not observed in corresponding comparative group
	Corresponding peptide sequence to above, unmodified
	Set 1 PTMs observed in corresponding comparative group
	Set 1 protein peptide sequences not detected in corresponding comparative group

*PTMs implicated are the acetylation/methylation of histones, ubiquitination and subsequent degradation of histone deacetylase by the proteosome, and carboxy-terminal cleavage of alpha-tubulin

Table 13: Detected Methylation sites (an addition of a methyl group, usually at lysine or arginine residues)

Annotation	Sequence	Modifications
6hrs - untreated		
HSP 70 (putative)	ITPSYVSFVDGER	Dimethyl(R)@13
HSP 70 (putative)	GVPKIEVTFTVDK	Methyl(E)@6; Oxidation(F)@9; Oxidation(K)@13
HSP 70 (putative)	DTTFAPEQISAMVLEK	Methyl(E)@7; Deamidated(Q)@8
HSP 70 (putative)	NAVVTVPAYFNDAQR	Methyl(N)@1; Deamidated(N)@11; Oxidation(R)@15
HSP 70 (putative)	NAVVTVPAYFNDAQR	Methyl(T)@5; Oxidation(R)@15
HSP 70 (putative)	IEVTFTVDKNGILHVEAEDKGTGKSR	Phospho(T)@4; Deamidated(N)@10; Oxidation(D)@19; Methyl(T)@22
Glyceraldehyde-3-phosphate dehydrogenase	IVSNASCTTNCLAPLAK	Methyl(I)@1; Carbamidomethyl(C)@7; Methyl(T)@9; Carbamidomethyl(C)@11
Glyceraldehyde-3-phosphate dehydrogenase	CALSNIIPASTGAAK	Carbamidomethyl(C)@1; Methyl(L)@3
Glyceraldehyde-3-phosphate dehydrogenase	VPIGTVSVVDLVCR	Carbamidomethyl(C)@13; Methyl(R)@14
Glyceraldehyde-3-phosphate dehydrogenase	VLPELNGKLTGVAF	Oxidation(P)@3; Methyl(L)@9
Glyceraldehyde-3-phosphate dehydrogenase	AVTKLGINGFGRIGR	Phospho(T)@3; Methyl(L)@5; Oxidation(R)@12; Oxidation(R)@15
Translation elongation factor EF-1, subunit alpha	YEEIKKEVK	Methyl(K)@9
Translation elongation factor EF-1, subunit alpha	YEEIKKEVK	Methyl(K)@9
Translation elongation factor EF-1, subunit alpha	YEEIKKEVK	Methyl(K)@6
Translation elongation factor EF-1, subunit alpha	YEEIKKEVK	Methyl(K)@9
Translation elongation factor EF-1, subunit alpha	YEEIKKEVK	Methyl(K)@9
Endoplasmin homolog precursor	MNVSNSDQIKAMSGQK	Oxidation(N)@2; Deamidated(N)@5; Methyl(K)@16
Endoplasmin homolog precursor	GVVDSDDLPLNVSR	Methyl(D)@4; Methyl(R)@14
Endoplasmin homolog precursor	VDLINNLGTIAK	Phospho(T)@9; Methyl(I)@10; Oxidation(K)@12
Endoplasmin homolog precursor	NILSITDTGIGMTK	Methyl(N)@1; Phospho(S)@4
Endoplasmin homolog precursor	DNNVDNESNDK	Deamidated(N)@3; Phospho(S)@8; Methyl(D)@10
Endoplasmin homolog precursor	NIDVLFLTESVDESCIQR	Phospho(S)@10; Methyl(D)@12; Carbamidomethyl(C)@15; Deamidated(Q)@17
HSP70	DAGTIAGLNVMR	Oxidation(N)@9; dethiomethyl(M)@11; Methyl(R)@12

HSP70	DAGTIAGLNVMR	Methyl(N)@9; dethiomethyl(M)@11; Oxidation(R)@12
HSP70	SVHEVVLVGGSTR	Methyl(E)@4; Phospho(T)@12
HSP70	VLKDAMMDK	Methyl(D)@4; Oxidation(K)@9
Actin	SYELPDGNIITVGNER	Methyl(T)@11
Actin	SYELPDGNIITVGNER	Methyl(E)@15
Actin	TSEQSSDIEK	Phospho(T)@1; Deamidated(Q)@4; Methyl(D)@7; Oxidation(K)@10
Parasitophorous vacuole antigen	AGRSSGTGGSVGTKISPGSQGQGKVAGPQLPR	Phospho(T)@7; Methyl(S)@10; Formyl(K)@14
Parasitophorous vacuole antigen	RGLTLPSESPSESSSK	Phospho(R)@1; Phospho(T)@4; Oxidation(P)@10; Methyl(S)@15
Parasitophorous vacuole antigen	AGRSSGTGGSVGTK	Methyl(T)@7; Phospho(T)@13; Oxidation(K)@14
Parasitophorous vacuole antigen	NVGVSRDTLDK	Oxidation(D)@7; Phospho(T)@8; Methyl(L)@9
Parasitophorous vacuole antigen	SSALYVANCSKR	Phospho(S)@2; Oxidation(N)@8; Carbamidomethyl(C)@9; Methyl(S)@10; Oxidation(R)@12
RNA pseudouridylate synthase, putative	SETEASNKNVESNDNVDGK	Phospho(T)@3; Phospho(S)@6; Methyl(D)@14
RNA pseudouridylate synthase, putative	NEIYEIMINSLNK	Phospho(S)@10; Methyl(N)@12
RNA pseudouridylate synthase, putative	NSSNIRSSSNIR	Deamidated(R)@6; Methyl(S)@8; Phospho(S)@9
RNA pseudouridylate synthase, putative	QQNISNTSGNMKNSSNIR	Oxidation(N)@3; Deamidated(N)@10; Deamidated(N)@13; Dimethyl(R)@18
Dynein axonemal heavy chain	TNMNRNIFKALAKK	Deamidated(N)@4; Deamidated(N)@6; Oxidation(K)@13; Trimethyl(K)@14
Dynein axonemal heavy chain	ISIALNKLADAR	Methyl(I)@1; Phospho(S)@2
Dynein axonemal heavy chain	SNQKIYTNELNNITNENY	Phospho(S)@1; Oxidation(K)@4; Methyl(E)@16
Peptidase, putative	SSTSLNNKRGRKGKNK	Deamidated(R)@11; Methyl(K)@16
Peptidase, putative	DDTNIMNNFK	Phospho(T)@3; Methyl(N)@4; Deamidated(N)@8; Oxidation(K)@10
Peptidase, putative	NAENYVSTIFGRVQFLYK	Deamidated(N)@4; Phospho(T)@8; Methyl(R)@12; Oxidation(K)@18
Peptidase, putative	KDDINKNINEDINK	Oxidation(D)@3; Methyl(N)@9; Deamidated(N)@13
Hypothetical protein	KKQSEKEQYEQK	Oxidation(K)@1; Dehydrated(E)@10; Methyl(K)@12
Hypothetical protein	NNPEGIGNTGKR	Deamidated(N)@2; Phospho(T)@9; Methyl(K)@11
EMP1	ARPSGSAGGGAGGK	Methyl(K)@14
EMP1	ARPSGSAGGGAGGKKEDESAK	Methyl(S)@6; Phospho(S)@19
EMP1	NGESRSGSDGNK	Deamidated(N)@1; Phospho(S)@6; Methyl(S)@8

EMP1	RSVETSGSSGGSGATGKSDGSI	Deamidated(R)@1; Phospho(S)@2; Dioxidation(K)@17; Methyl(S)@21
EMP1	AASTISELAGITDTCKRVQKYYEHFNVGAAR	Phospho(S)@6; Carbamidomethyl(C)@15; Methyl(R)@31
EMP1	TATSEGSSESGR	Phospho(S)@8; Methyl(R)@12
10b antigen, putative	KRGSDLYNNSKKESANDYTNDNQMNNNTK	Methyl(D)@17; Oxidation(N)@20; Phospho(T)@28
Chloroquine resistance marker protein	VISSSKRDNSVKLNAKFSEYK	Methyl(D)@8; Phospho(S)@18; Oxidation(K)@21
Chloroquine resistance marker protein	HSSFTYNARNK	Phospho(S)@3; Methyl(T)@5; Oxidation(Y)@6
Chloroquine resistance marker protein	VDTSKCYNDTNKKNEK	Oxidation(D)@2; Phospho(T)@3; Carbamidomethyl(C)@6; Deamidated(N)@8; Trimethyl(K)@16
Chloroquine resistance marker protein	ISRNIKVSNCLNKSLKVK	Phospho(S)@2; Carbamidomethyl(C)@10; Deamidated(N)@12; Oxidation(K)@16; Methyl(K)@18
Ornithine aminotransferase	VLMMNTGAEASETAYKLCR	Deamidated(N)@5; Methyl(S)@11; Phospho(T)@13; Carbamidomethyl(C)@18; Deamidated(R)@19
Hypothetical protein	NTNKNKNTNK	Oxidation(N)@9; Methyl(K)@10
Hypothetical protein	ASKIIGLLNCK	Deamidated(N)@9; Carbamidomethyl(C)@10; Methyl(K)@11
Pyruvate kinase, putative	SAVETAESIQASLII	Methyl(S)@8
Pyruvate kinase, putative	QILEPNNVNLR	Methyl(E)@4
Dynein heavy chain	DDITQNYVNII	Methyl(D)@2; Deamidated(Q)@5
Dynein heavy chain	IHPAISSDL	Phospho(S)@6; Phospho(S)@7; Methyl(D)@8
Dynein heavy chain	LSKSYNEKR	Phospho(S)@2; Deamidated(N)@6; Trimethyl(K)@8; Phospho(R)@9
Dynein heavy chain	NITNLKNVVNEEISKSFDLLNDSLNNLNK	Phospho(T)@3; Methyl(N)@4; Deamidated(N)@7; Oxidation(N)@21
Dynein heavy chain	FSIEDNLKDCTK	Phospho(S)@2; Methyl(D)@5; Carbamidomethyl(C)@10
Dynein heavy chain	FSIEDNLKDCTKGNYNLK	Methyl(I)@3; Carbamidomethyl(C)@10; Phospho(T)@11
Dynein heavy chain	SKVILSSLLDQEHKWNNKK	Phospho(S)@1; Oxidation(D)@10; Trimethyl(K)@19
Merozoite surface protein 1 precursor	VITGLTETQK	Methyl(T)@6; Phospho(T)@8; Oxidation(K)@10

Merozoite surface protein 1 precursor	VDVTPKSQDPTK	Methyl(T)@4; Deamidated(Q)@8
Merozoite surface protein 1 precursor	NPPPANSGNTPNTLLDKNK	Phospho(S)@7; Oxidation(N)@9; Deamidated(N)@12; Methyl(D)@16
Merozoite surface protein 1 precursor	VVENSIEHK	Deamidated(N)@4; Phospho(S)@5; Methyl(I)@6
Merozoite surface protein 1 precursor	VVENSIEHK	Deamidated(N)@4; Phospho(S)@5; Methyl(I)@6
PfEMP1	EAPSGPASTASASVNSGNTATTGK	Glu->pyro-Glu@N-term; Phospho(T)@9; Trimethyl(K)@24
PfEMP1	IYKKQKGNCKKESAGATEF	Oxidation(Y)@2; Oxidation(K)@3; Carbamidomethyl(C)@9; Methyl(E)@18; Oxidation(F)@19
HECT-domain (ubiquitin-transferase), E3 putative	KQTQNGNNNSEICSTSSFLNSFVKNTNGNNKKK	Phospho(T)@3; Carbamidomethyl(C)@13; Oxidation(F)@18; Methyl(N)@25; Deamidated(N)@30
Hypothetical protein	ITYDYSSINSLKKLSYNNLTRASCY	Deamidated(N)@17; Oxidation(N)@18; Methyl(T)@20; Phospho(S)@23; Carbamidomethyl(C)@24
Hypothetical protein	KLKKIQLLNKR	Oxidation(K)@1; Methyl(L)@2; Oxidation(K)@3
Hypothetical protein PF14_0419	KNETNISPNSDIK	Oxidation(N)@2; Phospho(S)@7; Methyl(D)@11
Hypothetical protein PF14_0419	INTCKIINIK	Carbamidomethyl(C)@4; Methyl(K)@10
PfEMP1	ETVETDSTDGPK	Phospho(T)@2; Methyl(E)@4; Oxidation(D)@6
Hypothetical protein	NNSISSSTNNYYK	Methyl(S)@5; Phospho(T)@8; Deamidated(N)@9
Hypothetical protein	SNHNNKNNNNNK	Phospho(S)@1; Methyl(N)@5; Deamidated(N)@11
Hypothetical protein	NKLKNEKDLK	Oxidation(K)@4; Methyl(N)@5; Oxidation(K)@7
Hypothetical protein	GNVDDVNKNDSR	Methyl(D)@5; Deamidated(N)@9; Phospho(S)@11
Histone H2A	SAKGKTGRKK	Phospho(S)@1; Methyl(K)@5; Deamidated(R)@8; Dioxidation(K)@9
Histone H2A	GTSNSAKAGLQFPVGR	Deamidated(N)@4; Phospho(S)@5; Oxidation(P)@13; Methyl(R)@16
Histone H2A	ASKGTSNSAK	Phospho(T)@5; Methyl(S)@6; Deamidated(N)@7
Pre-mRNA splicing factor	FNTGSVGK	Methyl(S)@5; Oxidation(K)@8
Bromodomain, putative	TIVNNDNGTK	Phospho(T)@1; Methyl(T)@9

Hypothetical protein	NLSKGIIGSASIFIK	Phospho(S)@3; Methyl(S)@11; Oxidation(F)@13
Hypothetical protein	NLSKGIIGSASIFIK	Phospho(S)@3; Oxidation(F)@13; Methyl(K)@15
Hypothetical protein	NLSKGIIGSASIFIK	Phospho(S)@3; Oxidation(F)@13; Methyl(K)@15
Hypothetical protein	NLSKGIIGSASIFIK	Phospho(S)@3; Methyl(S)@11; Oxidation(K)@15
Hypothetical protein	NLSKGIIGSASIFIK	Phospho(S)@3; Oxidation(F)@13; Methyl(I)@14
Hypothetical protein	NLSKGIIGSASIFIK	Phospho(S)@3; Methyl(I)@14; Oxidation(K)@15
Hypothetical protein	KLFNNVDTKTSGEESANSLLKEK	Deamidated(N)@5; Phospho(T)@8; Oxidation(K)@9; Methyl(S)@15
Hypothetical protein	TTDGGKTTDEGK	Methyl(T)@7; Phospho(T)@8
PfEMP1	DTSSGSNDNLK	Oxidation(D)@1; Phospho(S)@3; Oxidation(N)@7; Methyl(D)@8
PfEMP1	CAQTKNGSVVGGGSGGGNSDSK	Carbamidomethyl(C)@1; Phospho(S)@19; Methyl(D)@20; Oxidation(K)@22
Hypothetical protein	KNNNNKKNNKK	Trimethyl(K)@1; Deamidated(N)@5
Hypothetical protein	NSEEGNLSAENVP	Oxidation(N)@1; Methyl(E)@4; Deamidated(N)@6
Hypothetical protein	KNSGDKKKNSGDIKKNSGDK	Deamidated(N)@2; Dioxidation(K)@6; Methyl(D)@12; Oxidation(K)@20
PfEMP1	PADSPPAGPATDSGK	Phospho(S)@4; Methyl(D)@12; Phospho(S)@13; Oxidation(K)@15
PfEMP1	PADSPPAGPATDSGK	Phospho(S)@4; Phospho(T)@11; Methyl(S)@13; Oxidation(K)@15
PfEMP1	PADSPPAGPATDSGK	Phospho(S)@4; Methyl(T)@11; Phospho(S)@13; Oxidation(K)@15
PfEMP1	LSDIPSTNK	Oxidation(D)@3; Phospho(S)@6; Methyl(K)@9
PfEMP1	SGDTTGGKDGATGKSDGSICVPPR	Methyl(D)@3; Phospho(T)@4; Carbamidomethyl(C)@20; Oxidation(P)@23
Cell division cycle protein 48	CGDTNISSYER	Carbamidomethyl(C)@1; Phospho(T)@4; Deamidated(N)@5; Methyl(S)@8
Hypothetical protein	NSKHLK	Phospho(S)@2; Methyl(K)@6

Hypothetical protein	NNENSNDESDGGNNK	Methyl(S)@5; Phospho(S)@9
Conserved Plasmodium protein	QKRPKKQK	Deamidated(R)@3; Methyl(Q)@7
Conserved Plasmodium protein	NSNENSNENSNK	Oxidation(N)@3; Deamidated(N)@7; Methyl(N)@9
Tubulin alpha	LIAQVISSLTASLRF	Phospho(T)@10; Phospho(S)@12; Methyl(R)@14; Oxidation(F)@15
Hypothetical protein	NELIKTLGKLENSTVLNK	Deamidated(N)@12; Methyl(K)@18
Elongation factor 2	GDDKLLTGKQLLK	Methyl(K)@9
Elongation factor 2	STLTDSLVSKAGIISSKNAGDAR	Phospho(S)@6; Phospho(S)@15; Phospho(S)@16; Methyl(N)@18
Hypothetical protein	KGKTSNGGNTK	Oxidation(K)@1; Phospho(T)@4; Methyl(N)@6
Hypothetical protein	NINHITNTLNKRK	Oxidation(N)@1; Methyl(T)@6; Phospho(T)@8
Hypothetical protein	GKTSNGGNTKKEQQK	Phospho(T)@9; Trimethyl(K)@15
PfEMP3	NIFMSDIFKSFIK	Deamidated(N)@1; Oxidation(M)@4; Phospho(S)@5; Methyl(I)@7
Hypothetical protein	SMLEYYSRVAKRNCNR	Methyl(E)@4; Phospho(S)@7; Oxidation(K)@11; Carbamidomethyl(C)@14; Oxidation(N)@15
Ubiquitin transferase, putative	HEVNTKEDSTSSFNMSK	Methyl(E)@2; Phospho(T)@5; Phospho(S)@16
Ubiquitin transferase, putative	IFSENMLGEK	Oxidation(F)@2; Phospho(S)@3; Methyl(K)@10
Ubiquitin transferase, putative	LLLNMIHLNSDDNIYYK	Methyl(D)@11; Oxidation(N)@13; Oxidation(K)@17
Ubiquitin transferase, putative	SVILNHLSETSVISGITICK	Methyl(L)@7; Phospho(S)@11; Carbamidomethyl(C)@19
Hypothetical protein	RDDLTNINNK	Deamidated(R)@1; Methyl(D)@3

Hypothetical protein	LDTYNSEILK	Methyl(D)@2; Phospho(T)@3; Oxidation(K)@10
Polyubiquitin	TITLDVEPSDTIENVK	Methyl(D)@5
Polyubiquitin	TITLDVEPSDTIENVK	Methyl(D)@5
Polyubiquitin	TITLDVEPSDTIENVK	Methyl(D)@5
Polyubiquitin	TITLDVEPSDTIENVK	Methyl(D)@5
Polyubiquitin	TITLDVEPSDTIENVK	Methyl(D)@5
Polyubiquitin	TITLDVEPSDTIENVK	Methyl(D)@5
Polyubiquitin	TITLDVEPSDTIENVK	Methyl(D)@5
Polyubiquitin	TITLDVEPSDTIENVK	Methyl(D)@5
Polyubiquitin	TITLDVEPSDTIENVK	Methyl(D)@5
Ubiquitin-protein ligase 1	EDFSNVATSIIR	Glu->pyro-Glu@N-term; Phospho(S)@4; Methyl(N)@5
Ubiquitin-protein ligase 1	FTTTTNDKK	Phospho(T)@3; Methyl(N)@6
Hypothetical protein	SLIPLNCNGAIKKSSTNTQK	Phospho(S)@1; Carbamidomethyl(C)@7; Methyl(Q)@19
Hypothetical protein	ESHGEYKER	Glu->pyro-Glu@N-term; Phospho(S)@2; Methyl(E)@5
Probable tRNA-methyltransferase	KKIKNIKNKKNIKNK	Methyl(K)@9; Phospho(K)@10
Probable tRNA-methyltransferase	TTITTTTTTKK	Phospho(T)@4; Methyl(K)@11
Asparagine/aspartate rich protein	DGNKTLDGNK	Deamidated(N)@3; Methyl(K)@10
Exported serine/threonine protein kinase	TTEANSQSLSKYDF	Phospho(S)@6; Methyl(K)@11; Oxidation(Y)@12; Oxidation(F)@14
Exported serine/threonine protein kinase	TTEANSQSLSKYDF	Phospho(S)@6; Oxidation(K)@11; Methyl(D)@13; Oxidation(F)@14

Exported serine/threonine protein kinase	KIGEQIACTNNDK	Deamidated(Q)@5; Carbamidomethyl(C)@8; Phospho(T)@9; Deamidated(N)@10; Methyl(D)@12
Hypothetical protein	KEADSKIEHLKVEHSK	Oxidation(D)@4; Oxidation(K)@6; Trimethyl(K)@11; Phospho(S)@15
Hypothetical protein	SHYFSPMFK	Phospho(S)@1; Methyl(S)@5
Myosin PfM-C	KPVNSNVANDIR	Methyl(N)@6; Deamidated(R)@12
Proteasome 26S regulatory subunit, putative	TTTANNTDNNK	Phospho(T)@2; Oxidation(N)@5; Oxidation(N)@6; Methyl(K)@11
Ubiquitin carboxyl-terminal hydrolase family 2, putative	MNMKSMTSFDK	Methyl(K)@4; Phospho(S)@5
Plasmepsin 1 precursor	SIENSHDR	Phospho(S)@1; Methyl(D)@7; Oxidation(R)@8
Plasmepsin 1 precursor	DLSIGSVDPVVVELK	Methyl(D)@8
Plasmepsin 1 precursor	DLSIGSVDPVVVELK	Methyl(D)@8
Plasmepsin 1 precursor	DLSIGSVDPVVVELK	Methyl(D)@8
Plasmepsin 1 precursor	GYLTIGGIEDR	Methyl(D)@10
Merozoite capping protein 1, putative	NVKSGKGSVSSSNK	Oxidation(N)@1; Methyl(S)@8; Phospho(S)@12
Hypothetical protein	SKMSDFSNAK	Oxidation(M)@3; Phospho(S)@7; Oxidation(N)@8; Methyl(K)@10
Hypothetical protein	YSNDMNEEIIKK	Phospho(S)@2; Methyl(K)@11; Oxidation(K)@12
DNA repair protein rhp16	QYIESFEMENADQQEEEK	Gln->pyro-Glu@N-term; Phospho(S)@5; Methyl(D)@12; Deamidated(Q)@14
Plasmepsin 4	ANAVVDSGTSTITAPTSFLNK	Phospho(S)@10; Oxidation(N)@20; Methyl(K)@21
Hypothetical protein	NDSNISNDSNK	Methyl(N)@1; Deamidated(N)@4; Phospho(S)@9

Hypothetical protein	VVDGENILK	Methyl(K)@9
Hypothetical protein	RKKMEAQKSVSFTK	Oxidation(M)@4; Methyl(S)@11
Myosin d	TLLNINLEGTKLSINK	Deamidated(N)@4; Methyl(I)@5; Phospho(S)@13; Deamidated(N)@15
26S proteasome subunit	EALGVALDARR	Methyl(L)@3; Oxidation(R)@10; Oxidation(R)@11
Hypothetical protein	NVYSVDNTSINLSR	Oxidation(Y)@3; Phospho(S)@4; Methyl(D)@6
S-adenosylhomocysteine hydrolase	HSLPDGLMRATDFLISGK	Methyl(L)@7; Phospho(T)@11; Oxidation(F)@13
Hypothetical protein	NKSYEKIKSKSVDFNK	Deamidated(N)@1; Phospho(S)@3; Methyl(E)@5; Oxidation(N)@15
PfEMP1	KMGADGSITESAMR	Oxidation(D)@5; Methyl(I)@8; Phospho(S)@11; Oxidation(M)@13
PfEMP1	SADGAPSGDKDGAICIPPR	Phospho(S)@1; Oxidation(D)@11; Carbamidomethyl(C)@15; Oxidation(P)@17; Methyl(R)@19
Histone H4	QGRTLYGFGANT	Methyl(R)@3; Phospho(T)@4
6-phosphofructokinase	DGGSSPTSSAKK	Phospho(S)@5; Methyl(S)@9; Oxidation(K)@11
Hypothetical protein	RLGGDSNNDNVATSK	Phospho(S)@6; Oxidation(N)@8; Methyl(N)@10
PfEMP1	QKQPADKVVSR	Methyl(K)@7; Phospho(S)@10; Oxidation(R)@11
PfEMP1	QPADKVVSRSGASPDTASPDTK	Oxidation(P)@2; Methyl(D)@4; Oxidation(K)@5; Phospho(T)@16
PfEMP1	VDDSGSGR	Trimethyl(R)@8
PfEMP1	VDDSGSGR	Trimethyl(R)@8
RNA helicase-1	KDELTLEGIR	Trimethyl(K)@1
RNA helicase-1	QGVHMVVGTPGR	Methyl(H)@4; Phospho(T)@9
Diaphanous homolog	DTPKSKGAPK	Phospho(T)@2; Methyl(S)@5; Oxidation(K)@10

Diaphanous homolog	SKGAPKGGKGGK	Phospho(S)@1; Methyl(K)@9; Oxidation(K)@12
Hypothetical protein	SNKSKAQSKGSK	Methyl(N)@2; Phospho(S)@4; Oxidation(K)@5; Deamidated(Q)@7
Hypothetical protein	STNKSVSNSAGTLNNK	Phospho(T)@12; Deamidated(N)@15; Methyl(K)@16
Hypothetical protein	SILSEDKTNMEIK	Methyl(S)@1; Phospho(S)@4; Oxidation(K)@7; Phospho(T)@8
Guanylyl cyclase	KTQTLSLMNINGK	Oxidation(K)@1; Methyl(Q)@3; Oxidation(M)@8
Hypothetical protein	NDDNINKNDDNINK	Oxidation(N)@1; Methyl(D)@2; Oxidation(N)@6
PfEMP1	DKLISGRGGVTAR	Trimethyl(R)@13
Hypothetical protein	EKNVKHKAPSK	Glu->pyro-Glu@N-term; Oxidation(N)@3; Phospho(S)@10; Methyl(K)@11
Hypothetical protein	SSATTFKSKTFVNGSLKEKKNLKNDIK	Phospho(T)@5; Oxidation(F)@6; Oxidation(N)@13; Methyl(S)@15
Hypothetical protein	ERNRERHMEK	Oxidation(R)@2; Methyl(E)@5; Oxidation(M)@8
Hypothetical protein	KNSDMDIYNISSFNK	Oxidation(M)@5; Methyl(D)@6; Phospho(S)@11
Hypothetical protein	SSNKSKSSNKSK	Methyl(N)@3; Oxidation(K)@4; Phospho(S)@8
Hypothetical protein	SKSSNKSKSSNKSK	Phospho(S)@4; Phospho(S)@9; Phospho(S)@13; Methyl(K)@14
Hypothetical protein	GLSSSPKGSK	Phospho(S)@3; Methyl(S)@5
Hypothetical protein	EKEKDKDIEKEKSKDTAK	Oxidation(D)@5; Oxidation(K)@6; Oxidation(D)@7; Methyl(D)@15
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Translation elongation factor EF-1, subunit alpha	YEEIKKEVK	Methyl(K)@6
Translation elongation factor EF-1, subunit alpha	KEPGAVTAKAPA	Oxidation(K)@1; Oxidation(P)@3; Phospho(T)@7; Trimethyl(K)@9
Translation elongation factor EF-1, subunit alpha	YEEIKKEVK	Methyl(K)@9
Translation elongation factor EF-1, subunit alpha	YEEIKKEVK	Methyl(E)@7
HECT-domain (ubiquitin-transferase), putative	NSNNEHVNNIIDNLNNNI	Phospho(S)@2; Oxidation(N)@4; Methyl(N)@13; Oxidation(N)@17
HECT-domain (ubiquitin-transferase), putative	NTNGNNKKK	Phospho(T)@2; Deamidated(N)@3; Methyl(N)@6; Oxidation(K)@7
HECT-domain (ubiquitin-transferase), putative	DFSYEMKEFLPFLKVSPIESKK	Methyl(D)@1; Phospho(S)@3; Oxidation(K)@22
HECT-domain (ubiquitin-transferase), putative	NSPNLSSAK	Methyl(N)@1; Phospho(S)@7
Heat shock binding protein 70	NAVVTVPAYFNDAQR	Methyl(T)@5; Deamidated(N)@11; Oxidation(R)@15
Heat shock protein	NTILSAVKDAEDWLNNNSNADSEALKQK	Methyl(L)@14; Phospho(S)@18
Actin	SYELPDGNIITVGNER	Methyl(N)@14
Actin	SYELPDGNIITVGNER	Methyl(E)@15
Endoplasmin homolog precursor	EKNILSITDTGIGMTK	Glu->pyro-Glu@N-term; Deamidated(N)@3; Phospho(T)@10; Methyl(K)@16
Endoplasmin homolog precursor	RSVTNPKDLELTNSIK	Phospho(T)@4; Methyl(K)@16
Hypothetical protein	SELSLSNEKFPNMNK	Methyl(S)@1; Phospho(S)@4; Deamidated(N)@14
Hypothetical protein	STKAYKKMDK	Phospho(S)@1; Phospho(T)@2; Oxidation(K)@3; Trimethyl(K)@10
Hypothetical protein	KESISGTRK	Methyl(E)@2
Hypothetical protein	DNVKNSSNGKNISEMK	Oxidation(N)@5; Oxidation(N)@8; Methyl(N)@11; Phospho(S)@13
HSP 70 (putative)	DAGTIAGLNVMR	Methyl(D)@1; Phospho(T)@4; Oxidation(N)@9
HSP 70	GGMPGGMNFPGGMPGAGMPGNAPAGSGPTVEE	Oxidation(M)@7; Oxidation(P)@14; Phospho(T)@29; Methyl(E)@32
Hypothetical protein	TDSSDDKKK	Methyl(S)@4

Hypothetical protein	LTTKDEDMLHSK	Oxidation(H)@10; Trimethyl(K)@12
Hypothetical protein	YTVHKDICK	Phospho(T)@2; Methyl(D)@6; Carbamidomethyl(C)@8; Oxidation(K)@9
Hypothetical protein	EKLYTNDSEKENK	Oxidation(K)@2; Phospho(T)@5; Deamidated(N)@6; Methyl(K)@13
Hypothetical protein	SSGSSKSSGSSKSSDSSK	Oxidation(K)@6; Methyl(K)@12; Phospho(S)@14; Carbamidomethyl(K)@18
Hypothetical protein	LYTNDSEKENKKK	Methyl(L)@1; Phospho(T)@3; Oxidation(N)@4; Oxidation(D)@5
Hypothetical protein	SSGSSKSSGSSKSSGSSKSSGSSK	Oxidation(K)@6; Phospho(S)@11; Methyl(S)@17; Oxidation(K)@18
Hypothetical protein	SSGSSKSSDSSK	Methyl(S)@8; Phospho(S)@11
Glyceraldehyde-3-phosphate dehydrogenase, putative	VPIGTVSVVDLVCR	Carbamidomethyl(C)@13; Methyl(R)@14
Glyceraldehyde-3-phosphate dehydrogenase, putative	AVTKLGINGFGRIGR	Phospho(T)@3; Methyl(L)@5; Oxidation(N)@8; Oxidation(R)@15
Glyceraldehyde-3-phosphate dehydrogenase, putative	AGRCALSNIIPASTGAAK	Carbamidomethyl(C)@4; Methyl(I)@10
Bromodomain, putative	EDTKIEEGRK	Phospho(T)@3; Methyl(E)@6; Oxidation(K)@10
Bromodomain, putative	EASNCAQEAYQK	Carbamidomethyl(C)@5; Methyl(Q)@7
PfEMP1	EKVNSGGTARSGGTSGTSSTSGDSGTNDINNK	Glu->pyro-Glu@N-term; Phospho(S)@5; Oxidation(R)@10; Methyl(S)@21
PfEMP1	KVPSDPPPAPAPAAPPSTPAAPKHPR	Phospho(S)@4; Methyl(D)@5; Oxidation(H)@24; Oxidation(P)@25
PfEMP1	SGGTSGTSSTSGDSGTNDINNK	Methyl(T)@4; Phospho(S)@5; Oxidation(D)@13; Oxidation(N)@17
Amine oxidase, flavin-containing, putative	SYSTSNVIIGDKKSDK	Oxidation(K)@13; Trimethyl(K)@16
Amine oxidase, flavin-containing, putative	TFNLDLLNTTSSNQK	Phospho(T)@1; Methyl(N)@3; Oxidation(N)@13
Amine oxidase, flavin-containing, putative	ESNSFINTPSNSFEK	Oxidation(N)@7; Phospho(T)@8; Oxidation(F)@13; Methyl(E)@14

Amine oxidase, flavin-containing, putative	VLSNYSK	Methyl(K)@7
PfEMP1	PADSPPAGPATDSGK	Phospho(S)@4; Methyl(D)@12; Phospho(S)@13; Oxidation(K)@15
PfEMP1	PADSPPAGPATDSGK	Phospho(S)@4; Phospho(T)@11; Methyl(D)@12; Oxidation(K)@15
PfEMP1	PADSPPAGPATDSGK	Phospho(S)@4; Phospho(T)@11; Methyl(D)@12; Oxidation(K)@15
PfEMP1	PADSPPAGPATDSGK	Phospho(S)@4; Phospho(T)@11; Oxidation(D)@12; Methyl(S)@13
PfEMP1	PADSPPAGPATDSGK	Phospho(S)@4; Methyl(T)@11; Phospho(S)@13; Oxidation(K)@15
PfEMP1	PADSPPAGPATDSGK	Phospho(S)@4; Methyl(D)@12; Phospho(S)@13; Oxidation(K)@15
PfEMP1	PADSPPAGPATDSGK	Phospho(S)@4; Phospho(T)@11; Methyl(D)@12; Oxidation(K)@15
PfEMP1	PADSPPAGPATDSGK	Phospho(S)@4; Methyl(D)@12; Phospho(S)@13; Oxidation(K)@15
PfEMP1	PADSPPAGPATDSGK	Phospho(S)@4; Phospho(T)@11; Oxidation(D)@12; Methyl(K)@15
PfEMP1	CKTQNGSDGSGGGNSEK	Carbamidomethyl(C)@1; Methyl(K)@2; Phospho(T)@3
Hypothetical protein	KLSYNNLTRASCYVNSR	Phospho(S)@3; Deamidated(N)@5; Oxidation(R)@9; Methyl(S)@11; Carbamidomethyl(C)@12
Hypothetical protein	YNRKNNKK	Deamidated(N)@2; Methyl(K)@8
Chloroquine resistance marker protein	IFNKNGSINDKINDNNKENIR	Oxidation(D)@14; Methyl(N)@15; Oxidation(K)@17
Chloroquine resistance marker protein	NENINNSKNISEMSETNNKMDNMETR	Methyl(E)@2; Oxidation(M)@13; Phospho(T)@16
Chloroquine resistance marker protein	DHIIKSQAAGQAYLEAK	Oxidation(D)@1; Phospho(S)@6; Methyl(Q)@7
Merozoite surface protein 1 precursor	EQAVLSSITQP	Glu->pyro-Glu@N-term; Methyl(S)@6; Phospho(S)@7

Merozoite surface protein 1 precursor	FPSSPPTTPPSPAKTDEQKK	Methyl(T)@8; Oxidation(K)@14; Phospho(T)@15; Oxidation(K)@20
Hypothetical protein	NKKNKSKHNNHKNNNKINNNTKKL	Oxidation(N)@13; Phospho(T)@21; Oxidation(K)@23; Methyl(L)@24
Hypothetical protein	TPNGANKEKTPNDAEK	Phospho(T)@1; Deamidated(N)@6; Methyl(D)@13; Oxidation(K)@16
Hypothetical protein	SNHNIKNDDNIK	Oxidation(H)@3; Methyl(N)@4
Ubiquitin-protein ligase 1	IEKTEMLTKKYNK	Phospho(T)@4; Methyl(T)@8; Oxidation(K)@10; Oxidation(K)@13
ubiquitin-protein ligase 1	EDFSNVATSIIR	Phospho(S)@4; Deamidated(N)@5
ubiquitin-protein ligase 1	EDFSNVATSIIR	Glu->pyro-Glu@N-term
ubiquitin-protein ligase 1	EDFSNVATSIIR	Glu->pyro-Glu@N-term; Phospho(S)@4; Phospho(T)@8; Oxidation(R)@12
ubiquitin-protein ligase 1	EDFSNVATSIIR	Phospho(S)@4
ubiquitin-protein ligase 1	EDFSNVATSIIR	Phospho(S)@4; Deamidated(N)@5
ubiquitin-protein ligase 1	EDFSNVATSIIR	Phospho(S)@9
ubiquitin-protein ligase 1	EDFSNVATSIIR	Phospho(S)@4; Oxidation(N)@5
ubiquitin-protein ligase 1	EDFSNVATSIIR	Phospho(S)@4
ubiquitin-protein ligase 1	FTTTTNDK	Phospho(T)@3; Oxidation(N)@6
ubiquitin-protein ligase 1	FTTTTNDK	Phospho(T)@2
ubiquitin-protein ligase 1	FTTTTNDK	Oxidation(F)@1; Phospho(T)@5; Oxidation(N)@6; Oxidation(K)@8
ubiquitin-protein ligase 1	FTTTTNDK	Phospho(T)@2; Oxidation(D)@7
ubiquitin-protein ligase 1	FTTTTNDK	Oxidation(F)@1; Phospho(T)@2

ubiquitin-protein ligase 1	FTTTTNDK	Phospho(T)@2; Phospho(T)@5
ubiquitin-protein ligase 1	FTTTTNDK	Oxidation(F)@1; Phospho(T)@3
ubiquitin-protein ligase 1	FTTTTNDK	Oxidation(F)@1; Phospho(T)@3
ubiquitin-protein ligase 1	FTTTTNDK	Oxidation(F)@1; Phospho(T)@3
ubiquitin-protein ligase 1	FTTTTNDK	Oxidation(F)@1; Phospho(T)@3
ubiquitin-protein ligase 1	FTTTTNDK	Oxidation(F)@1; Phospho(T)@3
ubiquitin-protein ligase 1	FTTTTNDK	Oxidation(F)@1; Phospho(T)@3
ubiquitin-protein ligase 1	FTTTTNDK	Oxidation(F)@1; Phospho(T)@5
ubiquitin-protein ligase 1	FTTTTNDK	Oxidation(F)@1; Phospho(T)@3
ubiquitin-protein ligase 1	FTTTTNDK	Oxidation(F)@1; Phospho(T)@3
ubiquitin-protein ligase 1	FTTTTNDK	Oxidation(F)@1; Phospho(T)@3
ubiquitin-protein ligase 1	FTTTTNDKKK	Oxidation(F)@1; Phospho(T)@2; Phospho(T)@3
ubiquitin-protein ligase 1	FTTTTNDKKK	Oxidation(K)@9
40S ribosomal subunit protein S14, putative	SKTPGPGAQSALR	Phospho(T)@3; Methyl(R)@13
HSP70	KQQITIQSSGGLSKEEIEK	Trimethyl(K)@1; Phospho(S)@13; Oxidation(K)@19
Hypothetical protein	KTFYLAAAGEGKKLR	Phospho(T)@2; Methyl(L)@14; Oxidation(R)@15
Hypothetical protein	SDSINSNNMER	Phospho(S)@1; Methyl(N)@5; Deamidated(N)@8
PfEMP1	TPRAAPQARTRR	Oxidation(P)@6; Deamidated(Q)@7; Phospho(T)@10; Methyl(R)@12

PfEMP1	SDGGACAPPRRR	Phospho(S)@1; Methyl(D)@2; Carbamidomethyl(C)@6; Oxidation(P)@9; Oxidation(R)@10
PfEMP1	KIWEGMLCGLSHAGGNDAIKSNQDYQYSEVK	Oxidation(W)@3; Methyl(E)@4; Oxidation(M)@6; Carbamidomethyl(C)@8; Phospho(S)@28
PfEMP1	YETLYEKARIAADNGGLDTSSGDIDPK	Oxidation(Y)@1; Phospho(S)@21; Methyl(D)@25
Rhoptry protein	NNSTNNSIECVNNK	Phospho(S)@3; Carbamidomethyl(C)@10; Methyl(K)@14
Rhoptry protein	NETNISPNSDIK	Phospho(S)@9; Oxidation(D)@10; Methyl(I)@11; Oxidation(K)@12
Hypothetical protein	KTMNKSNGMNKSNGMNK	Oxidation(K)@1; Phospho(T)@2; Methyl(K)@11; Oxidation(M)@15
Hypothetical protein	SNGMNKSNSMSKNKK	Deamidated(N)@5; Methyl(K)@15
Hypothetical protein	YGKDHSDQEKDSPSK	Oxidation(K)@3; Methyl(D)@11; Phospho(S)@12; Oxidation(P)@13
Hypothetical protein	YNTKGNTKGNTK	Methyl(N)@6; Phospho(T)@7; Oxidation(K)@12
DNA-directed RNA polymerase 3 largest subunit	ETKNLTLLEKAERETAMN	Glu->pyro-Glu@N-term; Phospho(T)@2; Oxidation(N)@4; Trimethyl(K)@10
Hypothetical protein	NSVGVTANAVGSTPGSSNTFSHRQREK	Phospho(S)@17; Deamidated(N)@18; Phospho(S)@21; Trimethyl(R)@25
PfEMP1	TRIPTRGASNNLVSVK	Carbamyl(R)@6; Phospho(S)@9; Methyl(N)@10; Oxidation(N)@11
PfEMP1	PPKPTGGPGAGESPAR	Oxidation(P)@4; Phospho(T)@5; Methyl(E)@12; Deamidated(R)@16
PfEMP1	AVVDGKANAEGGGQKGARGPNGGTEGANSGK	Methyl(D)@4; Deamidated(N)@21; Phospho(T)@24; Phospho(S)@29
Asparagine-rich antigen Pfa35-2	SGISDKYFNK	Phospho(S)@1; Methyl(D)@5; Oxidation(K)@10
Asparagine-rich antigen Pfa35-2	TEEKINEENK	Phospho(T)@1; Methyl(E)@8; Oxidation(K)@10

PfEMP1	EESGAPPAPPATDSGK	Glu->pyro-Glu@N-term; Methyl(E)@2; Phospho(S)@3
PfEMP1	YETEISGGGASGSSR	Oxidation(Y)@1; Methyl(E)@2; Phospho(T)@3; Oxidation(R)@15
Hypothetical protein	QVTEKTYDK	Phospho(T)@3; Methyl(E)@4; Oxidation(Y)@7
Hypothetical protein	SSKVGLYNNISDSLSK	Methyl(L)@6; Deamidated(N)@9; Phospho(S)@13
Hypothetical protein	RISTNNISRSESRSSK	Phospho(T)@4; Phospho(S)@10; Methyl(S)@12; Phospho(S)@15
Hypothetical protein	SGKNGENENVENENVENK	Phospho(S)@1; Trimethyl(K)@3; Deamidated(N)@9; Deamidated(N)@17
PfEMP1	EEINESKPGVNSEHGKYNK	Glu->pyro-Glu@N-term; Methyl(E)@5; Phospho(S)@6; Deamidated(N)@18
NAD(P)H-dependent glutamate synthase	SNTGEGGEAEER	Phospho(S)@1; Phospho(T)@3; Methyl(E)@8; Oxidation(R)@12
Hypothetical protein	YLPSPPIINEEK	Dioxidation(P)@5; Methyl(I)@8; Oxidation(K)@12
Hypothetical protein	KDKGNHKDTSNKNNNTDK	Phospho(S)@10; Methyl(N)@14
Chloroquine resistance marker protein	THSSQSKTQSTQSKTQSTQSKTQSTQR	Methyl(S)@6; Phospho(T)@11; Oxidation(K)@14; Deamidated(Q)@19
Chloroquine resistance marker protein	STQSKTKSTQSK	Phospho(S)@4; Dioxidation(K)@5; Methyl(T)@9; Oxidation(K)@12
Chloroquine resistance marker protein	SKTQSTQSKTHSTQSK	Deamidated(Q)@4; Phospho(T)@6; Methyl(S)@12
Chloroquine resistance marker protein	STQSKTKSTQSK	Deamidated(Q)@3; Phospho(T)@6; Methyl(Q)@10; Oxidation(K)@12
Chloroquine resistance marker protein	NSINQKVNFWELTK	Methyl(E)@11

Hypothetical protein	NNNSYNNNNY	Oxidation(N)@3; Oxidation(N)@8; Methyl(N)@9; Oxidation(Y)@10
Dynein beta chain	ISSVEAETQK	Phospho(S)@2; Methyl(E)@7
CTRP	LLVVGVSTASENK	Methyl(T)@8; Deamidated(N)@12
CTRP	LLVVGVSTASENK	Methyl(T)@8; Deamidated(N)@12
CTRP	LLVVGVSTASENK	Methyl(T)@8; Deamidated(N)@12
Serine/Threonine protein kinase, FIKK family	EDTNKDDIKNVY	Phospho(T)@3; Methyl(D)@7; Oxidation(N)@10
Hypothetical protein	YIISNNDSEKNESK	Phospho(S)@13; Methyl(K)@14
Ubiquitin transferase, putative	KKNMTTNNTCNK	Oxidation(K)@2; Methyl(N)@3; Phospho(T)@6; Carbamidomethyl(C)@10
Ubiquitin transferase, putative	NMNKCIGKGLYPNK	Oxidation(M)@2; Carbamidomethyl(C)@5; Methyl(L)@10; Deamidated(N)@13
Hypothetical protein	RKKKEKSKNTNMKTIVK	Phospho(S)@7; Phospho(T)@14; Methyl(K)@17
Hypothetical protein	HEQQSGYIKK	Methyl(E)@2; Phospho(S)@5; Oxidation(K)@10
Exopolyphosphatase	SIIDHHILNEEMKNK	Oxidation(D)@4; Methyl(E)@11; Oxidation(M)@12
Hypothetical protein	FNNSNESENSNINMYNK	Phospho(S)@7; Methyl(I)@12
Hypothetical protein	VTPNSNSNSNSNSSSSSNSSSSNNNHFEK	Phospho(S)@5; Deamidated(N)@12; Methyl(S)@21
Hypothetical protein	KQHIEFINLFNNNIFF	Methyl(Q)@2; Oxidation(H)@3; Oxidation(F)@10
Hypothetical protein	LISSVNIISDEFMQKYTNTNVTIEK	Phospho(S)@4; Methyl(K)@15; Phospho(T)@19; Phospho(T)@22
Hypothetical protein	ENCDLLKLKITFQIIKTMIYVFNLIQKIYK	Carbamidomethyl(C)@3; Phospho(T)@11; Oxidation(N)@23; Methyl(K)@30
Hypothetical protein	TENTNDINEEVRNEQK	Phospho(T)@4; Trimethyl(K)@16
Ubiquitination factor,NosA, essential for cellular differentiation	YVINNSHSSDEGEEDVSSY	Deamidated(N)@5; Phospho(S)@9; Methyl(E)@13

Ubiquitination factor,NosA, essential for cellular differentiation	GSNNTSTNNNTTH	Phospho(T)@5; Methyl(S)@6; Oxidation(N)@10; Phospho(T)@12
Hypothetical protein	TKSIFSISNEKKNTYFSK	Oxidation(K)@2; Deamidated(N)@9; Methyl(E)@10; Oxidation(N)@13
Hypothetical protein	TTDGGKTTDGGK	Methyl(T)@1; Phospho(T)@2; Oxidation(D)@9; Oxidation(K)@12
Iswi protein homologue	NSSNTKSSSNTKSSSNTKNK	Methyl(S)@3; Deamidated(N)@4; Oxidation(K)@12; Phospho(S)@13
Iswi protein homologue	NSSNTKNSSNTK	Oxidation(N)@4; Methyl(K)@6; Phospho(S)@9; Oxidation(K)@12
Iswi protein homologue	NSSNTKNSSNTKSSSNTK	Phospho(T)@5; Methyl(S)@13; Deamidated(N)@16
PfEMP1	CIPSGDKAATSGEGDSGPSR	Carbamidomethyl(C)@1; Methyl(T)@10; Phospho(S)@11; Oxidation(P)@18
PfEMP2	APTSWKCIPSGDKAATSGEGDSGPSRKR	Methyl(T)@3; Phospho(S)@4; Carbamidomethyl(C)@7; Oxidation(P)@24; Deamidated(R)@28
Ecto-nucleoside triphosphate diphosphohydrolase 1, putative	GNINNSNK	Methyl(I)@3; Oxidation(N)@4; Phospho(S)@6
Hypothetical protein	NDSINDKIESKENNNKPCYKKQSSSHR	Methyl(D)@2; Phospho(S)@3; Oxidation(K)@7; Oxidation(N)@15; Carbamidomethyl(C)@18
Hypothetical protein	SGISSNFIEDKK	Phospho(S)@5; Methyl(I)@8; Oxidation(D)@10
Hypothetical protein	NEFLALFLTK	Deamidated(N)@1; Methyl(E)@2; Phospho(T)@9
Hypothetical protein	APIFGSPSNKDDKDKTPIFGSPSNKDDK	Oxidation(P)@7; Methyl(S)@8; Phospho(T)@16
Hypothetical protein	AGESSQSSSGSETPSQPDPK	Deamidated(Q)@6; Methyl(S)@11; Oxidation(P)@14; Phospho(S)@15
Hypothetical protein	MAPTSDGGGTKDESAK	Methyl(T)@4; Oxidation(D)@12; Oxidation(K)@16
PfEMP1	MARPGSGGGGSSQDAK	dethiomethyl(M)@1; Deamidated(R)@3; Phospho(S)@6; Trimethyl(K)@16
PfEMP1	LDFNNPEQTFRPATNCGP	Methyl(N)@4; Phospho(T)@14; Carbamidomethyl(C)@16
PfEMP1	GTEISDGGSGSGAAGGGGGR	Phospho(S)@5; Methyl(S)@11

Hypothetical protein	QNKDNKQNKDNK	Gln->pyro-Glu@N-term; Deamidated(Q)@7; Oxidation(N)@8; Methyl(N)@11
Hypothetical protein	QNSKSALSSKPGVKSSLSSKPGVK	Gln->pyro-Glu@N-term; Phospho(S)@5; Methyl(S)@16; Oxidation(P)@21
Hypothetical protein	LTNNNNSI	Methyl(L)@1; Phospho(T)@2
Exported serine/threonine protein kinase	KTPHNSDMCPNNIRSSSNTVGMVFNK	Phospho(T)@2; Methyl(S)@6; Oxidation(D)@7; Carbamidomethyl(C)@9
Hypothetical protein	HTDNTTNATTLYK	Oxidation(H)@1; Methyl(T)@6; Phospho(T)@10; Oxidation(K)@13
Hypothetical protein	FTNEISTEENCIYAYITRNQNK	Phospho(T)@2; Methyl(S)@6; Carbamidomethyl(C)@11
60S ribosomal subunit protein L8	LPSGAKKTIDAKARAMVGVVGAGGRIDK	Phospho(S)@3; Methyl(K)@7; Oxidation(D)@27; Oxidation(K)@28
Guanylyl cyclase	SISQSNTLYNK	Phospho(S)@5; Methyl(T)@7; Oxidation(K)@11
Guanylyl cyclase	TIDILNQSGIR	Methyl(N)@6; Phospho(S)@8; Oxidation(R)@11
Erythrocyte membrane protein 3	RENPDGEPLNTPEIHVIRPSDLMDK	Phospho(T)@11; Methyl(D)@21
Hypothetical protein	TNEESYKR	Phospho(T)@1; Methyl(E)@4; Deamidated(R)@8
Hypothetical protein	ESISKHIKGSPSRDK	Oxidation(K)@5; Methyl(K)@8
Zinc finger transcription factor (krox1)	SDASKKDDISAK	Phospho(S)@1; Oxidation(D)@2; Oxidation(D)@7; Methyl(D)@8
Hypothetical protein	SGGQFTVPRNSTSGRKR	Deamidated(Q)@4; Phospho(T)@6; Methyl(R)@9; Dioxidation(R)@17
Hypothetical protein	DQSGGQYTVPRKSTDCR	Phospho(S)@3; Methyl(Q)@6; Carbamidomethyl(C)@16
Hypothetical protein	NAALILR	Oxidation(N)@1; Methyl(L)@4
Dynein heavy chain, putative	TNFKIAITHSPISNLYRDR	Phospho(T)@1; Methyl(I)@7

Dynein heavy chain, putative	MIDFDDDDNNNIYDESK	Methyl(D)@5; Oxidation(N)@10; Phospho(S)@16
Hypothetical protein	GLISEDNNNNNNK	Methyl(N)@9
Dynein heavy chain, putative	VKVTHIKNYIKNFK	Phospho(T)@4; Iodo(H)@5; Methyl(K)@14
Metallophosphoesterase	STKPLSDLSPSYGK	Phospho(T)@2; Oxidation(K)@3; Methyl(S)@6; Oxidation(P)@10
Hypothetical protein	QDGSFSNIAPTNKNNKNYDDDNNK	Deamidated(N)@7; Phospho(T)@11; Methyl(K)@13; Deamidated(N)@15
Dynein heavy chain, putative	ITFAGACNPPTDAGRNPLSNR	Phospho(T)@2; Carbamidomethyl(C)@7; Methyl(N)@8; Oxidation(P)@9; Deamidated(N)@20
Dynein heavy chain, putative	LGGNPFGPAGTGKTESVK	Phospho(T)@11; Phospho(T)@14; Methyl(K)@18
PfEMP1	MGPPGITGTQGETAK	Oxidation(M)@1; Phospho(T)@7; Deamidated(Q)@10; Methyl(E)@12
PfEMP1	EIEKANGTSNGTTIR	Phospho(T)@12; Methyl(R)@15
Hypothetical protein	LLSKELESKLKDSNEKKK	Phospho(S)@3; Methyl(K)@9
Hypothetical protein	MNKHISNHKKNHNK	Phospho(S)@6; Methyl(H)@8; Deamidated(N)@11
Hypothetical protein	INNTPQSYNTPQSY	Oxidation(N)@3; Dioxidation(P)@5; Phospho(S)@7; Methyl(S)@13
Hypothetical protein	KINNTPQSYNTPQSY	Methyl(S)@14
Zinc finger protein Xfin, putative	KNGGKDVSKNSK	Methyl(D)@6; Oxidation(K)@9; Phospho(S)@11
GA27480	AEATNLRGRNSENK	Oxidation(N)@5; Methyl(N)@10; Phospho(S)@11
Zinc finger protein Xfin, putative	KNGGKDVSKNSK	Trimethyl(K)@1; Phospho(S)@8; Oxidation(K)@12
Cell division cycle protein 48 homologue, putative	GVLLYGPPGSGK	Methyl(K)@12
Normocyte binding protein 2a	SGTDHTNSSESTTDDNTNDR	Phospho(T)@3; Methyl(T)@6; Deamidated(N)@7

Hypothetical protein	KIFLSTDFLK	Methyl(S)@5; Phospho(T)@6; Oxidation(K)@10
Hypothetical protein	TLLAKAVAGEANVPFFNISGSDFIEVF	Phospho(T)@1; Methyl(L)@3; Deamidated(N)@17
Ornithine aminotransferase	VPYDDLEALEK	Methyl(D)@5; Oxidation(K)@11
Hypothetical protein	VSTNLSRTSNARNRGVK	Methyl(T)@8; Phospho(S)@9; Oxidation(N)@10
Hypothetical protein	FQDKPKSLKNK	Methyl(L)@8; Oxidation(K)@9; Oxidation(K)@11
MORN repeat protein, putative	FILFIFYFISK	Oxidation(Y)@7; Oxidation(F)@8; Methyl(I)@9; Phospho(S)@10
PfEMP1	RITDPNDQATVCR	Deamidated(R)@1; Phospho(T)@3; Deamidated(N)@6; Carbamidomethyl(C)@12; Methyl(R)@13
ATP-dependent DNA helicase	NSENSSTSN	Phospho(S)@2; Methyl(E)@3; Oxidation(N)@4
Asparagine--tRNA ligase	IKESEKNPSVDKSEK	Methyl(E)@5; Phospho(S)@9; Phospho(S)@13
12hr untreated		
heat shock protein 70	QATKDAGAIAGLNVLR	Phospho(T)@3; Oxidation(D)@5; Methyl(R)@16
12hr treated		
18hrs - untreated		
Chaperone protein DnaK	IINEPTAAALAYGLDK	Tyr->Phe@12; Methyl(L)@14
Heat shock protein	MINDAEKFADEDK	Dioxidation(M)@1; Methyl(I)@2; Oxidation(D)@12
Luminal binding protein	NAVVTVPAYFNDAQR	Methyl(N)@1; Oxidation(R)@15

Heat shock protein	SRGITITNDK	Deamidated(R)@2; Phospho(T)@7; Dimethyl(K)@10
Heat shock protein	NNIDLRTDKR	Oxidation(R)@6; Methyl(D)@8; Oxidation(R)@10
Heat shock protein	EDKNTILSAVK	Methyl(T)@5; Phospho(S)@8
Heat shock protein	GTGKSRGITI	Phospho(S)@5; Phospho(T)@9; Methyl(I)@10
Heat shock protein	GTGKSRGITITNDKGR	Methyl(T)@2; Phospho(S)@5; Oxidation(R)@6
Heat shock protein	GTGKSRGITITNDKGR	Phospho(T)@11; Methyl(R)@16
Chaperone protein DnaK	IINEPTAAALAYGLDK	Oxidation(P)@5; Phospho(T)@6; Dimethyl(K)@16
Heat shock protein, putative	MINDAEKFADEDKNLR	Oxidation(N)@3; Carbamyl(K)@7; Oxidation(F)@8; Dimethyl(R)@16
Heat shock protein	NLREKVEAK	Oxidation(N)@1; Deamidated(R)@3; Methyl(K)@9
Heat shock protein	QATKDAGTIAGLNIVRI	Gln->pyro-Glu@N-term; Oxidation(K)@4; Methyl(D)@5; Phospho(T)@8
Endoplasmin precursor, putative	GVVDSDDLPLNVSR	Methyl(D)@6; Oxidation(P)@9; Oxidation(N)@11; Dehydrated(S)@13
Endoplasmin precursor, putative	GVVDSDDLPLNVSR	Methyl(D)@6; Methyl(R)@14
Endoplasmin precursor, putative	GVVDSDDLPLNVSR	Methyl(D)@6; Dioxidation(P)@9; Dehydrated(S)@13
Endoplasmin homolog precursor	SVTNPKDLELTNSIK	Phospho(T)@3; Oxidation(N)@4; Methyl(K)@15
Endoplasmin homolog precursor	EGKKNKETLR	Phospho(T)@8; Methyl(L)@9
Endoplasmin homolog precursor	SFELTEEEKKKEQQMQK	Phospho(S)@1; Methyl(E)@8; Oxidation(K)@11; Oxidation(M)@15
Endoplasmin homolog precursor	EKNILSITDTGIGMTKVDLINNLGTIAK	Glu->pyro-Glu@N-term; Oxidation(N)@3; Phospho(S)@6; Methyl(K)@16
Molecular chaperone of HSP90 family	ELISNAADALEK	Methyl(E)@1; Phospho(S)@4; Oxidation(N)@5
Molecular chaperone of HSP90 family	ELISNAADALEK	Phospho(S)@4; Methyl(E)@11; Oxidation(K)@12

Molecular chaperone of HSP90 family	ELISNAADALEK	Glu->pyro-Glu@N-term; Phospho(S)@4; Methyl(D)@8; Oxidation(K)@12
Endoplasmin homolog precursor	ELTEEEKKKEQQMQKMYKALIDVISDTLK	Methyl(E)@6; Deamidated(Q)@14; Oxidation(M)@16; Dioxidation(K)@18
Endoplasmin homolog precursor	EQLQQNKILKAVSKR	Methyl(E)@1; Phospho(S)@13
Endoplasmin homolog precursor	FLSLSDESVLGEEK	Methyl(S)@8; Oxidation(K)@14
Endoplasmin homolog precursor	GPSDDVSDSSGEKKEVKRDRDTLEEI	Methyl(D)@8; Oxidation(K)@17; Oxidation(D)@21; Phospho(T)@22
Endoplasmin precursor, putative	GVVDSDDLPLNVSR	Methyl(D)@6; Oxidation(N)@11; Dehydrated(S)@13; Oxidation(R)@14
Endoplasmin precursor, putative	GVVDSDDLPLNVSR	Methyl(D)@6; Methyl(R)@14
Endoplasmin precursor, putative	GVVDSDDLPLNVSR	Methyl(D)@6; Val->Leu@12
Endoplasmin precursor, putative	GVVDSDDLPLNVSR	Methyl(D)@6; Methyl(R)@14
Endoplasmin precursor, putative	GVVDSDDLPLNVSR	Methyl(D)@6; Methyl(R)@14
Endoplasmin precursor, putative	KDNNVDNESNDKSDE	Oxidation(N)@4; Oxidation(N)@7; Methyl(K)@12
Regulator of G-protein signalling 14 [	VKADNILFYRLAEMK	Oxidation(D)@4; Oxidation(F)@8; Methyl(E)@13; dethiomethyl(M)@14
Heat-shock protein	KKKTGEDKNADESKEENEDEEK	Dioxidation(K)@3; Dioxidation(K)@8; Phospho(S)@13; Dimethyl(K)@22
Heat shock protein 86	LGIHEDNANR	Oxidation(N)@9; Methyl(R)@10
Heat-shock protein	YSAYLVADHVVVISK	Phospho(S)@2; Methyl(D)@8; Oxidation(H)@9; Oxidation(K)@15
Heat-shock protein	DKIRYESITDTQKL	Oxidation(R)@4; Phospho(T)@9; Trimethyl(K)@13
Heat-shock protein	CLDMFSELAENKENYKK	Carbamidomethyl(C)@1; Methyl(D)@3; Oxidation(M)@4; Phospho(S)@6

Heat shock protein 90, putative	ELISNASDALDK	Glu->pyro-Glu@N-term; Phospho(S)@4; Deamidated(N)@5; Methyl(S)@7
Heat shock protein 90, putative	ELISNASDALDK	Methyl(N)@5
Heat shock protein 86	IMKAQALRDNSMTSYMLSK	Phospho(T)@13; Oxidation(M)@16; Methyl(K)@19
Heat shock protein 86	NDLINNLGTIAR	Methyl(N)@1; Oxidation(D)@2; Oxidation(R)@12
Heat shock protein 86	TNNTLTIEDSGIGMTKNDLINNLGTIAR	Deamidated(N)@3; Methyl(I)@7; Oxidation(D)@9; Phospho(S)@10
heat shock protein,, putative	DAGTIAGLNVMR	Carbamidomethyl@N-term; Methyl(N)@9; dethiomethyl(M)@11; Oxidation(R)@12
HSP 70	QNHITITNDKGR	Deamidated(N)@8; Methyl(D)@9
Heat shock protein,, putative	DAGTIAGLNVMR	Methyl(N)@9; Carbamyl(R)@12
HSP 70	GKDLSKNSR	Methyl(D)@3; Phospho(S)@8; Oxidation(R)@9
HSP 70	KNRGKDLSKNSR	Oxidation(K)@1; Phospho(S)@8; Methyl(N)@10; Phospho(S)@11
HSP 70	NRGKDLSKNSRALRR	Oxidation(D)@5; Phospho(S)@7; Trimethyl(K)@8
HSP 70	NRGKDLSKNSRALRR	Methyl(D)@5; Phospho(S)@7; Deamidated(R)@11; Carbamyl(R)@15
HSP 70	PGNAPAGSGPTVEEV	Phospho(S)@8; Methyl(E)@14
Elongation factor 1 alpha	AGMVLNFAPSAVVSECK	Deamidated(N)@6; Methyl(E)@15; Carbamidomethyl(C)@16
Elongation factor 1 alpha	YEEIKKEVK	Methyl(K)@6
Elongation factor 1 alpha	YEEIKKEVK	Methyl(K)@6
Elongation factor 1 alpha	YEEIKKEVK	Methyl(K)@6
Elongation factor 1 alpha	APSAVVSECKSVEMHK	Oxidation(P)@2; Phospho(S)@3; Carbamidomethyl(C)@9; Oxidation(K)@10; Methyl(K)@16

Elongation factor 1 alpha	FLNIDSKIDKRSGK	Phospho(S)@12; Methyl(K)@14
Elongation factor 1 alpha	IDKRSGKVVEENPK	Oxidation(D)@2; Oxidation(K)@3; Oxidation(P)@13; Methyl(K)@14
Elongation factor 1 alpha	YEEIKKEVK	Oxidation(Y)@1; Methyl(E)@7
Elongation factor 1 alpha	YEEIKKEVK	Methyl(K)@9
Elongation factor 1 alpha	YEEIKKEVK	Methyl(K)@6
Mature parasite-infected erythrocyte surface antigen	QVEDGIKENDTEGNDK	Methyl(D)@4
Mature parasite-infected erythrocyte surface antigen	QVEDGIKENDTEGNDK	Methyl(D)@4
Mature parasite-infected erythrocyte surface antigen	QVEDGIKENDTEGNDK	Methyl(D)@4
Mature parasite-infected erythrocyte surface antigen	QVEDGIKENDTEGNDK	Methyl(D)@4
Mature parasite-infected erythrocyte surface antigen	DKVIEQEKEKEEVK	Methyl(D)@1; Oxidation(K)@2
Mature parasite-infected erythrocyte surface antigen	DKVIEQEKEKEEVK	Methyl(D)@1; Oxidation(K)@2
Mature parasite-infected erythrocyte surface antigen	VIGQEIITEEVK	Methyl(I)@2
Mature parasite-infected erythrocyte surface antigen	VIGQEIITEEVK	Methyl(I)@2
Mature parasite-infected erythrocyte surface antigen	EDVNEKDTANKDK	Methyl(D)@2; Oxidation(N)@4; Phospho(T)@8; Oxidation(K)@13
Mature parasite-infected erythrocyte surface antigen	GDVNEEGPENKDK	Oxidation(N)@4; Oxidation(N)@10; Methyl(D)@12
Mature parasite-infected erythrocyte surface antigen	HVNVMGESKETDESK	Oxidation(M)@5; Methyl(S)@8; Carbamyl(K)@9
Mature parasite-infected erythrocyte surface antigen	ITEESKDREGNK	Phospho(T)@2; Dimethyl(K)@12
Mature parasite-infected erythrocyte surface antigen	VIGQEIITEEVK	Methyl(I)@2
Mature parasite-infected erythrocyte surface antigen	VIGQEIIVEEVK	Methyl(E)@10
Mature parasite-infected erythrocyte surface	VIGQEVIIEEVKK	Methyl(E)@5
Merozoite surface protein-1	KTIDQNKNADNEEGKK	Phospho(T)@2; Deamidated(N)@11; Dimethyl(K)@16
Merozoite surface protein-1	LNSLNNPHNVLQNFSVFFNK	Methyl(N)@9; Oxidation(F)@14; Deamidated(N)@19
Merozoite surface protein-1	NPPPANSGNTPNTLLDKNK	Methyl(N)@6; Phospho(S)@7; Oxidation(P)@11
Merozoite surface protein-1	LLEVYNLTPEEENELKSCD	Methyl(N)@6; Carbamidomethyl(C)@18

Merozoite surface protein-1	DQVVTGEAISVTMDNI	Oxidation(D)@1; Phospho(T)@5; Methyl(T)@12; Oxidation(M)@13
Merozoite surface protein-1	ITKLSDLKAIDDKIDLFK	Phospho(T)@2; Methyl(S)@5; Methyl(D)@6
Merozoite surface protein-1	KEAEIAETENTLENTK	Phospho(T)@8; Trimethyl(K)@16
Merozoite surface protein-1	KKEAEIAETENTLENTK	Oxidation(K)@2; Phospho(T)@16; Methyl(K)@17
Merozoite surface protein-1	KLLDKINEIKNPPPANSGNTPNTLLDK	Oxidation(N)@7; Phospho(T)@23; Methyl(D)@26; Oxidation(K)@27
Merozoite surface protein-1	KTIDQNKNADNEEGKK	Methyl(D)@10; Oxidation(K)@15
Merozoite surface protein-1	KTIDQNKNADNEEGKKK	Phospho(T)@2; Methyl(N)@6; Oxidation(N)@8; Oxidation(K)@17
Merozoite surface protein-1	LKDTLQLSFDLYNK	Methyl(D)@10; Oxidation(Y)@12; Oxidation(K)@14
Merozoite surface protein-1	LSDLKAIDDK	Phospho(S)@2; Oxidation(D)@3; Methyl(K)@5
Merozoite surface protein 1, precursor	LTEEIKSSENKILEKNFKGLTHSANGSLEVSDIVK	Deamidated(N)@16; Carbamyl(K)@18; Methyl(T)@21; Phospho(S)@31
Merozoite surface protein-1	NKKVDVTPK	Phospho(T)@7; Methyl(K)@9
Merozoite surface protein-1	SYICHKYILVSNSSMDQK	Carbamidomethyl(C)@4; Methyl(I)@8; Phospho(S)@11
Merozoite surface protein-1	TDEQKKESKFLPFLTNIETLYNNLVNK	Dimethyl(K)@6; Phospho(S)@8
Merozoite surface protein-1	TGLEADIKKLTEEIK	Methyl(T)@1; Oxidation(K)@9; Phospho(T)@11
Merozoite surface protein-1	TIDQNKNADNEEGKK	Methyl(I)@2
Merozoite surface protein-1	VDVTPKSQDPTK	Oxidation(D)@9; Phospho(T)@11; Trimethyl(K)@12
Pyruvate kinase	QILEPNNVNLRSKK	Deamidated(Q)@1; Methyl(I)@2; Oxidation(R)@11; Phospho(S)@12
Pyruvate kinase	FKYKNSAAGASMQSAANITLR	Methyl(K)@4; Phospho(S)@11; Deamidated(R)@21
Pyruvate kinase	GVTCIKVGSFQGTDIVIR	Phospho(T)@3; Carbamidomethyl(C)@4; Methyl(K)@6; Oxidation(D)@14; Oxidation(R)@18

Pyruvate kinase	LIADGSVSCK	Phospho(S)@6; Methyl(S)@8; Carbamidomethyl(C)@9
Pyruvate kinase	NSAAGASMQSAANITLR	Oxidation(N)@13; Methyl(L)@16; Oxidation(R)@17
Pyruvate kinase	QILEPNNVNLRSKK	Methyl(I)@2; Oxidation(P)@5; Deamidated(N)@6; Phospho(S)@12
Chaperone protein DNAK, putative	QATKDAGKIAGLDVLR	Oxidation(D)@5; Methyl(L)@15; Oxidation(R)@16
HSP 70	QLEDFKDKISDSDKDELR	Methyl(Q)@1; Oxidation(D)@4
HSP 70	MTNKKQQITIQSSGGLSK	Methyl(K)@4
HSP 70	LTRAKLEELCHDLLK	Deamidated(R)@3; Carbamidomethyl(C)@10; Oxidation(H)@11; Oxidation(D)@12; Methyl(L)@13
HSP 70	CVKNTLLSEKSR	Carbamidomethyl(C)@1; Methyl(T)@5; Phospho(S)@11
Chaperone protein DNAK, putative	LVGGMTRMPK	Methyl(L)@1; Oxidation(M)@8; Oxidation(P)@9
HSP 70	IVRASNGDAWIEAQGK	Phospho(S)@5; Oxidation(N)@6; Methyl(D)@8
HSP 70	KQQITIQSSGGLSKEEIEK	Phospho(T)@5; Methyl(I)@6; Oxidation(K)@19
HSP 70	NTLLSEKSRSLCTSK	Methyl(E)@6; Oxidation(K)@7; Oxidation(R)@9; Carbamidomethyl(C)@12; Phospho(S)@14
HSP 70	QAITNPENTVYATKR	Methyl(Q)@1; Oxidation(Y)@11; Phospho(T)@13
HSP 70	RFIGRKYDEDATKK	Arg->Orn(R)@1; Methyl(E)@9; Oxidation(D)@10; Phospho(T)@12
HSP 70, homologue	TTPSVVAFTNDNQR	Phospho(S)@4; Methyl(R)@14
Chain A, Crystal Structure Of Phosphoglycerate Kinase	KGAITIVGGGDTASLVEQQNK	Phospho(T)@5; Methyl(E)@17; Oxidation(N)@20; Oxidation(K)@21
Para-aminobenzoic acid synthetase	EPSRISFNSIVQKEQYIENVRK	Deamidated(N)@8; Phospho(S)@9; Methyl(I)@10; Oxidation(Y)@16
Chain A, Crystal Structure Of Phosphoglycerate Kinase	ANKEDVEKFQNDLTK	Oxidation(K)@3; Methyl(E)@4; Phospho(T)@14
Phosphoglycerate kinase	ELPGVLALSN	Methyl(E)@1; Phospho(S)@9; Oxidation(N)@10

Phosphoglycerate kinase	ELPGVLALSN	Methyl(L)@2; Phospho(S)@9; Oxidation(N)@10
Chain A, Crystal Structure Of Phosphoglycerate Kinase	FQNDLTK	Methyl(Q)@2; Oxidation(N)@3
Para-aminobenzoic acid synthetase	FSYMGNLDGILGDIIEYYIDGK	Methyl(D)@13
Para-aminobenzoic acid synthetase	FSYMGNLDGILGDIIEYYIDGK	Methyl(D)@13
Phosphoglycerate kinase	IGTSLFDEAGSK	Methyl(I)@1; Phospho(T)@3; Oxidation(D)@7; Oxidation(K)@12
Chain A, Crystal Structure Of Phosphoglycerate Kinase	LGNKLSISDLKDIK	Methyl(I)@7; Phospho(S)@8; Oxidation(K)@11; Oxidation(K)@14
Para-aminobenzoic acid synthetase	NMISIGAGGAITIK	Phospho(S)@4; Phospho(T)@12; Methyl(I)@13; Oxidation(K)@14
Rhoptry-associated protein 1	KDEVIEKTEVSKK	Oxidation(D)@2; Trimethyl(K)@7; Phospho(S)@11
Rhoptry-associated protein 1	KKELTVIVSR	Methyl(E)@3; Phospho(S)@9; Methyl(R)@10
Rhoptry-associated protein 1	KTFSGIGFNLTEKEAK	Phospho(T)@11; Trimethyl(K)@13
Rhoptry-associated protein 1	SSSPSSTKSSSPSNVK	Methyl(K)@16
Rhoptry-associated protein 1	TDMLSLQNEESKIPNDKSANSKLATR	Phospho(T)@1; Oxidation(M)@3; Oxidation(P)@14; Methyl(D)@16
Glyceraldehyde-3-phosphate dehydrogenase, putative	IVSNASCTTNCLAPLAK	Methyl(I)@1; Carbamidomethyl(C)@7; Carbamidomethyl(C)@11
Glyceraldehyde-3-phosphate dehydrogenase, putative	LVSWYDNEWGYSNR	Methyl(L)@1; Trp->Phe@9
Glyceraldehyde-3-phosphate dehydrogenase, putative	IVSNASCTTNCLAPLAK	Methyl(S)@6; Carbamidomethyl(C)@7; Carbamidomethyl(C)@11
Glyceraldehyde-3-phosphate dehydrogenase, putative	IVSNASCTTNCLAPLAK	Methyl(I)@1; Carbamidomethyl(C)@7; Carbamidomethyl(C)@11
Glyceraldehyde-3-phosphate dehydrogenase, putative	IVSNASCTTNCLAPLAK	Methyl(I)@1; Carbamidomethyl(C)@7; Carbamidomethyl(C)@11

Glyceraldehyde-3-phosphate dehydrogenase, putative	IVSNASCTTNCLAPLAK	Methyl(I)@1; Carbamidomethyl(C)@7; Carbamidomethyl(C)@11
Glyceraldehyde-3-phosphate dehydrogenase, putative	IVSNASCTTNCLAPLAK	Methyl(S)@6; Carbamidomethyl(C)@7; Carbamidomethyl(C)@11
Glyceraldehyde-3-phosphate dehydrogenase, putative	VPIGTVSVVDLVCR	Carbamidomethyl(C)@13; Methyl(R)@14
Glyceraldehyde-3-phosphate dehydrogenase, putative	CALSNIIPASTGAAK	Carbamidomethyl(C)@1; Methyl(S)@4; Deamidated(N)@5
Glyceraldehyde-3-phosphate dehydrogenase, putative	IVSNASCTTNCLAPLAK	Methyl(S)@6; Carbamidomethyl(C)@7; Carbamidomethyl(C)@11
Glyceraldehyde-3-phosphate dehydrogenase, putative	AGRCALSNIIPASTGAAK	Carbamidomethyl(C)@4; Methyl(S)@7; Oxidation(N)@8; Phospho(S)@13; Phospho(T)@14
Glyceraldehyde-3-phosphate dehydrogenase, putative	IVSNASCTTNCLAPLAK	Methyl(I)@1; Carbamidomethyl(C)@7; Carbamidomethyl(C)@11
Glyceraldehyde-3-phosphate dehydrogenase, putative	CALSNIIPASTGAAK	Carbamidomethyl(C)@1; Methyl(L)@3
Glyceraldehyde-3-phosphate dehydrogenase, putative	VSVFAEKDPSQIPWGK	Deamidated(Q)@11; Methyl(I)@12
Actin	SYELPDGNIITVGNER	Methyl(T)@11
Actin, putative	YPIEHGIVTNWDDMEK	Methyl(H)@5
Actin	SYELPDGNIITVGNER	Methyl(E)@15
Actin	SYELPDGNIITVGNERF	Phospho(S)@1; Methyl(E)@3; Oxidation(R)@16; Oxidation(F)@17
Actin, putative	YPIEHGIVTNWDDMEK	Methyl(E)@4; Deamidated(N)@10
Hypothetical protein	NYNYSIMKHRYSEFL	Oxidation(Y)@2; Methyl(I)@6; Oxidation(F)@14
Cell division cycle protein 48 homologue,	GVLLYGPPGSGK	Methyl(K)@12
Cell division cycle protein 48 homologue, putative	GVLLYGPPGSGK	Methyl(K)@12
Cell division cycle protein 48 homologue, putative	GVLLYGPPGSGKTCIAR	Methyl(L)@4; Phospho(T)@13; Carbamidomethyl(C)@14
Hypothetical protein	IEKLTNINNITNDINNNIIL	Oxidation(N)@9; Methyl(N)@12
Hypothetical protein	NNSPKNEIEKNK	Methyl(N)@2; Oxidation(P)@4; Carbamyl(K)@10; Carbamyl(K)@12

Hypothetical protein	NEKHLSLILKK	Oxidation(N)@1; Oxidation(K)@3; Methyl(I)@8
Hypothetical protein	RKMKSTNNVLATNEK	Trimethyl(K)@4; Phospho(S)@5; Phospho(T)@12; Deamidated(N)@13
Hypothetical protein	NINIINNNNMIK	Oxidation(N)@1; Methyl(N)@8; Oxidation(M)@10
Hypothetical protein	NYNYSIMKHRYSEFL	Oxidation(Y)@2; Methyl(H)@9; Oxidation(F)@14
Hypothetical protein	TNDINNNIILEELSNR	Oxidation(N)@5; Deamidated(N)@7; Phospho(S)@14; Dimethyl(R)@16
Hypothetical protein	AYIPQNSLIK	Deamidated(N)@6; Phospho(S)@7; Dimethyl(K)@10
Hypothetical protein	CYTNIQKFNSRHYFK	Carbamidomethyl(C)@1; Methyl(N)@9; Phospho(S)@10; Oxidation(H)@12
Cell division cycle protein 48 homologue, putative	GVLLYGPPGSGK	Methyl(K)@12
Hypothetical protein	HKDISQGCKMK	Phospho(S)@5; Methyl(Q)@6; Carbamidomethyl(C)@8
Cell division cycle protein 48 homologue, putative	IKFDPLYKTK	Methyl(I)@1; Phospho(T)@9; Oxidation(K)@10
Cell division cycle protein 48 homologue, putative	KALVDENNGENK	Methyl(E)@6; Oxidation(K)@12
Hypothetical protein	KEQLTNRTK	Methyl(K)@1; Deamidated(Q)@3; Phospho(T)@5
Hypothetical protein	KMKSTNNVLATNEK	Methyl(N)@6
Hypothetical protein	KRKMKSTNNVLATNEK	Methyl(T)@7; Oxidation(K)@16
Cell division cycle protein 48 homologue, putative	LSPDVKLEEL	Phospho(S)@2; Methyl(L)@10
Cell division cycle protein 48 homologue, putative	QNSIDPALR	Methyl(D)@5
Cell division cycle protein 48 homologue, putative	QNSIDPALRR	Oxidation(P)@6; Methyl(R)@10
Hypothetical protein	QSFLHSKLKRTK	Deamidated(R)@10; Phospho(T)@11; Methyl(K)@12

Hypothetical protein	RHSTAILNHNISNLK	Trimethyl(R)@1; Deamidated(N)@8; Phospho(S)@12
Cell division cycle protein 48 homologue, putative	RSVSQADLIK	Oxidation(R)@1; Phospho(S)@2; Methyl(I)@9
Hypothetical protein	SLNNLKNKNDIIR	Phospho(S)@1; Methyl(K)@8; Oxidation(N)@9; Oxidation(D)@10
Hypothetical protein	TDKSYRSHTK	Methyl(T)@1; Phospho(S)@4
Hypothetical protein	TIYINNGPMKKDTK	Phospho(T)@1; Oxidation(Y)@3; Methyl(I)@4; Oxidation(N)@5
Hypothetical protein	VEVDETLTYHK	Oxidation(D)@4; Methyl(T)@6
Hypothetical protein	YCIGILLNSSLISSNK	Carbamidomethyl(C)@2; Deamidated(N)@8; Deamidated(N)@15; Methyl(K)@16
Hypothetical protein	YKYAERIVKSVFR	Methyl(E)@5; Phospho(S)@10; Oxidation(R)@13
Elongattion factor 2	ETVTEESTITCLGK	Carbamidomethyl(C)@11; Methyl(K)@14
Elongattion factor 2	RRGIVISEEQK	Oxidation(R)@1; Oxidation(R)@2; Phospho(S)@7; Methyl(K)@11
Elongattion factor 2	VAVKPKDSK	Oxidation(P)@5; Phospho(S)@8; Methyl(K)@9
Enolase (2-phosphoglycerate dehydratase)	DVQIVGDDLLVTNPTR	Methyl(N)@13; Phospho(T)@15; Carbamyl(R)@16
Enolase (2-phosphoglycerate dehydratase)	IEESLGNNAVFAGEKFRLQL	Methyl(E)@3; Oxidation(N)@7; Oxidation(N)@8; Deamidated(Q)@19
Enolase (2-phosphoglycerate dehydratase)	TEQKKIDNLMVEELDGSK	Phospho(T)@1; Methyl(E)@2
Enolase (2-phosphoglycerate dehydratase)	TPNNDKSLVK	Methyl(T)@1
Ornithine aminotransferase	ALSGGHYPISAILANDDVML	Phospho(S)@3; Oxidation(P)@8; Methyl(I)@9
Ornithine aminotransferase	PDILNAMINQAK	Oxidation(P)@1; Methyl(K)@12
RhopH2	VSIKYGAEQGVGSADSNTK	Oxidation(N)@17; Methyl(K)@19
RhopH2	QSLPIIDHVYHKDLKTLK	Phospho(S)@2; Trimethyl(K)@12; Oxidation(K)@18

RhopH2	NLSRYIDIKKELNDEK	Oxidation(D)@7; Methyl(E)@11; Deamidated(N)@13; Dioxidation(K)@16
RhopH2	QLMSAIRKYVTTLTK	Phospho(S)@4; Oxidation(Y)@9; Methyl(K)@15
High molecular weight rhoptry protein-2	YLLDNSNDIKK	Methyl(L)@3; Deamidated(N)@5
HSP 60	APGFGEHRKALIHDIAVMTGAK	Deamidated(R)@8; Methyl(D)@14; Phospho(T)@19
HSP 60	EKNSNIGFNAQEGK	Oxidation(K)@2; Oxidation(N)@3; Oxidation(N)@5; Methyl(E)@12
HSP 60	FGSDARTAMLTGCNK	Phospho(S)@3; Oxidation(M)@9; Carbamidomethyl(C)@13; Dimethyl(K)@15
HSP 60	LDDPQVVSYLGK	Methyl(D)@2; Phospho(S)@8
s-adenosylmethionine synthetase	VSIDEQSPDIAQCVHENR	Carbamidomethyl(C)@13; Methyl(E)@16
Hypothetical protein	FVLGGPAADAGLTGRK	Methyl(D)@9; Phospho(T)@13
s-adenosylmethionine synthetase	KNYIFIFGEITTKAK	Phospho(T)@12; Methyl(K)@13; Oxidation(K)@15
Membrane-associated calcium-binding protein	QTRSDESSGVK	Oxidation(D)@5; Methyl(E)@6; Phospho(S)@8; Oxidation(K)@11
HSP 101	GALKLYNSLSK	Methyl(L)@5; Deamidated(N)@7; Phospho(S)@10
HSP 101	GDVPKELQGYTVISLNFR	Methyl(Q)@8; Phospho(S)@14; Deamidated(N)@16
HSP 101	FEKTKKDKDGK	Methyl(K)@3; Phospho(T)@4
HSP 101	EQLKKYYEEYVITGER	Deamidated(Q)@2; Oxidation(K)@5; Methyl(E)@8; Phospho(T)@13
HSP 101	EPPIELQNSLKEAQQK	Phospho(S)@9; Methyl(E)@12
HSP 101	SNTIIIMTSNLGAELFKK	Methyl(S)@1; Oxidation(N)@2; Phospho(T)@3; Oxidation(K)@18
14-3-3 protein, putative	EASNCAQEAYQK	Methyl(N)@4; Carbamidomethyl(C)@5
14-3-3 protein, putative	ANVHNKNVAATYR	Phospho(T)@11; Oxidation(Y)@12; Methyl(R)@13

14-3-3 protein, putative	ASWRIISSVEQKEMSK	Phospho(S)@2; Oxidation(W)@3; Methyl(E)@10; Deamidated(Q)@11
Phosphoribosylpyrophosphate synthetase	ESLNDLFNIKS	Deamidated(N)@4; Methyl(L)@6; Phospho(S)@11
Lactate dehydrogenase	AKFDEAIAETK	Oxidation(F)@3; Oxidation(D)@4; Trimethyl(K)@11
Rhoptry-associated protein 2	RSSSLALVGTNNNDPIFAYCEK	Oxidation(R)@1; Phospho(S)@4; Carbamidomethyl(C)@20; Methyl(E)@21
RNA helicase	GIKPILNGYDTIGQAQSGTGK	Trimethyl(K)@3; Oxidation(N)@7
RNA helicase	VLVTTDLLAR	Methyl(T)@5; Carbamyl(R)@10
RNA helicase	VLVTTDLLAR	Methyl(L)@2
Chaperonin cpn60, mitochondrial precursor	GILDSSINSPNYLSKHR	Methyl(D)@4; Phospho(S)@5; Oxidation(Y)@12
Chaperonin cpn60, mitochondrial precursor	RSPNNKNRLFINK	Phospho(S)@2; Oxidation(P)@3; Methyl(L)@9; Oxidation(K)@13
Hypothetical protein	LNALIPLQTALRTHAK	Deamidated(N)@2; Phospho(T)@9; Methyl(T)@13
Hypothetical protein	ILTSSLPIIMENNR	Oxidation(M)@10; Oxidation(N)@12; Methyl(R)@14
Hypothetical protein	AGLKTIKTLK	Methyl(K)@7; Phospho(T)@8
Hypothetical protein	EVGIALLNVFTSKTYTNK	Methyl(I)@4; Phospho(T)@11
Hypothetical protein	IDMISNKIGLSNFK	Oxidation(M)@3; Phospho(S)@11; Dimethyl(K)@14
Hypothetical protein	ISPDSVEGIKK	Methyl(K)@11
Hypothetical protein	NISKGLSHPILISANK	Oxidation(K)@4; Phospho(S)@7; Methyl(I)@12; Phospho(S)@13
Hypothetical protein	NISKGLSHPILISANK	Oxidation(N)@1; Phospho(S)@3; Methyl(S)@7; Phospho(S)@13
Hypothetical protein	NKLSRGSAIK	Methyl(N)@1; Oxidation(K)@2; Phospho(S)@4; Deamidated(R)@5
Hypothetical protein	SALSKMNNKKEDKQLWQK	Phospho(S)@1; Oxidation(W)@16; Methyl(K)@18
Hypothetical protein	SVIILDKFKSYPR	Oxidation(P)@12; Methyl(R)@13

Hypothetical protein	TVSENSDK	Phospho(S)@6; Methyl(K)@8
Ring-infected erythrocyte surface antigen	VDNLGRSGGDIIK	Deamidated(N)@3; Methyl(R)@6
Ring-infected erythrocyte surface antigen	THLKKSSKSAK	Oxidation(K)@4; Methyl(K)@5; Phospho(S)@7
Ring-infected erythrocyte surface antigen	THLKKSSKSAK	Phospho(T)@1; Methyl(L)@3; Phospho(S)@7
Vacuolar ATP synthase catalytic subunit a	GRLTYIAPDGSYTLKDK	Methyl(L)@3; Phospho(T)@4; Oxidation(D)@9
Vacuolar ATP synthase subunit A, putative	LAEMPADSGYPAYLGARLASFYER	Methyl(S)@8; Phospho(S)@20; Oxidation(R)@24
Karyopherin beta	EYISAIDNAIAALGDVVLM	Phospho(S)@4; Methyl(D)@7; Oxidation(D)@15
Karyopherin beta	DNSLKSLSIEALVTIPER	Phospho(S)@8; Phospho(T)@14; Dimethyl(R)@18
Karyopherin beta	EQAVTAIAVIAGVIEEDFLKYYSTVVPMMK	Glu->pyro-Glu@N-term; Deamidated(Q)@2; Phospho(T)@5; Methyl(T)@24
Karyopherin beta	KLNNILNPN	Oxidation(N)@7; Methyl(N)@9
Hypothetical protein	CFQEGKYEEAVK	Carbamidomethyl(C)@1; Trimethyl(K)@12
Hypothetical protein	CFQEGKYEEAVK	Carbamidomethyl(C)@1; Trimethyl(K)@12
Hypothetical protein	CFQEGKYEEAVK	Carbamidomethyl(C)@1; Trimethyl(K)@12
Hypothetical protein	CFQEGKYEEAVK	Carbamidomethyl(C)@1; Trimethyl(K)@12
Hypothetical protein	CFQEGKYEEAVK	Carbamidomethyl(C)@1; Trimethyl(K)@12
Hypothetical protein	CFQEGKYEEAVK	Carbamidomethyl(C)@1; Trimethyl(K)@12
Hypothetical protein	CFQEGKYEEAVK	Carbamidomethyl(C)@1; Trimethyl(K)@12
Hypothetical protein	CFQEGKYEEAVK	Carbamidomethyl(C)@1; Trimethyl(K)@12
Hypothetical protein	CFQEGKYEEAVK	Carbamidomethyl(C)@1; Trimethyl(K)@12

Hypothetical protein	CFQEGKYEEAVK	Carbamidomethyl(C)@1; Trimethyl(K)@12
Hypothetical protein	CFQEGKYEEAVK	Carbamidomethyl(C)@1; Trimethyl(K)@12
Tubulin alpha	DVNAAVATIKTK	Methyl(D)@1; Deamidated(N)@3; Phospho(T)@8; Oxidation(K)@12
Tubulin alpha	DVNAAVATIKTKRTI	Deamidated(N)@3; Methyl(T)@11; Oxidation(K)@12; Phospho(T)@14
Tubulin alpha	GDVVPKDVNAAVATIK	Oxidation(P)@5; Oxidation(D)@7; Methyl(N)@9; Phospho(T)@14
Tubulin alpha	QLFHPEQLISGKEDAANNFAR	Methyl(E)@6; Phospho(S)@10; Deamidated(N)@18
T-complex protein beta subunit	IEEIIIGEDK	Carbamyl@N-term; Methyl(I)@5
T-complex protein beta subunit	IEEIIIGEDK	Carbamyl@N-term; Methyl(D)@9
T-complex protein beta subunit	TVTNDGATILKSVWLDNPVSK	Deamidated(N)@4; Phospho(S)@12; Methyl(K)@21
T-complex protein beta subunit	ILTPLNIEGTR	Phospho(T)@3; Oxidation(P)@4; Methyl(E)@8
Hypothetical protein	KNGGKDVSKNSK	Methyl(D)@6; Oxidation(K)@9; Phospho(S)@11
Hypothetical protein	KNGGKDVSKNSK	Methyl(D)@6; Oxidation(K)@9; Phospho(S)@11
HSP 70, putative	IINEPTAAAIAYGLDK	Tyr->Phe@12; Methyl(L)@14
Hypothetical protein	KKNGGKDVSK	Dioxidation(K)@2; Oxidation(K)@6; Methyl(D)@7; Phospho(S)@9
Hypothetical protein	KNGGKDVSKNSK	Deamidated(N)@2; Methyl(D)@6; Oxidation(K)@9; Phospho(S)@11
Hypothetical protein	ATSGDTHLGGEDFDNK	Ser->Ala@3; Dimethyl(K)@16
Heat shock protein SSB	QATKDAGAIAGLNVLRI	Gln->pyro-Glu@N-term; Dioxidation(K)@4; Methyl(I)@9; Dioxidation(R)@16
Stress-seventy subfamily A protein	EAQNNGPTVEEV	Glu->pyro-Glu@N-term; Methyl(N)@5; Phospho(T)@8

HSP 70, putative	IINEPTAAAIAYGLDK	Phospho(T)@6; Dimethyl(K)@16
HSP 70	LSKDDIDR	Methyl(D)@5
HSP 70	LSKDDIDR	Methyl(D)@5
Heat shock protein SSB	QATKDAGAIAGLNVLR	Gln->pyro-Glu@N-term; Phospho(T)@3; Oxidation(N)@13; Methyl(R)@16
Hypothetical protein	QNQITITNDKGRLSK	Trimethyl(K)@10; Phospho(S)@14
Erythrocyte membrane protein 3	NKASKGQQNNDLENDGLK	Phospho(S)@4; Methyl(N)@10; Deamidated(N)@14
Erythrocyte membrane protein 3	ESQDSSSEKSLKEK	Gln->Pro@3; Methyl(S)@10; Oxidation(K)@12
Erythrocyte membrane protein 3	TKKESQDSSSEKSLK	Oxidation(K)@2; Methyl(K)@3; Phospho(S)@10; Oxidation(K)@15
Erythrocyte membrane protein 3	NTPSEGQPNTGLK	Deamidated(Q)@7; Oxidation(P)@8; Methyl(N)@9
Erythrocyte membrane protein 3	RASRRPMMVKMQR	Phospho(S)@3; Oxidation(M)@7; Deamidated(Q)@12; Dimethyl(R)@13
Erythrocyte membrane protein 3	NTPSEGQPNTGLK	Oxidation(P)@8; Deamidated(N)@9; Methyl(L)@12
Erythrocyte membrane protein 3	DIRNKDLKSIGNMEQQNTGLKNTPSK	Deamidated(N)@12; Methyl(Q)@15; Phospho(S)@25
Erythrocyte membrane protein 3	DLSNKDMKNKELLNKDISNK	Phospho(S)@3; Methyl(K)@10; Oxidation(N)@14; Deamidated(N)@19
Erythrocyte membrane protein 3	ELRNKGSDGLK	Methyl(E)@1; Phospho(S)@7
Erythrocyte membrane protein 3	EQKKNDAQKAK	Methyl(K)@9
Erythrocyte membrane protein 3	EQKKNDAQKAK	Methyl(K)@9
Erythrocyte membrane protein 3	EQKKNDAQKAK	Methyl(K)@11
Erythrocyte membrane protein 3	GQQNTGLKNTPNER	Oxidation(N)@4; Oxidation(N)@9; Oxidation(P)@11; Trimethyl(R)@14
Erythrocyte membrane protein 3	GQQNTGLKNTPSEGQQNTGLK	Oxidation(P)@11; Oxidation(N)@17; Phospho(T)@18; Trimethyl(K)@21
Erythrocyte membrane protein 3	GSEGLKENAELKNKELQNKGSEGLK	Oxidation(N)@13; Deamidated(Q)@17; Methyl(E)@22

Erythrocyte membrane protein 3	LKRSLAQVLGNTR	Oxidation(R)@3; Phospho(S)@4; Methyl(T)@12; Oxidation(R)@13
Erythrocyte membrane protein 3	LSSRGVRDPRTKEALK	Phospho(S)@3; Deamidated(R)@7; Deamidated(R)@10; Methyl(K)@16
Erythrocyte membrane protein 3	NDAQKAKDLTK	Methyl(N)@1; Oxidation(D)@8; Phospho(T)@10
Erythrocyte membrane protein 3	NDAQKAKDLTKK	Oxidation(N)@1; Methyl(D)@2
Erythrocyte membrane protein 3	NKASKGQQNNDLENDGLK	Phospho(S)@4; Methyl(Q)@7; Deamidated(N)@9
Erythrocyte membrane protein 3	NKELRNKGSDGLK	Methyl(E)@3; Oxidation(R)@5; Phospho(S)@9
Erythrocyte membrane protein 3	NKSSFPDK	Deamidated(N)@1; Methyl(K)@2; Phospho(S)@4
Erythrocyte membrane protein 3	NSASKGQQNTGLK	Methyl(K)@13
Erythrocyte membrane protein 3	NSASKGQQNTGLKNTPSEGQQNNDLKNAPNER	Phospho(T)@10; Oxidation(K)@13; Deamidated(N)@23; Methyl(E)@31
Erythrocyte membrane protein 3	NTPSGGQQNTGLKNTPNER	Methyl(N)@1; Phospho(T)@2; Oxidation(P)@3
Erythrocyte membrane protein 3	QQNTGLKNAANK	Oxidation(N)@3; Methyl(K)@12
Erythrocyte membrane protein 3	QQNTGLKNAANK	Gln->pyro-Glu@N-term; Methyl(N)@3; Phospho(T)@4
Erythrocyte membrane protein 3	QQNTGLKNTASK	Methyl(Q)@2; Deamidated(N)@3; Deamidated(N)@8; Phospho(T)@9
Erythrocyte membrane protein 3	RENPDGEPLNTPEIHVIRPSDLMDKGENKSAGHPFK	Phospho(T)@11; Methyl(R)@18; Deamidated(N)@28
Erythrocyte membrane protein 3	RSLAQVLGNTR	Deamidated(N)@9; Phospho(T)@10; Methyl(R)@11
Erythrocyte membrane protein 3	RSLAQVLGNTR	Methyl(S)@2; Oxidation(N)@9; Phospho(T)@10; Deamidated(R)@11
Erythrocyte membrane protein 3	RSLAQVLGNTR	Deamidated(Q)@5; Phospho(T)@10; Methyl(R)@11
Erythrocyte membrane protein 3	SLKEKVNGEALKEK	Phospho(S)@1; Oxidation(K)@3; Methyl(E)@4; Oxidation(N)@7
Hypothetical protein	ESRKSKKSKKKETETDEK	Phospho(S)@8; Methyl(E)@12; Phospho(T)@13

Hypothetical protein	LDVKEANEIVQDVLQEF	Oxidation(N)@7; Methyl(D)@12
Hypothetical protein	MYGLFSSHYLNSRFSR	Methyl(S)@7; Oxidation(H)@8; Phospho(S)@15
Hypothetical protein	REFETLINSVR	Methyl(E)@2
Helicase	FENRILVSTDLFGR	Methyl(D)@10
Macrophage migration inhibitory factor homolog	SNNSALADQITK	Oxidation(N)@3; Oxidation(D)@8; Deamidated(Q)@9; Methyl(K)@12
t-complex protein 1, gamma subunit	ISGATIVNR	Oxidation(N)@8; Trimethyl(R)@9
Macrophage migration inhibitory factor homolog	ITSIGGINR	Methyl(I)@7
Hypothetical protein	KKKKKKKKKKKK	Oxidation(K)@5; Methyl(K)@8
t-complex protein 1, gamma subunit	KSITEAVASALEIIPK	Phospho(T)@4; Methyl(L)@11; Oxidation(P)@15
t-complex protein 1, gamma subunit	YAKVEKIPGGDITDSYVLK	Methyl(K)@6; Oxidation(D)@14
Hypothetical protein	GVPQTGKEGAEGGVNKENQMK	Phospho(T)@5; Oxidation(N)@15; Dimethyl(K)@21
Hypothetical protein	NALSNENGNLDDLK	Methyl(N)@1
Hypothetical protein	ITNPFEDMLK	Methyl(N)@3; Oxidation(P)@4; Oxidation(M)@8
Hypothetical protein	NNDLLKNKQLLKEAISK	Deamidated(Q)@9; Methyl(K)@12; Phospho(S)@16
T-complex protein 1, zeta subunit	GIDPISLDLLAKENIMALRR	Phospho(S)@6; Methyl(K)@12; Arg->Orn(R)@20
Hypothetical protein	FDTEGQIVSL	Methyl(D)@2; Deamidated(Q)@6
Hypothetical protein	FDTEGQIVSLK	Methyl(D)@2; Phospho(T)@3; Oxidation(K)@11
Hypothetical protein	KNKRSLDNKSDGPLKKSKIDDEGQFEK	Phospho(S)@5; Oxidation(D)@21; Methyl(E)@26

Hypothetical protein	MKLGFFIK	Oxidation(M)@1; Methyl(K)@2; Oxidation(F)@6
Hypothetical protein	MLTKKNTLKNSLSNGISK	Phospho(S)@13; Methyl(K)@18
Hypothetical protein	NSLSNGISKR	Phospho(S)@8; Trimethyl(K)@9
Hypothetical protein	NSLSNGISKR	Phospho(S)@8; Trimethyl(K)@9
Hypothetical protein	SLDNKSDGPLK	Oxidation(K)@5; Phospho(S)@6; Methyl(L)@10
6-phosphofructokinase	AERQIPISIIGVPK	Methyl(E)@2; Phospho(S)@8
6-phosphofructokinase	SGDKNAANKGGADGLVK	Methyl(D)@3; Deamidated(N)@8
6-phosphofructokinase	SASHVVLECALQTR	Carbamidomethyl(C)@9; Methyl(Q)@12; Phospho(T)@13
6-phosphofructokinase	AERQIPISIIGVPK	Methyl(E)@2; Phospho(S)@8
6-phosphofructokinase	AERQIPISIIGVPK	Methyl(E)@2; Phospho(S)@8
6-phosphofructokinase	DTKSGDKNAANKGGADGLVK	Phospho(S)@4; Methyl(K)@7; Oxidation(N)@8; Deamidated(N)@11
6-phosphofructokinase	MDTKSGDKNAANK	Phospho(T)@3; Methyl(K)@13
6-phosphofructokinase	SGDKNAANK	Methyl(K)@4
6-phosphofructokinase	SGDKNAANKGGADGLVK	Methyl(D)@3; Deamidated(N)@8
Acid phosphatase	GQILNAKYFK	Deamidated(N)@5; Methyl(K)@7
Acid phosphatase	GQILNAKYFK	Deamidated(N)@5; Methyl(K)@7
26S protease subunit regulatory subunit 6a, putative	MVRDAFNLAK	Methyl(K)@10
Dynein beta chain	SDKIKSNLDILKSKK	Methyl(N)@7; Phospho(S)@13; Carbamyl(K)@14
Hypothetical protein	GCEVIVSGKLRAQR	Carbamidomethyl(C)@2; Phospho(S)@7; Deamidated(Q)@13; Methyl(R)@14

Hypothetical protein	GCEVIVSGKLRAQR	Carbamidomethyl(C)@2; Phospho(S)@7; Deamidated(Q)@13; Methyl(R)@14
Dynein beta chain	DVMLNICKFSR	Carbamidomethyl(C)@7; Dimethyl(K)@8; Phospho(S)@10; Deamidated(R)@11
Dynein beta chain	NLVTNNTVNSNNTR	Oxidation(N)@1; Deamidated(N)@5; Methyl(N)@9; Deamidated(N)@12
26s proteasome aaa-atpase subunit rpt3	STNVKVIMATNR	Methyl(N)@3; Phospho(T)@10; Arg->Orn(R)@12
Hypothetical protein	NIVTSNMVTTY	Methyl(T)@10
60S Acidic ribosomal protein P2	LMCVLGGNENPSTK	Carbamidomethyl(C)@3; Deamidated(N)@8; Methyl(K)@14
60S Acidic ribosomal protein P2	KLQNIGGGVAAAPAGAAAVETAEAK	Trimethyl(K)@1; Oxidation(N)@4; Phospho(T)@21
Vacuolar ATP synthase subunit b	AEASRVNALAAVRNYKVCPR	Phospho(S)@4; Dimethyl(R)@13; Carbamidomethyl(C)@18
Vacuolar ATP synthase subunit b	GYPGYMYSDLSTIYERAGR	Oxidation(Y)@7; Methyl(S)@8
Plasmepsin 4	IDNALFTFYLPVHDK	Methyl(D)@2
T-complex protein 1, alpha subunit	TKYPVSSVNVIK	Methyl(S)@6; Phospho(S)@7
T-complex protein 1, alpha subunit	LTNGQIRLTLSSIDGTEK	Phospho(T)@2; Oxidation(D)@14; Methyl(E)@17; Oxidation(K)@18
26S proteasome regulatory subunit	LVIGTRVSLDMTTLTVMK	Oxidation(R)@6; Phospho(S)@8; Oxidation(M)@17; Methyl(K)@18
26S proteasome regulatory subunit	TLLARAMASNINCNFMR	Phospho(T)@1; Methyl(N)@10; Carbamidomethyl(C)@13
ZYRO0F11946p	YIGESARIIR	Oxidation(R)@7; Methyl(I)@9; Oxidation(R)@10
Eukaryotic translation initiation factor	NEKDKLAEQNLETLDVTK	Deamidated(N)@10; Methyl(E)@12; Dehydrated(T)@17
Eukaryotic translation initiation factor	LTPLSEDVISR	Methyl(L)@1; Oxidation(P)@3; Phospho(S)@5; Oxidation(R)@11
Elongation factor 1-gamma, putative	LNMPNFELGKDNK	Methyl(L)@1
QF122 antigen	MKKEKQNVDITEADIIRK	Oxidation(M)@1; Phospho(T)@11; Methyl(I)@16

QF122 antigen	LSQSNQTTNTK	Deamidated(Q)@3; Methyl(T)@8; Deamidated(N)@9; Phospho(T)@10
QF122 antigen	SKEVVKGGDQK	Phospho(S)@1; Methyl(D)@9; Deamidated(Q)@10
T-complex protein eta subunit	GGAKQFIEEVER	Methyl(K)@4; Deamidated(Q)@5; Oxidation(F)@6
Plasmepsin 1 precursor	DLSIGSVDPVVVELK	Methyl(D)@8
Plasmepsin 1 precursor	DLSIGSVDPVVVELK	Methyl(D)@8
Plasmepsin 1 precursor	DLSIGSVDPVVVELK	Methyl(D)@8
Plasmepsin 1 precursor	DLSIGSVDPVVVELK	Methyl(D)@8
Plasmepsin 1 precursor	DLSIGSVDPVVVELK	Methyl(D)@8
Leucine aminopeptidase	LTVVFEINVDK	Methyl(T)@2
Leucine aminopeptidase	LTVVFEINVDK	Methyl(T)@2; Oxidation(F)@5
Leucine aminopeptidase	LTVVFEINVDK	Methyl(T)@2; Oxidation(F)@5
Leucine aminopeptidase	LTVVFEINVDK	Methyl(T)@2; Oxidation(F)@5
Leucine aminopeptidase	LTVVFEINVDK	Methyl(T)@2; Oxidation(F)@5
Leucine aminopeptidase	YFSSLCKFLPISEK	Methyl(L)@5; Carbamidomethyl(C)@6
Hypothetical protein	LFTRAVEKR	Methyl(R)@9
Hypothetical protein	LNELNNLRDNYSKK	Oxidation(D)@9; Oxidation(N)@10; Trimethyl(K)@14
Hypothetical protein	LTTFKSGEHHNK	Phospho(T)@3; Methyl(K)@12
Hypothetical protein	RDESVKNVETRR	Oxidation(D)@2; Methyl(S)@4; Oxidation(R)@11

Ribosomal phosphoprotein P0	ADEPKKEEAKK	Oxidation(D)@2; Oxidation(K)@6; Dimethyl(K)@11
Hypothetical protein	GSGYGGNFGRGGYRSGGGMGGGFR	Deamidated(N)@7; Dimethyl(R)@14; Oxidation(M)@19; Gly->Ser@22
Hypothetical protein	GSGYGGNFGRGGYRSGGGMGGGFR	Ser->Met@2; Deamidated(R)@10; Oxidation(R)@14; Methyl(R)@24
cAMP-dependent protein kinase regulatory subunit	QVLMTLNKK	Methyl(Q)@1; Phospho(T)@5; Oxidation(N)@7
26S proteasome subunit	EALGVALDARR	Methyl(E)@1; Oxidation(R)@10; Oxidation(R)@11
Lysine--tRNA ligase	MINIIKEHK	Oxidation(M)@1; Deamidated(N)@3; Methyl(E)@7; Oxidation(H)@8
Lysine--tRNA ligase	EHKIELPNPPTAAK	Oxidation(P)@7; Oxidation(P)@10; Methyl(T)@11; Oxidation(K)@14
Lysine--tRNA ligase	IELPNPPTAAK	Methyl(L)@3; Deamidated(N)@5
Lysine--tRNA ligase	IMRVSASGQKLR	Phospho(S)@7; Methyl(R)@12
TCP-1/cpn60 chaperonin family, putative	LATETVMMILK	Methyl(T)@5
Cysteine protease	AGRSSGTGGSVGTK	Deamidated(R)@3; Phospho(T)@13; Methyl(K)@14
Cysteine protease	ELTRPITTIQIHSVSENKDTHLLESK	Phospho(T)@8; Methyl(I)@9; Oxidation(H)@12; Oxidation(D)@19
Cysteine protease	SSITHNSVSSSNITKSNKNTNK	Phospho(S)@7; Methyl(T)@20; Oxidation(N)@21; Oxidation(K)@22
ATP-dependent DNA helicase	MIKEGRISGR	Phospho(S)@8; Methyl(R)@10
ATP-dependent DNA helicase	KATEVTVQDVR	Oxidation(K)@1; Methyl(T)@3; Phospho(T)@6; Oxidation(R)@11
Hexokinase	GAAITAAVIALNADIPQLP	Phospho(T)@5; Methyl(I)@9; Deamidated(N)@12; Oxidation(D)@14
Hexokinase	GTYYAIDFGGTNFRAVR	Oxidation(Y)@4; Deamidated(N)@12; Dimethyl(R)@17

Cg4 protein	LGIDIGNDNSVVATINK	Methyl(N)@7; Phospho(T)@14
Cg4 protein	LTPTLVGFTEKER	Phospho(T)@4; Methyl(T)@9; Deamidated(R)@13
Early transcribed membrane protein 10.2	VKSKSSNGKSK	Oxidation(K)@4; Methyl(S)@6; Phospho(S)@10; Oxidation(K)@11
S-antigen	KSKNSIINMLIGMIR	Phospho(S)@2; Methyl(N)@4; Phospho(S)@5; Oxidation(M)@9
S-antigen	KSKNSIINMLIGMIR	Phospho(S)@2; Methyl(N)@4; Phospho(S)@5; Oxidation(M)@9
S-antigen	NKKSKNSIINMLIG	Phospho(S)@7; Oxidation(M)@11; Methyl(I)@13
Nascent polypeptide associated complex alpha chain	NNNDLVQSIMELS	Deamidated(N)@3; Oxidation(D)@4; Deamidated(Q)@7; Methyl(E)@11
Zinc finger transcription factor (krox1)	DDISAKSDASKK	Oxidation(K)@6; Methyl(S)@7; Phospho(S)@10; Oxidation(K)@12
Zinc finger transcription factor (krox1)	RSEGDKRSEGDKRSEGDKR	Deamidated(R)@1; Oxidation(R)@7; Methyl(D)@11; Oxidation(K)@12
Zinc finger transcription factor (krox1)	QRSESRRSNVSRR	Methyl(S)@5; Deamidated(N)@9; Oxidation(R)@12; Oxidation(R)@13
Zinc finger transcription factor (krox1)	RSNVTNKLSDR	Oxidation(N)@3; Methyl(L)@8; Phospho(S)@9
Zinc finger transcription factor (krox1)	SDASKKDDISAKSDVSRR	Oxidation(D)@8; Methyl(D)@14; Phospho(S)@16
Zinc finger transcription factor (krox1)	SESYRSESNRRSESDGRSESDGRSEGDRR	Oxidation(R)@10; Oxidation(R)@11; Phospho(S)@12; Methyl(E)@25
Zinc finger transcription factor (krox1)	SEVSRRSNVTNK	Trimethyl(R)@6; Phospho(S)@7; Oxidation(K)@12
Clathrin heavy chain	ILENKIDNNR	Oxidation(K)@5; Deamidated(N)@9; Methyl(R)@10
Hypothetical protein	NITTIFVITNK	Methyl(N)@1; Phospho(T)@9
Clathrin heavy chain	NNNFYDKK	Methyl(N)@1; Oxidation(Y)@5
Clathrin heavy chain	SNNPEAYKEVIEK	Phospho(S)@1; Methyl(E)@5
Ribosomal protein S2	AIFNALSKTY	Methyl(I)@2; Oxidation(F)@3; Oxidation(K)@8; Phospho(T)@9

PfEMP1	QMHQAAKKQLGSSSSR	Gln->pyro-Glu@N-term; Phospho(S)@15; Dimethyl(R)@16
Erythrocyte membrane protein 1	SFADIGDIIRGK	Phospho(S)@1; Methyl(D)@4; Oxidation(K)@12
Erythrocyte membrane protein 1	TVKQIARQMHQAAKKQLGSSSSRALK	Phospho(T)@1; Oxidation(K)@3; Methyl(I)@5
Hypothetical protein	NVKNMLIDIDNIK	Oxidation(M)@5; Methyl(D)@8; Oxidation(K)@13
Hypothetical protein	NIQSNNELLYTSK	Oxidation(N)@1; Oxidation(N)@5; Methyl(S)@12
Hypothetical protein	YDTISGHIISGDINSRNLK	Phospho(S)@5; Methyl(I)@8
Conserved Plasmodium protein, unkown	NYINNKMKNKNK	Oxidation(N)@1; Methyl(N)@4; Oxidation(N)@5; Oxidation(K)@12
Conserved Plasmodium protein, unkown	TTHIITELYQK	Methyl(I)@4
Conserved Plasmodium protein, unkown	TTHIITELYQK	Methyl(I)@4
Conserved Plasmodium protein, unkown	FNLNESSLLSTSLSR	Methyl(T)@11; Phospho(S)@12; Phospho(S)@14; Deamidated(R)@15
Conserved Plasmodium protein, unkown	KNNDKKKSK	Methyl(N)@3; Phospho(S)@8
Conserved Plasmodium protein, unkown	NDANKHTK	Oxidation(D)@2; Deamidated(N)@4; Oxidation(H)@6; Methyl(K)@8
Chain A, Re-Refinement Of Uncomplexed	SRTYEKDGTK	Phospho(T)@3; Trimethyl(K)@6; Oxidation(D)@7
Plasmepsin Ii		
Polyubiquitin	TITLDVEPSDTIENVK	Methyl(D)@5
Polyubiquitin	TITLDVEPSDTIENVK	Methyl(D)@5
Polyubiquitin	TITLDVEPSDTIENVK	Methyl(D)@5
Polyubiquitin	TITLDVEPSDTIENVK	Methyl(D)@5
Polyubiquitin	TITLDVEPSDTIENVK	Methyl(D)@5
Polyubiquitin	TITLDVEPSDTIENVK	Methyl(D)@5

Polyubiquitin	TITLDVEPSDTIENVK	Methyl(D)@5
Polyubiquitin	TITLDVEPSDTIENVK	Methyl(D)@5
Polyubiquitin	TITLDVEPSDTIENVK	Methyl(D)@5
Polyubiquitin	TITLDVEPSDTIENVK	Methyl(D)@5
Hypothetical protein	IVEAGSALENKK	Methyl(I)@1; Deamidated(N)@10; Oxidation(K)@12
Hypothetical protein	NNEKHLNIGSFSFYK	Oxidation(N)@7; Methyl(S)@10
DNA/RNA-binding protein	IAIGAASIMEK	Dioxidation(M)@9; Methyl(E)@10
Hypothetical protein	ENSKKNIDGLNNISGNGR	Phospho(S)@3; Oxidation(K)@5; Oxidation(N)@6; Methyl(L)@10
Hypothetical protein	ITSSSSEKSNLTLRIDRGMAATAK	Methyl(S)@4; Deamidated(N)@10; Phospho(T)@22
Hypothetical protein	NIDGLNNISGNGR	Oxidation(N)@6; Trimethyl(R)@13
Hypothetical protein	SKTRGGKRVQNVVEK	Oxidation(R)@4; Deamidated(R)@8; Methyl(E)@14; Oxidation(K)@15
Hypothetical protein	TISKNSPNLSSAKNIK	Phospho(T)@1; Phospho(S)@3; Methyl(K)@16
Hypothetical protein	TLEIGGNHFK	Methyl(T)@1
hsp70 interacting protein	PSGMPGGMPGGMPGGMPDLNSPEMK	Phospho(S)@21; Oxidation(P)@22; Trimethyl(K)@25
Actin, putative	YPIEHGIVTNWDDMEK	Methyl(H)@5
Actin, putative	YPIEHGIVTNWDDMEK	Methyl(E)@4; Deamidated(N)@10
Hypothetical protein	IGSKKGNVVSSK	Oxidation(K)@4; Methyl(K)@5; Phospho(S)@11
Hypothetical protein	YDCYKYNSGFSNYRDDASK	Carbamidomethyl(C)@3; Oxidation(K)@5; Oxidation(Y)@6; Methyl(R)@14
Hypothetical protein	YDCYKYNSGFSNYRDDASK	Carbamidomethyl(C)@3; Oxidation(Y)@4; Oxidation(Y)@6; Methyl(D)@16

Hypothetical protein	HVTIPTTPLTLEK	Phospho(T)@3; Methyl(T)@10; Oxidation(K)@13
Hypothetical protein	SKMSDFSNAKVNMGNKKSK	Phospho(S)@1; Methyl(K)@2; Deamidated(N)@15; Dioxidation(K)@19
CTRP	LLVVGVSTASENK	Methyl(E)@11
CTRP	LLVVGVSTASENK	Methyl(E)@11
CTRP	PTINNNNNNSSGSNNSSRTNIR	Oxidation(N)@5; Deamidated(N)@7; Methyl(N)@15; Dioxidation(R)@22
Hypothetical protein	NSSINFSFKNGKKGETTEK	Phospho(S)@7; Methyl(K)@9
ATP-dependent Clp protease subunit	LIGAAPGYVGYEQGGLLTDAVR	Methyl(I)@2
Hypothetical protein	VVTKAVQRSR	Phospho(T)@3; Dimethyl(K)@4; Deamidated(R)@10
Hypothetical protein	KKKGKNNNIK	Oxidation(K)@2; Methyl(N)@6
Hypothetical protein	KDNEIVSNTTTKK	Oxidation(N)@3; Phospho(T)@10; Methyl(T)@11
Hypothetical protein	INTYIILPNNK	Methyl(L)@7; Oxidation(N)@9
Hypothetical protein	ETTNKQNIKKVTKNDK	Oxidation(K)@10; Phospho(T)@12; Methyl(N)@14
Hypothetical protein	IKTNTNTKTQK	Methyl(T)@3; Deamidated(N)@6; Oxidation(K)@8; Phospho(T)@9
Putative esterase	TLLDFLK	Methyl(D)@4; Oxidation(K)@7
Malate:quinone oxidoreductase	VALKDSHTLR	Dimethyl(K)@4; Oxidation(H)@7; Phospho(T)@8
Hypothetical protein	ISINLDNVNK	Carbamidomethyl@N-term; Deamidated(N)@4; Methyl(K)@10
Hypothetical protein	SYDSININISNNQNPK	Deamidated(N)@8; Oxidation(N)@14; Oxidation(P)@15; Methyl(K)@16
Hypothetical protein	LYTNFHNEEKDHLK	Oxidation(N)@4; Oxidation(F)@5; Methyl(E)@8; Oxidation(H)@12

Surface protein	NKYISLYNKVK	Oxidation(N)@1; Phospho(S)@5; Oxidation(K)@9; Methyl(K)@11
Hypothetical protein	KKKKKKKKKKKK	Oxidation(K)@5; Methyl(K)@8
Hypothetical protein	YIHPYNINIWDKMK	Oxidation(M)@13; Methyl(K)@14
Hypothetical protein	RRGRPPGSTKLSK	Oxidation(R)@1; Oxidation(P)@6; Phospho(T)@9; Dimethyl(K)@13
Hypothetical protein	TMPIPLNNLNAYTTNNNDNNNK	Phospho(T)@1; Methyl(N)@10
Hypothetical protein	YLYQDKNVENTR	Methyl(Q)@4; Oxidation(D)@5
Hypothetical protein	FIGSNNTNSDSNVK	Methyl(N)@5; Oxidation(N)@6
Hypothetical protein	VADELIEK	Oxidation(D)@3; Dehydrated(E)@4; Dimethyl(K)@8
DNA packaging protein of prophage; terminase large subunit	VAEELVEK	Methyl(L)@5
Conserved Plasmodium protein, unkown	SNTTSSKLK	Deamidated(N)@2; Methyl(K)@9
Hypothetical protein	TKDHVIKANNKGSTR	Carbamyl@N-term; Trimethyl(K)@2; Oxidation(H)@4; Phospho(T)@14
Hypothetical protein	RTPKRKINKLENEKK	Deamidated(R)@1; Phospho(T)@2; Methyl(E)@11; Deamidated(N)@12
3D7Surf4.1; surface-associated interspersed gene 4.1	TPKVSAPAGGKKSK	Phospho(S)@5; Pro->pyro-Glu(P)@7; Dimethyl(K)@14
3D7Surf4.1; surface-associated interspersed gene 4.1	TPKVSAPAGGKK	Phospho(S)@5; Trimethyl(K)@12
3D7Surf4.1; surface-associated interspersed gene 4.1	TPKVSAPAGGK	Methyl(K)@3; Phospho(S)@5
Hypothetical protein	KSETEASNK	Methyl(N)@8; Oxidation(K)@9
60S ribosomal protein L10, putative	MLSCAGADRLQTGMR	Oxidation(M)@1; Phospho(S)@3; Carbamidomethyl(C)@4; Methyl(L)@10
Ribosomal L10	VDIGQVLLSIR	Methyl(Q)@5; Phospho(S)@9; Deamidated(R)@11
Ser/Thr protein kinase	LNGNINLK	Methyl(N)@2; Carbamyl(K)@8

Chain A, Crystal Structure Of Histo-Aspartic Protease (Hap)	LTSKAGTISGIFSKDLVTIGK	Phospho(S)@3; Oxidation(F)@12; Methyl(S)@13
Proteasome regulatory component	IGIESSLDVVGITAK	Methyl(L)@7; Phospho(T)@13
Proteasome regulatory component	LAATKMEIVVELLMGDIPDRSIFSNKIMYK	Phospho(T)@4; Dimethyl(K)@5; Oxidation(M)@14
Hypothetical protein	KSTLSNIQEVKADVK	Phospho(S)@5; Trimethyl(K)@15
Hypothetical protein	KKKKKKKKKKKK	Oxidation(K)@5; Methyl(K)@8
Hypothetical protein	RLNRNILSSLDMKKKKK	Oxidation(M)@12; Methyl(K)@17
Hypothetical protein	LINQEKELENIK	Methyl(E)@5; Deamidated(N)@10; Dioxidation(K)@12
Cell division cycle ATPase	AIANECKANFISVK	Carbamidomethyl(C)@6; Methyl(K)@14
Cell division cycle ATPase	FMSIGISAPK	Phospho(S)@3; Methyl(I)@4
Cell division cycle ATPase	IEFMKISVDEDK	Methyl(E)@2; Phospho(S)@7; Oxidation(K)@12
PfEMP1	SMLSRSAVDSGKGDK	Methyl(R)@5; Oxidation(D)@9; Oxidation(D)@14
Hypothetical protein	IDTNNKLDTNNK	Deamidated(N)@5; Methyl(D)@8; Deamidated(N)@11
Hypothetical protein	VDPTLISK	Oxidation(P)@3; Trimethyl(K)@8
40S ribosomal subunit protein S6	DKTEKKQNKTNNIKNDK	Phospho(T)@3; Oxidation(K)@9; Deamidated(N)@12; Methyl(D)@16
PfEMP1	DTTSGVVTTAPSSAK	Methyl(D)@1; Phospho(S)@4; Oxidation(P)@11
PfEMP1	TEISGGDGGGSSRKK	Methyl(S)@11; Phospho(S)@12; Oxidation(K)@15
Ring-infected erythrocyte surface antigen	VDNLGRSGGDIIK	Deamidated(N)@3; Methyl(R)@6
Ring-infected erythrocyte surface antigen	NKDAKSLSGNIANEINLINK	Methyl(D)@3; Phospho(S)@6; Deamidated(N)@10
Ring-infected erythrocyte surface antigen	TLHVPDTR	Methyl(D)@6

Ring-infected erythrocyte surface antigen	TLHVPDTR	Methyl(D)@6
Ring-infected erythrocyte surface antigen	TLHVPDTR	Oxidation(H)@3; Methyl(R)@8
PFG377 protein	LNQVLNDNKENKTIDNLDK	Deamidated(N)@2; Oxidation(N)@6; Methyl(N)@8; Phospho(T)@13
Hypothetical protein	QNEKQVHNKNK	Methyl(Q)@1; Oxidation(N)@2; Oxidation(H)@7; Deamidated(N)@8
Hypothetical protein	GGNSTNINK	Deamidated(N)@6; Methyl(I)@7; Oxidation(K)@9
Hypothetical protein	LGEMKKKKMDTK	Methyl(K)@8; Phospho(T)@11; Oxidation(K)@12
Hypothetical protein	SKTFVNGSLKEKK	Oxidation(K)@2; Phospho(T)@3; Oxidation(F)@4; Methyl(N)@6
Hypothetical protein	NDGVKNDGVK	Deamidated(N)@1; Methyl(D)@2
Hypothetical protein	SQVGNQDINTFR	Methyl(Q)@6; Oxidation(D)@7; Oxidation(F)@11
Hypothetical protein	ETKETDEQNKR	Methyl(E)@7; Carbamyl(R)@11
Hypothetical protein	KTNYEIINNYNDK	Phospho(T)@2; Oxidation(N)@8; Dimethyl(K)@13
Ubiquitin-protein ligase 1	TNDLLNNEIISLQNIANR	Oxidation(N)@2; Methyl(S)@11
Ubiquitin-protein ligase 1	IDNQEHNQKVK	Methyl(H)@6
Ubiquitin-protein ligase 1	IDNQEHNQKVK	Methyl(Q)@8
Ubiquitin-protein ligase 1	KNVSYVTFLNPSYVR	Oxidation(Y)@13; Methyl(R)@15
Ubiquitin-protein ligase 1	LHSGLFISIFK	Methyl(L)@1; Phospho(S)@8
DEAD/DEAH box helicase	TDDTTKLNEEKDFLYSR	Methyl(E)@9; Oxidation(F)@13; Oxidation(R)@17
EMP1	SFADIGDIIRGK	Phospho(S)@1; Methyl(D)@4; Oxidation(K)@12
Oligopeptide transport system permease protein	VTNIGPNITNVRLTFTNI	Methyl(T)@9; Oxidation(N)@10; Phospho(T)@14

Dynein heavy chain, putative	LQGEYKVK	Oxidation(Y)@5; Methyl(K)@6
Hypothetical protein	GNNSNNNNNKSNNNKTSHNNK	Deamidated(N)@8; Dimethyl(K)@10; Deamidated(N)@12; Deamidated(N)@20
PfEMP1	EQWTKIKGKYK	Glu->pyro-Glu@N-term; Phospho(T)@4; Methyl(K)@9; Trioxidation(Y)@10
EMP1	SFADIGDIIRGK	Phospho(S)@1; Methyl(D)@4; Oxidation(K)@12
PfEMP1	SKNTPGVTAMTPNTLY	Methyl(K)@2; Phospho(T)@4
Hypothetical protein	LTDLTTSPVSKR	Phospho(T)@6; Methyl(S)@7; Oxidation(R)@12
Hypothetical protein	ICDVNVLPCNGK	Carbamidomethyl(C)@2; Oxidation(D)@3; Oxidation(N)@5; Carbamidomethyl(C)@9; Methyl(K)@12
Hypothetical protein	TRGRSSSYVK	Phospho(T)@1; Deamidated(R)@4; Methyl(S)@5
Hypothetical protein	KGNIDKNK	Deamidated(N)@3; Oxidation(K)@6; Methyl(N)@7
Hypothetical protein	KKTYNYSKNHFKK	Oxidation(K)@1; Methyl(N)@9; Oxidation(H)@10
Hypothetical protein	YHYESLIDMLK	Oxidation(H)@2; Oxidation(Y)@3; Phospho(S)@5; Methyl(D)@8
Hypothetical protein	KKKKKKKKKKKK	Oxidation(K)@5; Methyl(K)@8
18hrs - treated		
Heat shock protein	IPKIQQIIKEFFNGK	Oxidation(P)@2; Methyl(Q)@5; Deamidated(N)@13
Heat shock protein	DTTFAPEQISAMVLEKMK	Methyl(D)@1; Oxidation(P)@6; Methyl(L)@14
Heat shock protein	GVPKIEVTFTVDK	Methyl(T)@8; Oxidation(F)@9; Oxidation(K)@13
Heat shock protein	ALTKDNHLLGK	Methyl(K)@4; Oxidation(N)@6; Oxidation(K)@11
Heat shock protein	DKLADKIEKEDK	Methyl(D)@5; Carbamyl(K)@12

Heat shock protein	GINPDEAVAYGAAIQAGII	Oxidation(P)@4; Oxidation(D)@5; Methyl(E)@6
Heat shock protein	GTGKSRGITITNDKGRLSK	Methyl(S)@5; Oxidation(R)@6; Deamidated(N)@12
78 kDa glucose-regulated protein precursor	KVLDDAKYEK	Methyl(K)@1; Oxidation(D)@5; Oxidation(K)@10
Heat shock protein	MINDAEKFADEDKNLR	Trimethyl(K)@7; Oxidation(F)@8; Oxidation(D)@12
Heat shock protein	MINDAEKFADEDKNLREK	Methyl(D)@12; Deamidated(R)@16; Oxidation(K)@18
Luminal binding protein	NAVVTVPAYFNDAQR	Methyl(T)@5; Oxidation(R)@15
Luminal binding protein	NAVVTVPAYFNDAQR	Methyl(N)@1; Oxidation(R)@15
Heat shock protein	VMDYFIKMFK	Oxidation(F)@5; Methyl(K)@10
Endoplasmin precursor, putative	GVVDSDDLPLNVSR	Methyl(S)@5; Methyl(R)@14
Endoplasmin homolog precursor	LSEPSTYKLIYKEYRKFLK	Oxidation(P)@4; Trioxidation(Y)@7; Trimethyl(K)@8; Oxidation(K)@12
Endoplasmin homolog precursor	VDLINNLGTIAK	Carbamyl@N-term; Oxidation(N)@5; Oxidation(N)@6; Methyl(K)@12
Endoplasmin homolog precursor	VDLINNLGTIAK	Methyl(D)@2; Deamidated(N)@6
Endoplasmin homolog precursor	VDLINNLGTIAK	Oxidation(D)@2; Deamidated(N)@6; Trimethyl(K)@12
Endoplasmin homolog precursor	DLELTNSIKIMYQSAK	Methyl(S)@7
Endoplasmin homolog precursor	DPRGATLKRGTR	Oxidation(K)@8; Methyl(R)@9
Endoplasmin homolog	ELISNAADALEK	Oxidation(D)@8; Methyl(L)@10; Oxidation(K)@12
Endoplasmin homolog	ELISNAADALEKIR	Glu->pyro-Glu@N-term; Methyl(E)@11
Endoplasmin homolog	ELISNAADALEKIR	Glu->pyro-Glu@N-term; Oxidation(N)@5; Methyl(D)@8; Oxidation(R)@14

Endoplasmin homolog precursor	ELISNAADALEKIRFLSLSDESVLGEEK	Deamidated(N)@5; Methyl(D)@8; Oxidation(F)@15
Endoplasmin precursor, putative	GVVDSDDLPLNVSR	Methyl(D)@6; Methyl(N)@11
Endoplasmin precursor, putative	GVVDSDDLPLNVSR	Methyl(S)@5; Methyl(R)@14
Endoplasmin precursor, putative	GVVDSDDLPLNVSR	Methyl(D)@6; Methyl(R)@14
Endoplasmin precursor, putative	GVVDSDDLPLNVSR	Methyl(D)@6; Methyl(S)@13
Endoplasmin homolog precursor	IVRKILDTFHKLYK	Methyl(I)@5; Oxidation(K)@11
Endoplasmin homolog precursor	LMKMNVSNSDQIKAMSGQK	Oxidation(M)@4; Oxidation(M)@15; Methyl(Q)@18; Oxidation(K)@19
Endoplasmin homolog precursor	MNVSNSDQIKAMSGQK	Oxidation(N)@2; Deamidated(Q)@8; Methyl(K)@16
Endoplasmin homolog precursor	MNVSNSDQIKAMSGQK	Oxidation(M)@1; Deamidated(N)@5; Methyl(S)@6; Oxidation(D)@7
Endoplasmin homolog precursor	VDLINNLGTIAKSGTSNFLEAISK	Deamidated(N)@5; Oxidation(K)@12; Methyl(S)@16; Oxidation(N)@17
Endoplasmin homolog	YMSFVKGVVDSDDLPLNVSR	Oxidation(D)@10; Methyl(R)@20
Glyceraldehyde-3-phosphate dehydrogenase, putative	IVSNASCTTNCLAPLAK	Methyl(I)@1; Carbamidomethyl(C)@7; Carbamidomethyl(C)@11
Glyceraldehyde-3-phosphate dehydrogenase, putative	IVSNASCTTNCLAPLAK	Methyl(I)@1; Carbamidomethyl(C)@7; Carbamidomethyl(C)@11
Glyceraldehyde-3-phosphate dehydrogenase, putative	IVSNASCTTNCLAPLAK	Methyl(N)@4; Carbamidomethyl(C)@7; Carbamidomethyl(C)@11
Glyceraldehyde-3-phosphate dehydrogenase, putative	IVSNASCTTNCLAPLAK	Methyl(S)@3; Carbamidomethyl(C)@7; Carbamidomethyl(C)@11
Glyceraldehyde-3-phosphate dehydrogenase, putative	LVSWYDNEWGYSNR	Methyl(L)@1; Trp->Phe@9
Glyceraldehyde-3-phosphate dehydrogenase, putative	LVSWYDNEWGYSNR	Methyl(L)@1; Trp->Phe@9
Glyceraldehyde-3-phosphate dehydrogenase, putative	LVSWYDNEWGYSNR	Methyl(L)@1; Trp->Phe@9

Glyceraldehyde-3-phosphate dehydrogenase, putative	CALSNIIPASTGAAK	Carbamidomethyl(C)@1; Methyl(L)@3
Glyceraldehyde-3-phosphate dehydrogenase, putative	DPSQIPWGKCQVDVVCESTGVFLTK	Carbamidomethyl(C)@10; Carbamidomethyl(C)@16; Methyl(S)@18; Oxidation(K)@25
Glyceraldehyde-3-phosphate dehydrogenase, putative	KVSVFAEKDPSQIPWGK	Methyl(E)@7; Oxidation(P)@10
Glyceraldehyde-3-phosphate dehydrogenase, putative	MAVTKLGINGFGR	Methyl(K)@5; Deamidated(N)@9; Oxidation(F)@11; Oxidation(R)@13
Glyceraldehyde-3-phosphate dehydrogenase, putative	SSIFDMKAGLALNDNFFK	Methyl(D)@5; Deamidated(N)@13; Oxidation(N)@15
Glyceraldehyde-3-phosphate dehydrogenase, putative	TKLGINGFGRIGRLVFR	Deamidated(R)@10; Oxidation(R)@13; Methyl(R)@17
Glyceraldehyde-3-phosphate dehydrogenase, putative	VPIGTVSVVDLVCR	Methyl(D)@10; Carbamidomethyl(C)@13
Actin	YPIEHGIVTNWDDMEK	Methyl(H)@5; Oxidation(M)@14
Actin, putative	YPIEHGIVTNWDDMEK	Methyl(E)@4; dethiomethyl(M)@14
Actin	SYELPDGNIITVGNER	Methyl(E)@15
Actin	DITTLAPSTMK	Oxidation(D)@1; Oxidation(P)@7; Methyl(T)@9; Dioxidation(M)@10
Actin, putative	ELPDGNIITVGNERFR	Oxidation(P)@3; Methyl(T)@9; Oxidation(F)@15; Oxidation(R)@16
Actin	GYGFSTSAEKEIVR	Methyl(T)@6
HSP 90	GVVDSEDLPLNISRESLQQNKILKVIK	Methyl(D)@7; Oxidation(P)@9; Carbamyl(R)@14; Deamidated(N)@20
HSP 90	NDLINNLGTIAR	Deamidated(N)@1; Deamidated(N)@6; Methyl(R)@12
HSP 90	CLDMFSELAENK	Carbamidomethyl(C)@1; Methyl(E)@7; Oxidation(N)@11; Oxidation(K)@12
HSP 90	DKIRYESITDTQK	Oxidation(Y)@5; Methyl(E)@6
HSP 90	EIFLRELISNASDALDK	Oxidation(R)@5; Oxidation(D)@13; Methyl(L)@15; Oxidation(K)@17
HSP 90	ELISNASDALDK	Ser->Ala@7; Methyl(D)@11
HSP 90	GFEVIYMVDPIDEYAVQQLK	Carbamyl@N-term; Methyl(D)@9

HSP 90	IIPDKTNNTLTIEDSGIGMTK	Oxidation(N)@7; Deamidated(N)@8; Methyl(D)@14
HSP 90	IMDDCEEIIPEWLNFVK	Oxidation(M)@2; Carbamidomethyl(C)@5; Oxidation(W)@12; Deamidated(N)@14; Methyl(K)@17
HSP 90	NADESKEENEDEEKK	Deamidated(N)@9; Trimethyl(K)@15
HSP 90	RAPFDMFENRK	Oxidation(P)@3; Oxidation(F)@4; Oxidation(M)@6; Methyl(E)@8
HSP 70	ATAGDTHLGGEDFDNR	Asp->Asn@5; Methyl(R)@16
HSP 70	DGIPPAPRKVPQIEVTFDIDANGILNVTAVEK	Oxidation(P)@11; Methyl(T)@16; Oxidation(F)@17; Oxidation(D)@18
HSP 70	NENVDIIANDQGNRTTPSYVAFTDTER	Oxidation(D)@10; Methyl(T)@16; Oxidation(P)@17; Oxidation(Y)@19
HSP 70	STGKQNHITITNDKGR	Methyl(K)@4; Oxidation(N)@6; Deamidated(N)@12; Dioxidation(R)@16
Lactate dehydrogenase	KAKIVLVGSGMIGGVMATL	Methyl(K)@3; Oxidation(M)@11; Oxidation(M)@16
Lactate dehydrogenase	AKFDEAIAETKRMK	Oxidation(K)@2; Oxidation(F)@3; Methyl(D)@4; Oxidation(R)@12
Lactate dehydrogenase	EWNRDDLLPLNNK	Glu->pyro-Glu@N-term; Oxidation(P)@9; Deamidated(N)@12; Methyl(K)@13
Lactate dehydrogenase	LNVCPRDVNAHIVGAHGNKMVLLK	Carbamidomethyl(C)@4; Methyl(N)@9; Deamidated(N)@18; Oxidation(M)@20
Elongation factor 1 alpha	IDKRSGKVVEENPK	Oxidation(D)@2; Oxidation(K)@3; Oxidation(P)@13; Methyl(K)@14
Elongation factor 1 alpha	YEEIKKEVK	Methyl(K)@9
Elongation factor 1 alpha	AGMVLNFAPSAVVSECK	Carbamyl@N-term; Methyl(N)@6; Carbamidomethyl(C)@16
Elongation factor 1 alpha	FEKESAEMGKGSFKY	Oxidation(F)@1; Oxidation(K)@3; Methyl(E)@4
Elongation factor 1 alpha	TIEKFEKESAEMGKGSFKYAWVLDK	Methyl(E)@11; Oxidation(F)@17; Oxidation(Y)@19; Oxidation(W)@21
Elongation factor 1 alpha	YAWVLDKLKAERER	Oxidation(K)@7; Methyl(K)@9; Oxidation(R)@12; Oxidation(R)@14

Elongation factor 1 alpha	YEEIKKEVK	Methyl(E)@7
Elongation factor 1 alpha	YEEIKKEVK	Methyl(K)@6
Elongation factor 1 alpha	YEEIKKEVK	Methyl(E)@7
Rhoptry-associated protein 1	TSTPSGTQTSGLKSSSPSSTK	Methyl(S)@5; Carbamyl(K)@13; Dioxidation(K)@21
Rhoptry-associated protein 1	NVADGINVNGDNNYGK	Oxidation(N)@9; Methyl(D)@11; Oxidation(K)@16
Rhoptry-associated protein 1	DDMEFKASPSVVK	Methyl(S)@10
Rhoptry-associated protein 1	FSSESFLENK	Methyl(E)@4
Rhoptry-associated protein 1	IGKESDEEPFMFSENK	Methyl(E)@8; Oxidation(M)@11; Oxidation(K)@16
Rhoptry-associated protein 1	IPNDKSANSKLATR	Oxidation(P)@2; Oxidation(D)@4; Methyl(S)@6; Oxidation(N)@8
Rhoptry-associated protein 1	IQYAKLINIR	Methyl(Q)@2; Oxidation(K)@5; Deamidated(N)@8
Rhoptry-associated protein 1	TDMLSLQNEESKIPNDK	Methyl(N)@15
Elongation factor 2	VFSGTVATGQKVR	Carbamyl@N-term; Deamidated(Q)@10; Methyl(R)@13
Elongation factor 2	AGIISSKNAGDARFTDTR	Deamidated(R)@13; Dimethyl(R)@18
Elongation factor 2	GIKVEMPQLDQYLDKL	Trimethyl(K)@3; Oxidation(Y)@12
Elongation factor 2	DSNKNSYKIIMNIRER	Methyl(D)@1; Oxidation(K)@4; Deamidated(N)@12; Oxidation(R)@16
Elongation factor 2	ANYLHSNFQWDK	Deamidated(N)@2; Methyl(N)@7; Deamidated(Q)@9; Oxidation(W)@10
Elongation factor 2, putative	LLTGKQLLK	Methyl(K)@9
Elongation factor 2, putative	MVPTSDKGR	Oxidation(P)@3; Carbamyl(K)@7; Methyl(R)@9
Elongation factor 2, putative	MVPTSDKGRFYAFGR	Oxidation(M)@1; Methyl(T)@4; Deamidated(R)@15
Elongation factor 2	VAVKPKDSKQLPK	Methyl(K)@9; Deamidated(Q)@10

Elongation factor 2	VEMPQLDQYLDKL	Deamidated(Q)@5; Deamidated(Q)@8; Methyl(D)@11; Oxidation(K)@12
Phosphoglycerate kinase	VKNMFHGNTNIIHISR	Oxidation(H)@6; Deamidated(N)@10; Methyl(I)@14
Phosphoglycerate kinase	NMISIGAGGAITIK	Carbamidomethyl@N-term; Methyl(I)@11
Phosphoglycerate kinase	MIIGGGMAYTF	Oxidation(M)@1; Methyl(I)@2; Oxidation(F)@11
Phosphoglycerate kinase	DDINKTTISISR	Methyl(D)@2; Oxidation(K)@5; Oxidation(R)@12
Phosphoglycerate kinase	EQYIENVRKCK	Glu->pyro-Glu@N-term; Methyl(Q)@2; Deamidated(N)@6; Carbamidomethyl(C)@10; Oxidation(K)@11
Phosphoglycerate kinase	FSYMGNLDGILGDIIEYYIDGK	Methyl(D)@13
Phosphoglycerate kinase	FSYMGNLDGILGDIIEYYIDGK	Methyl(D)@13
Phosphoglycerate kinase	FSYMGNLDGILGDIIEYYIDGK	Methyl(L)@7
Phosphoglycerate kinase	GIYSGCIGFLTFEGNFIFNIVIR	Carbamidomethyl(C)@6; Methyl(E)@13; Oxidation(F)@16
Phosphoglycerate kinase	GLLGEEVLFLNDCVGK	Carbamyl@N-term; Methyl(E)@6; Carbamidomethyl(C)@13
Phosphoglycerate kinase	ILYKEQNDNKK	Oxidation(Y)@3; Methyl(E)@5; Oxidation(K)@11
Phosphoglycerate kinase	ITATLPTINHLKK	Trimethyl(K)@13
Phosphoglycerate kinase	KEKYDINNK	Methyl(D)@5
Phosphoglycerate kinase	KGNNFSDAILNIFPGGSMTGSPK	Deamidated(N)@4; Methyl(D)@7; Deamidated(N)@11; Oxidation(M)@18
Phosphoglycerate kinase	KKNMISIGAGGAITIK	Trimethyl(K)@16
Phosphoglycerate kinase	KNMISIGAGGAITIK	Oxidation(K)@1; Oxidation(N)@2; Oxidation(M)@3; Methyl(K)@15
Phosphoglycerate kinase	KQMIIDYQYIDLHNLINNKNELEK	Oxidation(M)@3; Methyl(E)@23; Oxidation(K)@24

Phosphoglycerate kinase	MLGNKLSISDLKDIK	Deamidated(N)@4; Methyl(I)@8; Oxidation(D)@10; Oxidation(K)@15
Phosphoglycerate kinase	NMISIGAGGAITIK	Methyl(K)@14
Phosphoglycerate kinase	NMISIGAGGAITIK	Methyl(K)@14
Phosphoglycerate kinase	RKEKYDINNK	Methyl(K)@4; Oxidation(N)@8; Deamidated(N)@9; Oxidation(K)@10
Phosphoglycerate kinase	TVIWNGPQGVFEMPNFAK	Trimethyl(K)@18
Merozoite surface protein 1 precursor	MQIKKLTLLKEQLESK	Oxidation(M)@1; Oxidation(K)@5; Methyl(L)@8
Merozoite surface protein 1 precursor	KNENIKKLLDKINEIK	Oxidation(K)@7; Oxidation(D)@10; Carbamyl(K)@11; Trimethyl(K)@16
Merozoite surface protein 1 precursor	TIDQNKNADNEEGKKK	Methyl(E)@11
Merozoite surface protein 1 precursor	SQDPTKSVQIPK	Carbamyl@N-term; Deamidated(Q)@2; Methyl(I)@10; Dioxidation(P)@11
Merozoite surface protein 1 precursor	SGPSGTSPSSRSNTLPR	Deamidated(R)@11; Oxidation(N)@13; Methyl(L)@15; Oxidation(R)@17
Merozoite surface protein 1 precursor	KQIEKNIFTFNLNLNDILNSRLKK	Oxidation(N)@11; Methyl(N)@13; Deamidated(N)@19; Oxidation(K)@24
Merozoite surface protein 1 precursor	EEKEKFPSSPPTTPPSPAK	Oxidation(K)@3; Methyl(K)@5; Oxidation(P)@15; Oxidation(P)@17
Merozoite surface protein 1 precursor	EEKEKFPSSPPTTPPSPAK	Oxidation(K)@5; Oxidation(P)@7; Oxidation(P)@17; Trimethyl(K)@19
Merozoite surface protein 1 precursor	EKFPSSPPTTPPSPAKTDEQK	Glu->pyro-Glu@N-term; Oxidation(P)@8; Methyl(E)@19
Merozoite surface protein 1 precursor	ELGQDKMQIK	Deamidated(Q)@4; Methyl(Q)@8
Merozoite surface protein 1 precursor	EVIKNKNYTGNSPSENNKK	Oxidation(N)@7; Methyl(T)@9; Deamidated(N)@17; Oxidation(K)@19
Merozoite surface protein 1 precursor	FQDMLNISQHQCVK	Oxidation(D)@3; Oxidation(M)@4; Methyl(S)@8; Carbamidomethyl(C)@12
Merozoite surface protein 1 precursor	FYENILKNNDTYFNDDIK	Methyl(N)@8

Merozoite surface protein 1 precursor	HISSNEYIIEDSFK	Methyl(N)@5
Merozoite surface protein 1 precursor	INEKIITDNKERK	Deamidated(N)@2; Methyl(T)@7; Oxidation(K)@10; Deamidated(R)@12
Merozoite surface protein 1 precursor	ITKLSDLKAIDDKIDL	Oxidation(D)@6; Oxidation(K)@8; Oxidation(K)@13; Methyl(D)@15
Merozoite surface protein 1 precursor	KGISEKDFNHYYTLK	Trimethyl(K)@1; Oxidation(H)@10
Merozoite surface protein 1 precursor	KLINDDTKKDMLGK	Methyl(T)@7; Oxidation(K)@8
Merozoite surface protein 1 precursor	KVDVTPKSQDPTK	Methyl(T)@5; Oxidation(D)@10; Oxidation(P)@11
Merozoite surface protein 1 precursor	LNDNLHLGKKK	Methyl(D)@3; Oxidation(N)@4; Oxidation(K)@10
Merozoite surface protein 1 precursor	LNFYFDLLRAK	Deamidated(N)@2; Methyl(D)@6; Oxidation(K)@11
Merozoite surface protein 1 precursor	LNSLNNPHNVLQNFSVFFNK	Deamidated(N)@9; Oxidation(N)@13; Methyl(K)@20
Merozoite surface protein 1 precursor	NKKVDVTPK	Deamidated(N)@1; Oxidation(P)@8; Methyl(K)@9
Merozoite surface protein 1 precursor	NKNYTGNSPSENNKKVNEALKSYENFLPEAK	Deamidated(N)@13; Methyl(K)@15; Oxidation(P)@28; Oxidation(K)@31
Merozoite surface protein 1 precursor	PQPDVTPSPLSVRVSGSSGSTK	Deamidated(Q)@2; Oxidation(P)@7; Oxidation(R)@13; Methyl(K)@22
Merozoite surface protein 1 precursor	SNTLPRSNTSSGASPPADASDSDAKSYADLK	Oxidation(D)@23; Oxidation(K)@25; Methyl(D)@29; Oxidation(K)@31
Merozoite surface protein 1 precursor	TTIANINELIEGSK	Oxidation(N)@5; Methyl(E)@8
Merozoite surface protein 1 precursor	VTTVVTPPQPDVTPSPLSVR	Methyl(T)@6; Deamidated(Q)@9; Oxidation(P)@16; Deamidated(R)@20
Ornithine aminotransferase	FVADEVQTGLGR	Methyl(D)@4
Ornithine aminotransferase	IPENSAKIIVCNNNFSGR	Carbamidomethyl(C)@11; Methyl(N)@12; Deamidated(N)@14; Oxidation(R)@18
Ornithine aminotransferase	KYNVLFVADEVQTGLGR	Methyl(K)@1; Deamidated(N)@3; Oxidation(F)@6; Oxidation(R)@17

Ornithine aminotransferase	KYNVLFVADEVQTGLGR	Oxidation(N)@3; Methyl(L)@5; Deamidated(R)@17
RNA helicase-1	DPKTILVKKDELTLEGIR	Oxidation(P)@2; Methyl(E)@15; Oxidation(R)@18
Conserved Plasmodium protein, unknown	NIDEKVNESLEKKINEPINEILVETK	Methyl(I)@21
Conserved Plasmodium protein, unknown	EKLTNINNITNDINNNIILEELSNRNK	Deamidated(N)@11; Methyl(L)@22
Conserved Plasmodium protein, unknown	KFNNEYINEEK	Methyl(E)@5; Oxidation(N)@8
Conserved Plasmodium protein, unknown	KNFIAKINR	Oxidation(N)@2; Trimethyl(R)@9
Cell division cycle protein 48 homologue, putative	QNSIDPALRR	Oxidation(P)@6; Deamidated(R)@9; Methyl(R)@10
Conserved Plasmodium protein, unknown	KFNNEYINEEK	Methyl(N)@3; Oxidation(K)@11
Conserved Plasmodium protein, unknown	TNDLKLNNIIELNKEQNIQTKKGNI	Methyl(I)@9; Oxidation(N)@17; Deamidated(Q)@19; Deamidated(N)@24
Cell division cycle protein 48 homologue, putative	AAIRDAIDAEEMNK	Methyl(E)@11; Deamidated(N)@13; Oxidation(K)@14
Cell division cycle protein 48 homologue, putative	AARAAIRDAIDAEEMNK	Oxidation(R)@7; Methyl(D)@11; Oxidation(M)@15
Cell division cycle protein 48 homologue, putative	EDNTDKKALVDENNGENKVPKK	Oxidation(N)@3; Oxidation(K)@7; Methyl(E)@16
Conserved Plasmodium protein, unknown	EIIKGSYENDKNGKNYENGK	Oxidation(N)@12; Methyl(N)@15

Conserved Plasmodium protein, unknown	EITSNDLLCEYREEVLKKFNNEYINEEK	Carbamidomethyl(C)@9; Oxidation(R)@12; Methyl(E)@14; Oxidation(F)@19; Deamidated(N)@25
Conserved Plasmodium protein, unknown	EKTIYINNGPMKKDTK	Glu->pyro-Glu@N-term; Oxidation(K)@2; Methyl(D)@14
Conserved Plasmodium protein, unknown	HTKKNYLNKNIKNK	Oxidation(Y)@6; Trimethyl(K)@14
Conserved Plasmodium protein, unknown	IKVNENLK	Oxidation(K)@2; Methyl(K)@8
Conserved Plasmodium protein, unknown	ILNSKNYKAEWNKNKKNK	Oxidation(Y)@7; Oxidation(N)@14; Methyl(K)@15; Oxidation(K)@18
Cell division cycle protein 48 homologue, putative	IQVLPIDDTIEGLAK	Deamidated(Q)@2; Oxidation(P)@5; Methyl(I)@6
Cell division cycle protein 48 homologue, putative	KALVDENNGENKVPKK	Methyl(N)@7; Deamidated(N)@8
Conserved Plasmodium protein, unknown	KDINDIYINKKKINNIDFK	Methyl(I)@6; Deamidated(N)@15; Oxidation(K)@19
Conserved Plasmodium protein, unknown	KDNKLNHVSDKNITYNDK	Methyl(D)@2; Oxidation(K)@11; Deamidated(N)@12
Conserved Plasmodium protein, unknown	KIMNNINYISSQKK	Methyl(I)@2; Oxidation(N)@7; Oxidation(Y)@8
Conserved Plasmodium protein, unknown	LINTIMNPPAPK	Methyl(I)@2; Oxidation(N)@3; Oxidation(M)@6
Conserved Plasmodium protein, unknown	LNNIIELNK	Methyl(N)@2; Oxidation(N)@3
Conserved Plasmodium protein, unknown	LQQSPKVSINK	Methyl(S)@4; Oxidation(P)@5
Conserved Plasmodium protein, unknown	NDDKNIDEK	Deamidated(N)@5; Methyl(I)@6; Oxidation(D)@7
Conserved Plasmodium protein, unknown	NEHDNIIISK	Methyl(D)@4
Conserved Plasmodium protein, unknown	NIKGNNGYK	Oxidation(K)@3; Oxidation(Y)@8; Trimethyl(K)@9
Conserved Plasmodium protein, unknown	NKGEMIKENEK	Oxidation(M)@5; Methyl(I)@6; Oxidation(K)@11

Conserved Plasmodium protein, unknown	NKNDIIRTGKYANEK	Deamidated(N)@1; Methyl(K)@2; Oxidation(K)@15
Conserved Plasmodium protein, unknown	NYNKDTIHKSNENTHTNIK	Deamidated(N)@3; Oxidation(K)@9; Methyl(N)@13
Conserved Plasmodium protein, unknown	QHDTFQFTNLYNR	Deamidated(Q)@6; Trimethyl(R)@13
Cell division cycle protein 48 homologue, putative	QNSIDPALRR	Oxidation(P)@6; Methyl(R)@10
Cell division cycle protein 48 homologue, putative	QNSIDPALRR	Gln->pyro-Glu@N-term; Methyl(N)@2; Deamidated(R)@10
Cell division cycle protein 48 homologue, putative	REKTNGEVERR	Deamidated(N)@5; Methyl(E)@7
Conserved Plasmodium protein, unknown	RHSTAILNHNISNLK	Oxidation(R)@1; Oxidation(H)@2; Oxidation(H)@9; Methyl(K)@15
Conserved Plasmodium protein, unknown	RHSTAILNHNISNLK	Oxidation(R)@1; Oxidation(H)@2; Methyl(I)@11; Oxidation(K)@15
Conserved Plasmodium protein, unknown	RHSTAILNHNISNLK	Oxidation(R)@1; Oxidation(H)@2; Oxidation(N)@8; Methyl(N)@13
Conserved Plasmodium protein, unknown	SNIERKENGEEGDIIKDLNIYNDANK	Oxidation(N)@2; Oxidation(R)@5; Oxidation(N)@8; Methyl(D)@23
Conserved Plasmodium protein, unknown	TKISNVKDKNDKIYLNK	Deamidated(N)@5; Oxidation(K)@12; Oxidation(Y)@14; Methyl(K)@17
Conserved Plasmodium protein, unknown	VSNIIENTISPILIPNYKKIK	Deamidated(N)@3; Methyl(E)@6
Cell division cycle protein 48 homologue, putative	VVSQLLTLMDGIK	Methyl(Q)@4
Conserved Plasmodium protein, unknown	WIKLFENYPNKRFFR	Oxidation(P)@9; Methyl(R)@12; Oxidation(R)@15
Conserved Plasmodium protein, unknown	YKTYTKLLSK	Dioxidation(Y)@1; Methyl(S)@9; Oxidation(K)@10

14-3-3 protein, putative	ATDIAENELPSTH	Methyl(T)@12; Oxidation(H)@13
14-3-3 protein, putative	ASWRIISSVEQKEMSK	Methyl(I)@6
14-3-3 protein, putative	KEASNCAQEAYQKATDIAENELPSTHPIR	Carbamidomethyl(C)@6; Oxidation(Y)@11; Methyl(Q)@12; Deamidated(N)@20
14-3-3 protein, putative	SVAYKNAVGAR	Oxidation(N)@6; Methyl(R)@11
14-3-3 protein, putative	TLVEQCVNNDKDELTVEER	Methyl(L)@2; Carbamidomethyl(C)@6; Deamidated(N)@9
14-3-3 protein, putative	VEEELNNICQDILNLLTK	Carbamidomethyl(C)@9; Deamidated(Q)@10; Oxidation(N)@14; Methyl(K)@18
HSP 70	IINEPTAAALAFGLEK	Oxidation(F)@12; Methyl(E)@15
HSP 70	IVRASNGDAWIEAQGKK	Oxidation(N)@6; Dioxidation(W)@10; Methyl(K)@17
HSP 70	EVKATNGNTSLGGEDFDQR	Deamidated(N)@6; Methyl(E)@14; Deamidated(Q)@18
HSP 70	GVNPDEAVALGAAIQGGVLK	Deamidated(N)@3; Dioxidation(P)@4; Methyl(L)@10
HSP 70	KYDEDATKKEQKNLPYK	Oxidation(K)@12; Trimethyl(K)@17
HSP 70	QGKVIENSEGFR	Gln->pyro-Glu@N-term; Dimethyl(K)@3
HSP 70	QLEDFKDKISDSDKDELR	Methyl(E)@3; Oxidation(D)@4
HSP 70	QLEDFKDKISDSDKDELR	Methyl(E)@3; Oxidation(D)@4
HSP 70	YSPSQIGACVL	Methyl(S)@2; Carbamidomethyl(C)@9
Karyopherin beta	FNNAEDLIKVWLNHLPIKEDDAEGR	Oxidation(N)@2; Deamidated(N)@3; Oxidation(D)@6; Methyl(K)@9
Karyopherin beta	GECINLISCIVEDNSSSLVK	Methyl(E)@2; Carbamidomethyl(C)@3; Carbamidomethyl(C)@9
Karyopherin beta	ILSEKTDNDK	Methyl(D)@7; Oxidation(D)@9; Oxidation(K)@10
Karyopherin beta	MLLQILVDQDVR	Deamidated(Q)@4; Oxidation(D)@8; Methyl(D)@10
Karyopherin beta	NDLNNTVLSILK	Trimethyl(K)@12

Karyopherin beta	QAACYGVIQATK	Carbamidomethyl(C)@4; Methyl(Q)@9; Oxidation(K)@12
Membrane-associated calcium-binding protein	QTRSDESSGVK	Deamidated(Q)@1; Methyl(R)@3
Membrane-associated calcium-binding protein	QVQAEMGQIDSDKDGFISLNELNDAFAQNLDAK	Gln->pyro-Glu@N-term; Oxidation(M)@6; Trimethyl(K)@13; Oxidation(N)@20
s-adenosylmethionine synthetase	KIICDTYGGWGAHGGGAFSGKDASKVDR	Carbamidomethyl(C)@4; Oxidation(F)@18; Methyl(D)@27
RhopH2	YGAEQGVGSADSNTK	Methyl(Q)@5; Oxidation(D)@11; Deamidated(N)@13
RhopH3	GEEFKKLMDMELK	Methyl(D)@9; Oxidation(M)@10
RhopH4	ILWMHASSK	Methyl(H)@5
RhopH5	IQVSKIDDINNLNIYEHK	Deamidated(N)@11; Methyl(E)@16; Oxidation(H)@17; Oxidation(K)@18
RhopH6	KCHNVIGNIR	Carbamidomethyl(C)@2; Oxidation(H)@3; Methyl(N)@4; Deamidated(N)@8
RhopH7	KEYNEFLQDKR	Deamidated(N)@4; Methyl(L)@7; Oxidation(D)@9; Oxidation(K)@10
RhopH8	NTIKEGNEFLMSILHMK	Deamidated(N)@1; Oxidation(M)@11; Methyl(I)@13; Oxidation(M)@16
RhopH9	NTIKEGNEFLMSILHMK	Oxidation(K)@4; Oxidation(F)@9; Oxidation(M)@11; Methyl(L)@14
RhopH10	QRIYDMTINNAL	Methyl(I)@3; Deamidated(N)@9
RhopH11	QSLPIIDHVYHK	Methyl(Q)@1; Oxidation(H)@11
RhopH11	RVSNITNDMIK	Oxidation(R)@1; Oxidation(N)@4; Methyl(T)@6
RhopH11	VKGEEFKKLMDMELK	Oxidation(M)@12; Methyl(E)@13
RhopH11	YGAEQGVGSADSNTKLCSDILK	Oxidation(Y)@1; Oxidation(D)@11; Methyl(S)@12; Carbamidomethyl(C)@17
Phosphoethanolamine N-methyltransferase	IIFEANDILTK	Methyl(E)@4; Oxidation(K)@11
Acid phosphatase	GQILNAKYFK	Deamidated(N)@5; Methyl(K)@10

Rhoptry-associated protein, putative	DIKSMLSTDDYQSFFK	Oxidation(Y)@11; Deamidated(Q)@12; Methyl(S)@13
Rhoptry-associated protein, putative	FMENLDLYIMKESER	Oxidation(N)@4; Methyl(D)@6
Rhoptry-associated protein, putative	QYSNRAAENFK	Methyl(Q)@1; Oxidation(Y)@2
Protein disulfide isomerase	LIPEYNEAANMLNEKK	Methyl(I)@2; Deamidated(N)@6; Oxidation(N)@10
Protein disulfide isomerase	SLKSEPIPEDDKNAPVK	Trimethyl(K)@3; Oxidation(P)@15
GTP-binding nuclear protein ran/tc4	VCETIPMVLVGNKVDVKDRQVK	Carbamidomethyl(C)@2; Methyl(E)@3; Oxidation(P)@6; Oxidation(K)@17; Deamidated(Q)@20
Tubulin alpha	FDGALNVDVTEFQTNLVPYPR	Leu->Val@5; Methyl(E)@11
Hypothetical protein	SKTRGGKRVQNVVEK	Oxidation(R)@4; Deamidated(R)@8; Methyl(E)@14; Oxidation(K)@15
Hypothetical protein	TNNLEKFGELWLNARSTK	Oxidation(N)@13; Oxidation(R)@15; Methyl(K)@18
Hypothetical protein	QKINRLNSEENERIEK	Dioxidation(R)@5; Deamidated(N)@11; Methyl(E)@12
Hypothetical protein	GMNGININNDNDRDEDNNKDK	Deamidated(N)@9; Methyl(D)@12; Oxidation(R)@13; Oxidation(D)@14
Hypothetical protein	TIKAMELAMYESLGR	Methyl(E)@6; Oxidation(M)@9
Hypothetical protein	CYKNEMYDEKATMENNKK	Carbamidomethyl(C)@1; Oxidation(Y)@2; Dioxidation(K)@3; Methyl(E)@5
Hypothetical protein	IHHISSSNSNTIKIK	Oxidation(H)@3; Methyl(T)@11
Hypothetical protein	IRMKKNEFYESVK	Methyl(R)@2
Hypothetical protein	LAFMNSGEQGKVMK	Deamidated(N)@5; Methyl(K)@11; Oxidation(K)@14
Hypothetical protein	MFPKQLVIQETQKL	Oxidation(P)@3; Methyl(Q)@5
Hypothetical protein	MFPKQLVIQETQKL	Oxidation(M)@1; Methyl(Q)@5

Hypothetical protein	NSPNLSSAKNIK	Methyl(S)@2; Deamidated(N)@10
Hypothetical protein	NYSNEKSIYVKNSK	Methyl(N)@4
Hypothetical protein	QKMEENGSDDGLENIMPVK	Methyl(E)@5; Oxidation(D)@10; Oxidation(M)@16
Hypothetical protein	TISKNSPNLSSAKNIK	Methyl(L)@9; Deamidated(N)@14
Hypothetical protein	TLMNNDNDKINTK	Methyl(L)@2
Plasmepsin	IDNALFTFYLPVHDK	Methyl(D)@2
Plasmepsin	LNHDLYWQIDLDIHFGK	Oxidation(Y)@6; Oxidation(W)@7; Methyl(K)@17
Chaperonin cpn60, mitochondrial precursor	DKGILDSSINSPNYLSK	Methyl(D)@1; Oxidation(N)@10; Oxidation(P)@12; Dioxidation(Y)@14
Chaperonin cpn60, mitochondrial precursor	KDKGILDSSINSPNYLSK	Methyl(S)@12; Deamidated(N)@14
Chaperonin cpn60, mitochondrial precursor	RSPNNKNR	Methyl(R)@1; Oxidation(P)@3
Chaperonin cpn60	TSLITKEEYK	Methyl(K)@6; Oxidation(K)@10
Dynein beta chain	TNMNRNIFKALAKK	Deamidated(N)@4; Deamidated(N)@6; Oxidation(K)@13; Trimethyl(K)@14
Dynein beta chain	NEIKNSYNEFNK	Deamidated(N)@8; Methyl(E)@9
Dynein beta chain	KYQNKKNKK	Deamidated(Q)@3; Methyl(N)@7
Dynein beta chain	VDSKAININKEDEMVYTNINR	Methyl(E)@11; Oxidation(D)@12; Oxidation(N)@20; Oxidation(R)@21
Dynein beta chain	KINLKKKKK	Methyl(L)@4
Dynein beta chain	DTNYIQLLEKLLDNWINDIERLFK	Methyl(D)@1; Oxidation(Y)@4; Oxidation(W)@15; Deamidated(R)@21
Dynein beta chain	EAFNDPNDNQLKK	Methyl(K)@13

Dynein beta chain	EIKKETSMELSNDKKGKKKYQNK	Deamidated(N)@12; Methyl(D)@13; Deamidated(N)@22; Oxidation(K)@23
Dynein beta chain	FVFESAKNFKPNLNCY	Oxidation(F)@3; Methyl(S)@5; Oxidation(P)@11; Oxidation(N)@14; Carbamidomethyl(C)@15
Dynein beta chain	KSISILFKEHWALEENK	Trimethyl(K)@1
Dynein beta chain	NIFNNIENTLFK	Methyl(E)@7
Dynein beta chain	SLGDQLILQTER	Methyl(E)@11; Deamidated(R)@12
Dynein beta chain	SLGDQLILQTER	Methyl(L)@2; Deamidated(Q)@5
Dynein beta chain	VSVTDNVKSFMKK	Deamidated(N)@6; Oxidation(F)@10; Oxidation(M)@11; Methyl(K)@13
Conserved Plasmodium protein, unknown	KEELGNDYVEDMKLK	Methyl(K)@15
Conserved Plasmodium protein, unknown	SYPRVISKGSDAMK	Methyl(S)@10
Conserved Plasmodium protein, unknown	ILTSSLPIIMENNR	Oxidation(P)@7; Oxidation(M)@10; Methyl(E)@11
Conserved Plasmodium protein, unknown	EDKQLWQK	Oxidation(D)@2; Oxidation(K)@3; Deamidated(Q)@4; Methyl(K)@8
Conserved Plasmodium protein, unknown	FKSYPRVISKGSDAMKCAVGPEELSK	Methyl(S)@12; Oxidation(D)@13; Carbamidomethyl(C)@17
Conserved Plasmodium protein, unknown	ILTSSLPIIMENNR	Oxidation(M)@10; Methyl(E)@11; Oxidation(R)@14
Conserved Plasmodium protein, unknown	ILTSSLPIIMENNR	Oxidation(M)@10; Methyl(N)@13; Oxidation(R)@14
Conserved Plasmodium protein, unknown	KEELGNDYVEDMK	Oxidation(K)@1; Methyl(D)@7

Conserved Plasmodium protein, unknown	RNFHVSAFYALSK	Methyl(H)@4; Oxidation(Y)@9
Heat shock protein 101	ELQNSLKEAQQK	Deamidated(N)@4; Methyl(Q)@11
Heat shock protein 101	SLSDAVVK	Methyl(D)@4
Heat shock protein 101	DEEIRAIIESLLRYNK	Oxidation(R)@5; Methyl(E)@9; Dehydrated(S)@10
Heat shock protein 101	EKVRNGKLQGIYGRDEEIR	Glu->pyro-Glu@N-term; Oxidation(K)@7; Methyl(E)@17; Deamidated(R)@19
Heat shock protein 101	ETLALAEAAANKYKSPK	Methyl(L)@3; Oxidation(K)@12
Heat shock protein 101	FIESCSAFERR	Carbamidomethyl(C)@5; Methyl(S)@6
Heat shock protein 101	LYNSLSKSIIGNEDIIK	Methyl(L)@1; Deamidated(N)@3
Heat shock protein 101	SLSDAVVK	Methyl(D)@4
Pyruvate kinase, putative	LLYQSLVNAIETPISVQEAVAR	Carbamyl@N-term; Methyl(L)@6
Pyruvate kinase, putative	VGSFQGTDIVIR	Deamidated(Q)@5; Methyl(I)@11; Carbamyl(R)@12
Pyruvate kinase, putative	EEVSGGTNLMK	Methyl(E)@2; Oxidation(N)@8; Oxidation(M)@10
Pyruvate kinase, putative	LIRNLLGPRGR	Trimethyl(R)@3
Pyruvate kinase, putative	NPRPTRAEVTDVANAVL	Deamidated(N)@1; Methyl(L)@17
Pyruvate kinase, putative	QILEPNNVNLR	Oxidation(P)@5; Oxidation(N)@6; Oxidation(N)@7; Trimethyl(R)@11
Conserved Plasmodium protein, unknown	NSLSNGISKRK	Methyl(S)@4
Conserved Plasmodium protein, unknown	RSLDNKSDGPLK	Methyl(S)@2; Oxidation(K)@12

Phosphoribosylpyrophosphate synthetase	QRTKPNEIEK	Arg->Orn(R)@2; Oxidation(K)@4; Methyl(I)@8
Phosphoribosylpyrophosphate synthetase	VFAFATHGLFSGPAIDRIEK	Methyl(T)@6; Oxidation(H)@7; Oxidation(P)@13
Conserved Plasmodium protein, unknown	MNKQIRGGEKKKGR	Methyl(R)@6
Conserved Plasmodium protein, unknown	EQYEQKYSFELK	Methyl(E)@1; Deamidated(Q)@2
Conserved Plasmodium protein, unknown	FIIAYATDINKYTKR	Carbamyl@N-term; Oxidation(Y)@5; Methyl(I)@9; Deamidated(N)@10
Conserved Plasmodium protein, unknown	FLISNMNIYKKMVDSYIK	Methyl(N)@7; Oxidation(Y)@9; Oxidation(M)@12
Conserved Plasmodium protein, unknown	FSDDSTKSSNSSKSSHK	Trimethyl(K)@7; Oxidation(K)@13; Carbamyl(K)@17
Mitochondrial ribosomal protein L17 precursor, putative	HDNNRQYAYRLIANYVYDR	Carbamyl@N-term; Dioxidation(Y)@7; Carbamyl(R)@10; Methyl(D)@18
Conserved Plasmodium protein, unknown	LEIQNIYLRNMHKFK	Methyl(N)@5
Enolase	GVQKAIKNINEIIAPK	Deamidated(Q)@3; Deamidated(N)@10; Methyl(E)@11; Oxidation(P)@15
Enolase	NNWGVMVSHR	Deamidated(N)@2; Methyl(H)@9; Deamidated(R)@10
Ring-infected erythrocyte surface antigen precursor	SAKKLQQRTQANK	Methyl(K)@4; Oxidation(R)@8; Deamidated(Q)@10
Ring-infected erythrocyte surface antigen precursor	RLTVLNQIAWK	Methyl(Q)@7; Oxidation(W)@10
26S proteosome ATPase	IEFPLPDRKQKR	Methyl(E)@2; Deamidated(R)@8
hsp70), putative	DIEALELIGSGWR	Oxidation(D)@1; Methyl(I)@2

hsp70), putative	DNYTAPFFKHKDVQLK	Oxidation(H)@10; Methyl(K)@11
hsp70), putative	NINLNIGCVISVPCNFSQR	Oxidation(N)@1; Carbamidomethyl(C)@8; Carbamidomethyl(C)@14; Methyl(R)@19
Plasmepsin 2 precursor	HTGFLTIGGIEER	Methyl(T)@2; Deamidated(R)@13
Tubulin beta	QITHSLGGGTGSGMGTL	Methyl(L)@17
proteasome 26S regulatory subunit	SQIDKFQYSSDQYVK	Methyl(S)@9; Oxidation(D)@11; Deamidated(Q)@12; Oxidation(K)@15
proteasome 26S regulatory subunit	INNSLDTPIAK	Methyl(S)@4
PfEMP1	GNNRNVTGGACAPLR	Dimethyl(R)@4; Deamidated(N)@5; Carbamidomethyl(C)@11; Deamidated(R)@15
PfEMP1	TVGNTVVSGEPQTQGEASSPSDKESSQSDKLR	Methyl(E)@10; Deamidated(Q)@14; Deamidated(R)@32
Hypothetical protein	RINEKDNDTDR	Trimethyl(R)@1
Hypothetical protein	YFTQKNEQFK	Dioxidation(K)@5; Methyl(N)@6
Conserved Plasmodium protein, unknown	LDGEIKKFLLLSK	Methyl(E)@4
Conserved Plasmodium protein, unknown	IRRSEFSMIK	Oxidation(R)@3; Oxidation(M)@8; Methyl(K)@10
Conserved Plasmodium protein, unknown	KLLYYQKNQKDMEK	Oxidation(K)@1; Oxidation(Y)@5; Methyl(Q)@6; Oxidation(N)@8
Conserved Plasmodium protein, unknown	KPKKENLYYKYNCAR	Oxidation(P)@2; Oxidation(K)@10; Methyl(N)@12; Carbamidomethyl(C)@13; Deamidated(R)@15
Conserved Plasmodium protein, unknown	VHDNNNYSSMHK	Oxidation(H)@2; Deamidated(N)@4; Methyl(N)@6
Conserved Plasmodium protein, unknown	VLKRAAYELSHNPR	Methyl(L)@2; Deamidated(R)@4

Conserved Plasmodium protein, unknown	VSIIPPSNVKY	Methyl(N)@8; Oxidation(Y)@11
Conserved Plasmodium protein, unknown	YNTKPSPPPTYTLKVDKK	Methyl(S)@6; Oxidation(K)@17; Oxidation(K)@18
Conserved Plasmodium protein, unknown	NSNENSNENSNK	Oxidation(N)@3; Deamidated(N)@11; Methyl(K)@12
Conserved Plasmodium protein, unknown	STSLSLSSFELNNK	Methyl(S)@5; Oxidation(F)@9; Oxidation(N)@13; Oxidation(K)@14
Conserved Plasmodium protein, unknown	TLLKKIPNKLK	Methyl(I)@6; Carbamyl(K)@11
Polyubiquitin	TITLDVEPSDTIENVK	Methyl(D)@5
Polyubiquitin	TITLDVEPSDTIENVK	Methyl(I)@2
Polyubiquitin	TITLDVEPSDTIENVK	Methyl(D)@5
Polyubiquitin	TITLDVEPSDTIENVK	Methyl(D)@5
Polyubiquitin	TITLDVEPSDTIENVK	Methyl(D)@5
Polyubiquitin	TITLDVEPSDTIENVK	Methyl(L)@4
Polyubiquitin	TITLDVEPSDTIENVK	Methyl(D)@5
Polyubiquitin	TITLDVEPSDTIENVK	Methyl(D)@5
Polyubiquitin	TITLDVEPSDTIENVK	Methyl(D)@5
Polyubiquitin	TITLDVEPSDTIENVK	Methyl(D)@5
Polyubiquitin	TITLDVEPSDTIENVK	Methyl(D)@5

Polyubiquitin	TITLDVEPSDTIENVK	Methyl(D)@5
Polyubiquitin	LIFAGKQLEDGR	Deamidated(Q)@7; Methyl(L)@8
Polyubiquitin	TITLDVEPSDTIENVK	Methyl(T)@3
Polyubiquitin	TITLDVEPSDTIENVK	Methyl(E)@7
Polyubiquitin	TITLDVEPSDTIENVK	Methyl(D)@5
26S proteasome subunit	EALGVALDARR	Methyl(E)@1; Oxidation(R)@10; Oxidation(R)@11
Hypothetical protein	EKDEKEKDEKEK	Glu->pyro-Glu@N-term; Oxidation(D)@3; Methyl(E)@6
26s protease regulatory subunit s 10b	GVLLYGPPGTGKTLLAR	Methyl(T)@10
26s protease regulatory subunit s 10b	GVLLYGPPGTGKTLLAR	Methyl(L)@4; Deamidated(R)@17
Hypothetical protein	MYDEKFNSSNDKSGK	Methyl(D)@3; Deamidated(N)@10
Hypothetical protein	NNITLDDGSYEEQSCARK	Methyl(D)@7; Carbamidomethyl(C)@15; Oxidation(K)@18
Hypothetical protein	DRYNGGGENIDRYNGGGENIDR	Deamidated(N)@4; Methyl(N)@14
Hypothetical protein	FGKNIRREMHNHSGMHYINYKVLK	Methyl(R)@6; Oxidation(K)@24
Ribosomal phosphoprotein P0	GVSNVAALSR	Methyl(S)@3; Deamidated(N)@4; Deamidated(R)@10
Ribosomal phosphoprotein P0	MVENPEAFAAVAAPASAAK	Methyl(E)@6; Oxidation(F)@8; Oxidation(P)@14
Ribosomal phosphoprotein P0	NTRIRTALK	Deamidated(R)@5; Methyl(L)@8
Ribosomal phosphoprotein P0	SEIRNIILDNKSPAPAR	Deamidated(N)@5; Methyl(L)@8; Oxidation(P)@13
PFG377 protein	NYNKRIEIK	Methyl(N)@3

Hypothetical protein	ILFFYVNSVINSNDSKMKLHPNFEK	Dehydrated(S)@8; Methyl(I)@10; Oxidation(N)@11
PFG377 protein	IPKKTEQDVLEVSKFR	Oxidation(P)@2; Oxidation(K)@4; Methyl(K)@14; Deamidated(R)@16
Hypothetical protein	LNLFNKELYKLITK	Oxidation(N)@5; Oxidation(K)@6; Methyl(E)@7; Oxidation(Y)@9
Dimethyladenosine transferase	RLATFFVFLGNNGKK	Deamidated(N)@12; Methyl(K)@15
Hypothetical protein	SCLDNLQFFKR	Carbamidomethyl(C)@2; Methyl(R)@11
PFG377 protein	TRDSEGSESDVPKDK	Oxidation(D)@3; Oxidation(D)@14; Trimethyl(K)@15
Hypothetical protein	HDVNVSSDSSSEVGEIKHK	Methyl(S)@9
Similar to zinc finger protein 638	LYQQVYDFEKVETCCK	Methyl(Q)@4; Oxidation(D)@7; Carbamidomethyl(C)@14; Carbamidomethyl(C)@15
Conserved Plasmodium protein, unknown	KNITYDINEENKVER	Oxidation(N)@2; Oxidation(Y)@5; Oxidation(D)@6; Trimethyl(R)@15
Conserved Plasmodium protein, unknown	KNTNKNKNTNKNKNKNK	Deamidated(N)@4; Deamidated(N)@6; Trimethyl(K)@17
Conserved Plasmodium protein, unknown	NEQINKLQKYNNKIK	Deamidated(N)@1; Deamidated(N)@5; Methyl(K)@15
Conserved Plasmodium protein, unknown	NKNLNKMNQMNK	Deamidated(N)@1; Methyl(N)@3; Carbamyl(M)@7
Conserved Plasmodium protein, unknown	NKNTNKNKNK	Deamidated(N)@7; Methyl(K)@10
Conserved Plasmodium protein, unknown	NKNTNKNKNKNK	Oxidation(N)@3; Deamidated(N)@11; Methyl(K)@12
Conserved Plasmodium protein, unknown	NLNKMNQMNKMNQMNK	Carbamyl(M)@5; Deamidated(N)@9; Oxidation(M)@11; Dimethyl(K)@16
Conserved Plasmodium protein, unknown	NTNKNKNKNKNTNKNKK	Deamidated(N)@7; Oxidation(K)@10; Methyl(N)@11; Deamidated(N)@13
Conserved Plasmodium protein, unknown	YNDLEGSDEIYK	Oxidation(Y)@1; Methyl(E)@5; Oxidation(D)@8
Conserved Plasmodium protein, unknown	YNDLEGSDEIYKRK	Methyl(D)@3; Oxidation(K)@12; Arg->Orn(R)@13; Oxidation(K)@14

SET domain protein, putative	NDDIRNDDDKNDENEENTK	Oxidation(N)@6; Methyl(D)@7; Oxidation(D)@12
SET domain protein, putative	CFNLVEFNKDTIFYK	Carbamidomethyl(C)@1; Methyl(L)@4; Oxidation(N)@8; Oxidation(K)@15
SET domain protein, putative	ENSDEGKMQKGK	Methyl(E)@5; Oxidation(M)@8; Deamidated(Q)@9
SET domain protein, putative	LNNTSKNNISNNNNNMLK	Oxidation(N)@3; Methyl(N)@7; Deamidated(N)@8
SET domain protein, putative	NVLCDGEERVSYNRNK	Carbamidomethyl(C)@4; Methyl(S)@11; Deamidated(N)@15
SET domain protein, putative	RYFNNNGKNKR	Methyl(N)@6
SET domain protein, putative	VHKEYFTLRNILMDDNLLNNIIRNK	Oxidation(N)@10; Oxidation(M)@13; Methyl(D)@15; Arg->Orn(R)@23
SET domain protein, putative	YTGVNNNNSSIIMSLKKCDK	Deamidated(N)@8; Carbamidomethyl(C)@18; Methyl(D)@19
hsp70), putative	NQASRNPENTVFDAKR	Carbamyl@N-term; Deamidated(N)@9; Oxidation(D)@13; Trimethyl(K)@15
hsp70), putative	IEARNNLENYCYNVK	Oxidation(R)@4; Oxidation(N)@9; Carbamidomethyl(C)@11; Methyl(K)@15
hsp70), putative	IINEPTAAAIAYGLDK	Methyl(I)@10
hsp70), putative	LSGDQSSAVKDLLL	Methyl(S)@7; Oxidation(D)@11
hsp70), putative	NRIEARNNLENYCYNVK	Carbamidomethyl(C)@13; Trimethyl(K)@17
hsp70), putative	RLRTQCEKAKR	Oxidation(R)@1; Deamidated(R)@3; Carbamidomethyl(C)@6; Methyl(E)@7; Carbamyl(R)@11
Merozoite surface antigen 2 precursor	NAETNPKGKGEVQEP	Methyl(E)@3; Oxidation(P)@6; Oxidation(P)@15
Merozoite surface antigen 2 precursor	ENGNNNRNNENELK	Glu->pyro-Glu@N-term; Oxidation(N)@5; Methyl(N)@6
Merozoite surface antigen 2 precursor	NAETNPKGKGEVQEP	Methyl(E)@3; Oxidation(P)@6; Oxidation(P)@15
Hypothetical protein	QNINEEDNNINNSIKTAR	Gln->pyro-Glu@N-term; Methyl(N)@8

Hypothetical protein	QNINEEDNNINNSIKTAR	Gln->pyro-Glu@N-term; Methyl(E)@6; Oxidation(K)@15; Oxidation(R)@18
Nuclear DNA binding protein G2p	NKAKNNEEANQEN	Methyl(E)@12
Hypothetical protein	NQEVAISNISSTIINEK	Deamidated(N)@1; Methyl(E)@3
Hypothetical protein	NDKNEKNDKNEKNDKNEK	Oxidation(N)@4; Methyl(N)@13
Conserved Plasmodium protein, unknown	IMENNYNIAYK	Oxidation(M)@2; Deamidated(N)@7; Methyl(I)@8
Hypothetical protein	KADPSFSFSSSSSSSF	Methyl(D)@3
RhopH3	FILTKDDASKPEK	Oxidation(F)@1; Oxidation(D)@6; Methyl(D)@7
RhopH3	GIDNLMKSTRYDK	Methyl(D)@12
Exported protein 2 (Exp-2)	GDLAATSALTTVIKDP	Methyl(S)@7
Exported protein 2 (Exp-2)	SHTLYTHITPDAVPQLPK	Methyl(T)@9; Oxidation(P)@17; Oxidation(K)@18
Conserved Plasmodium protein, unknown	QIETFSVDMFNF	Methyl(E)@3
Conserved Plasmodium protein, unknown	SSILDKIDLNPSDIKKMCPR	Oxidation(P)@11; Oxidation(D)@13; Oxidation(M)@17; Carbamidomethyl(C)@18; Methyl(R)@20
Hypothetical protein	QKDQELKNIIQEYDER	Oxidation(K)@2; Oxidation(D)@3; Methyl(Q)@4
Hypothetical protein	MNEHVNKLQNELIKR	Methyl(N)@2; Oxidation(N)@10; Oxidation(R)@15
Ethylene-inducible protein hever	RISEGASMIRTK	Methyl(S)@3; Oxidation(M)@8; Deamidated(R)@10
Ethylene-inducible protein hever	RTVNNEIK	Methyl(K)@8
Ethylene-inducible protein hever	SVEQAKIAEEAGAIGVMVLENI	Oxidation(K)@6; Methyl(I)@14; Deamidated(N)@21

Clathrin heavy chain	IYIDLNKDPENFLK	Methyl(D)@4; Oxidation(N)@6; Oxidation(D)@8; Oxidation(K)@14
Rifin	VVIVLVMVIIY	Methyl(I)@3
Ribosomal protein L10, putative	DEYQQYKKKGRI	Methyl(E)@2; Deamidated(Q)@5; Oxidation(R)@11
Ribosomal protein L10, putative	DEYQQYKKKGRI	Methyl(E)@2; Deamidated(Q)@5; Oxidation(R)@11
Ribosomal protein L10, putative	FIREKGPLDK	Oxidation(F)@1; Methyl(L)@8; Oxidation(K)@10
Hypothetical protein	QNIILLNNINNFYFNK	Methyl(N)@8; Oxidation(F)@14; Oxidation(N)@15; Oxidation(K)@16
Hypothetical protein	KNFLDINNIR	Methyl(N)@2
Hypothetical protein	YNYMEFLGMNIIKKK	Deamidated(N)@2; Methyl(I)@11; Oxidation(K)@15
Conserved Plasmodium protein, unknown	EIENIKRQLFHLEYSKIHSR	Glu->pyro-Glu@N-term; Methyl(E)@3; Oxidation(H)@11; Oxidation(H)@18
Conserved Plasmodium protein, unknown	LNEEENEKDK	Methyl(E)@5
Conserved Plasmodium protein, unknown	NLLFLSFHNMTMK	Methyl(K)@13
Conserved Plasmodium protein, unknown	YENLKNENIK	Methyl(N)@3
Hypothetical protein	ITYKKMIAKFERK	Methyl(E)@11
Hypothetical protein	NNERNNERKSETNKWTCQYR	Oxidation(N)@6; Trimethyl(R)@8; Carbamidomethyl(C)@17; Deamidated(Q)@18
Hypothetical protein	ITYKKMIAKFERK	Methyl(E)@11
Hypothetical protein	ITYKKMIAKFERK	Methyl(E)@11
Hypothetical protein	TNEQKDKQIEK	Oxidation(K)@5; Methyl(D)@6; Deamidated(Q)@8; Oxidation(K)@11
Hypothetical protein	GIISSNETNDTNHTNR	Methyl(N)@12; Oxidation(H)@13; Deamidated(N)@15

Hypothetical protein	LKNNIKNSDDIINNYFSK	Deamidated(N)@3; Trimethyl(K)@18
Hypothetical protein	NERSNIIMSKENMNK	Deamidated(N)@1; Methyl(I)@7; Oxidation(M)@8
Hypothetical protein	QQNISNTSGNMKNSSNIR	Methyl(I)@17; Oxidation(R)@18
Hypothetical protein	YISFNDDSDVISTNDEENVDRSDDSESNDDK	Methyl(D)@30
Hypothetical protein	LENLLNQIEKKIKEK	Methyl(E)@14
Hypothetical protein	KQMNLEMMKK	Methyl(E)@6; Oxidation(M)@8
Hypothetical protein	LENLLNQIEKKIKEK	Methyl(E)@14
Hypothetical protein	LENLLNQIEKKIKEK	Methyl(E)@14
Hypothetical protein	IISVYGSIKKYMKILFLKFTK	Dioxidation(Y)@5; Methyl(K)@9
Eukaryotic translation initiation factor 3 subunit 10	ERDRDRDRDRDIK	Oxidation(R)@4; Methyl(D)@5; Oxidation(R)@6; Oxidation(K)@13
Eukaryotic translation initiation factor 3 subunit 10	IRNILNYADENIQK	Arg->Orn(R)@2; Oxidation(N)@3; Methyl(D)@9; Oxidation(K)@14
Eukaryotic translation initiation factor 3 subunit 10	KEELARKGEKLRIKEEKHK	Deamidated(R)@6; Deamidated(R)@12; Trimethyl(K)@19
Formin binding protein	RDRDRDRER	Dimethyl(R)@9
PfEMP1	FYKELKESEYGK	Methyl(K)@3; Oxidation(K)@12
PfEMP1	FYKELKESEYGK	Methyl(K)@3; Oxidation(K)@12
PfEMP1	QKYETEISNSGSCGGSGGVKGR	Methyl(Q)@1; Oxidation(K)@2; Oxidation(Y)@3; Carbamidomethyl(C)@13; Phospho(S)@16
PfEMP1	RPDSSASGTKLTDFIK	Oxidation(P)@2; Oxidation(D)@3; Methyl(T)@9

Hypothetical protein	LSESNESNKLSESNESNKLSESNESNK	Oxidation(N)@5; Deamidated(N)@14; Dimethyl(K)@18
Hypothetical protein	NNVVHNKKNNIYINEFK	Oxidation(N)@10; Methyl(I)@11
Hypothetical protein	RIGNRKVYNK	Methyl(R)@5; Deamidated(N)@9
Peptidase family C50, putative	KIINLKKYPKIK	Oxidation(K)@1; Oxidation(P)@9; Methyl(K)@12
Peptidase family C50, putative	ISSNISITRSL	Methyl(S)@10
Peptidase family C50, putative	ESKNIIKGSQECAEVK	Oxidation(N)@4; Trimethyl(K)@7; Carbamidomethyl(C)@12
PfEMP1	QLLDPLIYRMDLANGK	Deamidated(Q)@1; Methyl(D)@4; Oxidation(M)@10
PfEMP1	SQKLENSENPLFK	Methyl(N)@9
Hypothetical protein	ENKSESNSMKR	Methyl(S)@8
6-phosphofructokinase	VKNKDDLIAIENIVAKLK	Oxidation(D)@6; Methyl(K)@18
Hypothetical protein	DINIVNGNINKEKK	Deamidated(N)@8; Methyl(E)@12
DNAJ domain protein	EEKTIELTLEIEK	Lys->Allysine(K)@3; Methyl(E)@12; Oxidation(K)@13
Hypothetical protein	NINEDINKNINEDINK	Deamidated(N)@7; Methyl(N)@9; Oxidation(N)@15; Oxidation(K)@16
Hypothetical protein	KGKNKNNNNNKNNDDNNNIDDNK	Deamidated(N)@13; Oxidation(N)@17; Methyl(D)@21
Hypothetical protein	NVIEFSRYGVTNK	Methyl(R)@7; Oxidation(Y)@8; Deamidated(N)@12
Hypothetical protein	YVCKKSYLLINLLLR	Carbamidomethyl(C)@3; Carbamyl(K)@5; Deamidated(N)@11; Methyl(R)@15
Dynein heavy chain	KLQNDFKKIKVDRK	Methyl(D)@12; Oxidation(K)@14

Dynein heavy chain	EKNKEKNLQNGINGTNEK	Deamidated(N)@3; Oxidation(K)@4; Methyl(E)@5; Oxidation(N)@7
Dynein heavy chain	LFLSAAIPNEKDTKLLPEKLLKKCFR	Oxidation(P)@17; Methyl(K)@22; Carbamidomethyl(C)@24; Oxidation(F)@25; Deamidated(R)@26
Dynein heavy chain	QKFAQENKVPIDK	Oxidation(K)@2; Methyl(E)@6; Oxidation(N)@7
Dynein heavy chain	VNDVENILIKK	Oxidation(N)@6; Methyl(K)@11
Dynein heavy chain	WILAGVALFLSD	Methyl(L)@3
SNF2-family protein	MVLDTLVVQGLNKK	Methyl(K)@14
Hypothetical protein	TGTRTSTRTSTR	Methyl(R)@12
6-phosphogluconate dehydrogenase, decarboxylating	LNLGEIAR	Methyl(L)@3
Hypothetical protein	SATYLLKIEIEK	Methyl(T)@3; Ubiquitination GG(K)@12
Hypothetical protein	KKQNEKEKEKEK	Oxidation(K)@1; Methyl(E)@5; Oxidation(K)@10; Oxidation(K)@12
Hypothetical protein	QKQNEKEKEKEK	Oxidation(K)@2; Methyl(Q)@3; Oxidation(K)@10; Oxidation(K)@12
Hypothetical protein	KEKQKQNEKEKEKEKEKEK	Deamidated(N)@7; Dioxidation(K)@11; Methyl(E)@18
Hypothetical protein	ALMNNAYKLMQIKR	Methyl(L)@9; Deamidated(Q)@11
Hypothetical protein	NYVKANFIKCKEKK	Carbamidomethyl(C)@10; Methyl(K)@14
Ubiquitin carboxyl-terminal hydrolase family 2, putative	GGDNKGGDKKGGDNKGGDK	Oxidation(K)@5; Oxidation(K)@9; Methyl(K)@10
Ubiquitin carboxyl-terminal hydrolase family 2, putative	NNSMDAVNSVNHVNR	Methyl(N)@14
Ubiquitin carboxyl-terminal hydrolase family 2, putative	YEQKYEHQGSSVK	Deamidated(Q)@3; Methyl(H)@7; Deamidated(Q)@8; Oxidation(K)@13

Key		
	Proteins (Set 1) implicated in alpha,beta unsaturated sequiterpene lactone induced cell growth inhibition*	
	Set 1 PTMs not observed in corresponding comparative group	
	Corresponding peptide sequence to above, unmodified	
	Set 1 PTMs observed in corresponding comparative group	
	Set 1 protein peptide sequences not detected in corresponding comparative group	
*PTMs implicated are the acetylation/methylation of histones, ubiquitination and subsequent degradation of histone deacetylase by the proteomsome, and carboxy-terminal cleavage of the alpha tubulin		

Table 14: Detected Ubiquitination sites (post-translational modification of a protein by the covalent attachment (via an isopeptide bond) of one or more ubiquitin monomers

Annotation	**Sequence**	**Modifications**
6hrs - untreated		
HSP70	IINEPTAAALAYGLDK	Tyr->Ala@12; Ubiquitination GG(K)@16
HSP70	IINEPTAAALAFGLEK	Oxidation(F)@12; Ubiquitination GG(K)@16
HSP70	IINEPTAAALAFGLEK	Oxidation(F)@12; Ubiquitination GG(K)@16
HSP70	IINEPTAAALAFGLEK	Oxidation(F)@12; Ubiquitination GG(K)@16
HSP70	IINEPTAAALAFGLEK	Oxidation(F)@12; Ubiquitination GG(K)@16

EMP1	ECKGISEVK	Carbamidomethyl(C)@2; Ubiquitination GG(K)@3; Phospho(S)@6; Phospho(K)@9
Hypothetical protein	SKKCQKPHTFVNTVKNSNK	Phospho(S)@1; Carbamidomethyl(C)@4; Oxidation(N)@18; Ubiquitination GG(K)@19
Hypothetical protein	QIVDSVLTVMLENENKEVIIQEGTK	Ubiquitination GG(K)@16; Deamidated(Q)@21; Phospho(T)@24
Dynein heavy chain	DTKDAYIKQSEIKKKENDVKNKIK	Phospho(T)@2; Ubiquitination GG(K)@3; Oxidation(K)@20; Oxidation(K)@24
Merozoite surface protein 1 precursor	PSSPPTTPPSPAKTDEQK	Ubiquitination GG(K)@13; Phospho(T)@14
PfEMP1	NKLPEDIQEKYINDDK	Oxidation(D)@15; Ubiquitination GG(K)@16
Hypothetical protein	NPFKINPMSGLIK	Oxidation(F)@3; Deamidated(N)@6; Phospho(S)@9; Ubiquitination GG(K)@13
Hypothetical protein	INVSNNMLKQLNQTK	Deamidated(N)@5; Phospho(T)@14; Ubiquitination GG(K)@15
Hypothetical protein	ENVTKANGMK	Oxidation(N)@2; Oxidation(M)@9; Ubiquitination GG(K)@10
GTPase Ran	LILVGDGGVGKTTFVKR	Dehydrated(T)@12; Phospho(T)@13
GTPase Ran	LILVGDGGVGK	
GTPase Ran	LILVGDGGVGK	
GTPase Ran	LILVGDGGVGK	
GTPase Ran	LILVGDGGVGK	
GTPase Ran	LILVGDGGVGK	
Ribosomal protein S25, putative	VITPSAIAEKYK	Oxidation(P)@4; Ubiquitination GG(K)@12
Elongation factor 2	VFSGTVATGQK	Oxidation(F)@2; Phospho(S)@3; Ubiquitination GG(K)@11
Hypothetical protein	KYSTTFNKQFKK	Oxidation(Y)@2; Deamidated(N)@7; Ubiquitination GG(K)@8; Deamidated(Q)@9
Hypothetical protein	SNNLLNGSAQNVNTNDSKK	Oxidation(N)@6; Phospho(S)@17; Ubiquitination GG(K)@19
Merozoite capping protein 1, putative	KSSTSTQKKK	Ubiquitination GG(K)@1; Oxidation(K)@10

Merozoite capping protein 1, putative	KSSTSTQKKK	Ubiquitination GG(K)@1; Oxidation(K)@8
Merozoite capping protein 1, putative	KSSTSTQKKK	Ubiquitination GG(K)@1; Oxidation(K)@9
Hypothetical protein	EREQDREMEQEKEKEK	Deamidated(Q)@4; Oxidation(R)@6; Oxidation(K)@14; Ubiquitination GG(K)@16
Hypothetical protein	NKIVIHKNNKSNTK	Ubiquitination GG(K)@2; Carbamyl(K)@14
Hypothetical protein	EKNNKNNKKKK	Oxidation(N)@3; Oxidation(N)@4; Ubiquitination GG(K)@11
S-adenosylhomocysteine hydrolase	VKDISLAPFGK	Ubiquitination GG(K)@2; Phospho(S)@5; Oxidation(P)@8
PfEMP1	AKEKADVASR	Ubiquitination GG(K)@2; Phospho(S)@9; Oxidation(R)@10
PfEMP1	WVVQKEQEWK	Deamidated(Q)@4; Oxidation(K)@5; Ubiquitination GG(K)@10
Metacaspase-like protein, putative	NKIIYINDANITNDKFK	Deamidated(N)@7; Phospho(T)@12; Oxidation(K)@15; Ubiquitination GG(K)@17
6hrs - treated		
Hypothetical protein	SSDSSKSSDSSKSSDSSK	Ser->Glu@7; Phospho(S)@11; Ubiquitination GG(K)@18
Hypothetical protein	SNQSSSENMSDVISSKRYSDKSSDSSK	Oxidation(N)@2; Phospho(S)@5; Oxidation(K)@16; Ubiquitination GG(K)@27
Hypothetical protein	SSGSSKSSGSSKSSGSSKSSGSSKSSGSYK	Oxidation(K)@6; Phospho(S)@7; Carbamyl(K)@12; Ubiquitination GG(K)@18
PfEMP1	NKYQTEISGGGASGGASGRSRK	Oxidation(Y)@3; Phospho(S)@20; Ubiquitination GG(K)@22
Hypothetical protein	NKNATSNNNSSFSK	Deamidated(N)@3; Phospho(T)@5; Ubiquitination GG(K)@14
Chloroquine resistance marker protein	NRKMLLPNNLKNSK	Deamidated(N)@1; Deamidated(N)@9; Phospho(S)@13; Ubiquitination GG(K)@14

Chloroquine resistance marker protein	EPTNSILLNK	Oxidation(P)@2; Deamidated(N)@4; Oxidation(N)@9; Ubiquitination GG(K)@10
GTPase Ran	LILVGDGGVGKTTFVKR	Ubiquitination GG(K)@11; Phospho(T)@12; Phospho(T)@13; Oxidation(R)@17
Hypothetical protein	TLSDSKYGSFKNK	Phospho(S)@9; Oxidation(F)@10; Ubiquitination GG(K)@13
LRR domain-containing protein	TQQLSAHSLQQQMYPQQMTSQVHSSFHAQK	Phospho(S)@8; Deamidated(Q)@17; Deamidated(Q)@29; Ubiquitination GG(K)@30
Hypothetical protein	EKIMSMAKKMMNIEKNIHVK	Phospho(S)@5; Ubiquitination GG(K)@9; Deamidated(N)@16; Oxidation(H)@18
PfEMP1	EKKKANKEAYR	Ubiquitination GG(K)@3; Oxidation(Y)@10; Deamidated(R)@11
PfEMP1	GNKKKSENKREKEK	Oxidation(K)@5; Deamidated(N)@8; Ubiquitination GG(K)@12; Oxidation(K)@14
Hypothetical protein	RKTMNKSNGMNKSNGMNK	Ubiquitination GG(K)@2; Phospho(T)@3; Oxidation(M)@10
PfEMP1	SVETSGSSGGSGATGKSDGSICI	Phospho(S)@7; Ubiquitination GG(K)@16; Carbamidomethyl(C)@22
PfEMP1	KNYTSLEELEKTLKCNGSDK	Oxidation(Y)@3; Phospho(T)@4; Ubiquitination GG(K)@11; Carbamidomethyl(C)@15; Deamidated(N)@16
Hypothetical protein	SPYQNSVHPSYHVHKNIEKK	Phospho(S)@1; Deamidated(N)@5; Oxidation(K)@19; Ubiquitination GG(K)@20
Hypothetical protein	NYNSNNKNYNSK	Deamidated(N)@6; Oxidation(N)@10; Phospho(S)@11; Ubiquitination GG(K)@12
PfEMP3	INQIDSIDFSKYK	Oxidation(N)@2; Phospho(S)@6; Oxidation(Y)@12; Ubiquitination GG(K)@13
PfEMP3	KNATLLGSK	Deamidated(N)@2; Phospho(S)@8; Ubiquitination GG(K)@9
Erythrocyte membrane-associated giant protein antigen 332	VLGKNEHHEDHLKGK	Ubiquitination GG(K)@15
Hypothetical protein	KLIIYYEVDNK	Ubiquitination GG(K)@11
Hypothetical protein	DKTPIFGSPSNKDDKDK	Phospho(S)@8; Oxidation(D)@16; Ubiquitination GG(K)@17

Hypothetical protein	NVLSPKDNHKSEDNHK	Ubiquitination GG(K)@6; Oxidation(H)@15
60S ribosomal protein L8	AGVAHHKYRVKR	Oxidation(H)@6; Oxidation(R)@9; Ubiquitination GG(K)@11
PyRhopH2	KELNDEKAYKQLMSAIRKYVTTLTK	Ubiquitination GG(K)@1; Oxidation(Y)@9; Oxidation(K)@18; Phospho(T)@22
PfEMP3	SKEAISAYIELK	Phospho(S)@1; Ubiquitination GG(K)@2
Rhoptry-associated protein 1	ASPSVVKTSTPSGTQTSGLK	Phospho(T)@8; Deamidated(Q)@15; Ubiquitination GG(K)@20
Lysine decarboxylase	THVNNKSDVMIIIPSEDHLNPHIIHK	Phospho(T)@1; Ubiquitination GG(K)@26
Cell division cycle protein 48	IPLLKTNILRTNETNKSMNTFK	Oxidation(K)@5; Phospho(T)@11; Ubiquitination GG(K)@22
RNA polymerase I, putative	NSNSDQASK	Phospho(S)@8; Ubiquitination GG(K)@9
PfEMP1	CIPTSGDKTDTSENGAPR	Carbamidomethyl(C)@1; Phospho(S)@5; Ubiquitination GG(K)@8; Oxidation(N)@14; Oxidation(P)@17
Asparagine--tRNA ligase, putative	ISEVNVEHKK	Phospho(S)@2; Ubiquitination GG(K)@10
Ribonuclease, putative	KKDSFNNMQSSSFLSDK	Ubiquitination GG(K)@2; Oxidation(M)@8; Phospho(S)@10; Oxidation(K)@17
18hrs - untreated		
HSP90	STETFAFNADIR	Protein Terminal Acetyl@N-term
HSP90	STETFAFNADIR	Protein Terminal Acetyl@N-term
HSP90	STETFAFNADIR	Protein Terminal Acetyl@N-term
HSP90	IGLKEYVDRMK	Protein Terminal Acetyl@N-term; Deamidated(R)@9
HSP90	STETFAFNADIR	Protein Terminal Acetyl@N-term
HSP90	STETFAFNADIR	Protein Terminal Acetyl@N-term

HSP90	STETFAFNADIR	Protein Terminal Acetyl@N-term; Phospho(T)@2
HSP70	ASAKGSKPNLPESNI	Protein Terminal Acetyl@N-term; Phospho(S)@6
HSP70	MASAKGSKPNLPESNIAIGIDLGTTYSCVGVWR	Protein Terminal Acetyl@N-term; Phospho(S)@3; Dioxidation(Y)@26; Carbamidomethyl(C)@28; Oxidation(W)@32
Phosphoglycerate kinase	LGNKLSISDLKDIKNK	Protein Terminal Acetyl@N-term; Phospho(S)@6; Phospho(S)@8; Phospho(K)@16
Phosphoglycerate kinase	KSSVVSLF	Protein Terminal Acetyl@N-term; Phospho(S)@6
Glyceraldehyde-3-phosphate dehydrogenase, putative	AVTKLGINGFGR	Protein Terminal Acetyl@N-term; Oxidation(K)@4; Oxidation(F)@10; Oxidation(R)@12
Glyceraldehyde-3-phosphate dehydrogenase, putative	AVTKLGINGFGRIGR	Protein Terminal Acetyl@N-term; Phospho(T)@3; Deamidated(R)@15
Glyceraldehyde-3-phosphate dehydrogenase, putative	AVTKLGINGFGRIGR	Protein Terminal Acetyl@N-term; Phospho(T)@3; Oxidation(K)@4; Dioxidation(R)@12
Actin	GEEDVQALVVDNGSGNVK	Protein Terminal Acetyl@N-term; Deamidated(N)@12
Actin	GEEDVQALVVDNGSGNVK	Protein Terminal Acetyl@N-term; Deamidated(N)@12
Actin	GEEDVQALVVDNGSGNVK	Protein Terminal Acetyl@N-term
Actin	GEEDVQALVVDNGSGNVK	Protein Terminal Acetyl@N-term; Deamidated(N)@16
Actin	GEEDVQALVVDNGSGNVK	Protein Terminal Acetyl@N-term; Deamidated(N)@12
Actin	GEEDVQALVVDNGSGNVK	Protein Terminal Acetyl@N-term
Actin	GEEDVQALVVDNGSGNVK	Protein Terminal Acetyl@N-term; Deamidated(N)@12
Actin	GEEDVQALVVDNGSGNVK	Protein Terminal Acetyl@N-term
Cell division cycle protein 48	EDNTDKKALVDENNGENK	Protein Terminal Acetyl@N-term; Phospho(T)@4; Deamidated(N)@14; Oxidation(N)@17

Elongation factor 2	VNFTVDQVR	Protein Terminal Acetyl@N-term; Oxidation(F)@3
Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)	AHVITRINAR	Protein Terminal Acetyl@N-term; Phospho(T)@5; Dioxidation(R)@6; Deamidated(N)@8
Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)	AHVITRINAR	Protein Terminal Acetyl@N-term; Carbamyl(R)@6; Oxidation(N)@8; Oxidation(R)@10
HSP60	MVKQVAANTNDK	Protein Terminal Acetyl@N-term; Phospho(T)@9; Carbamyl(K)@12
HSP60	MVKQVAANTNDK	Protein Terminal Acetyl@N-term; Oxidation(K)@12
14-3-3 protein	ADAMRTL	Protein Terminal Acetyl@N-term
14-3-3 protein	LIEMADAMR	Protein Terminal Acetyl@N-term; Oxidation(M)@4
HSP70	MYTTPTSINLKTK	Protein Terminal Acetyl@N-term; Phospho(T)@3; Phospho(S)@7; Phospho(T)@12
Phosphoethanolamine N-methyltransferase	NRNYISSGGLEATK	Protein Terminal Acetyl@N-term; Dehydrated(T)@13
Erythrocyte membrane protein 3	ATIKKYHIRGR	Protein Terminal Acetyl@N-term; Phospho(T)@2; Oxidation(K)@4; Oxidation (Y)@6
T-complex protein 1, gamma subunit	MLKNPGTVLVFKPNTK	Protein Terminal Acetyl@N-term; Deamidated(N)@4
T-complex protein 1, gamma subunit	MLKNPGTVLVFKPNTK	Protein Terminal Acetyl@N-term; Deamidated(N)@4
Elongation factor 1-gamma, putative	ISKNINKTK	Protein Terminal Acetyl@N-term; Phospho(S)@2; Oxidation(N)@4; Phospho(T)@8
Conserved GTP-binding protein, putative	MGLVGLPNVGK	Protein Terminal Acetyl@N-term; Oxidation(P)@7; Oxidation(K)@11
Chaperonin, 60 kDa	SHLMSLPIVLLK	Protein Terminal Acetyl@N-term
PIESP2 erythrocyte surface protein (putative/hypothetical)	GKRSYPKSGHK	Protein Terminal Acetyl@N-term; Carbamyl(K)@7; Phospho(S)@8; Oxidation (H)@10
Lysyl-tRNA synthetase	MRVSASGQKLR	Protein Terminal Acetyl@N-term; Phospho(S)@4; Oxidation(K)@9

Lysyl-tRNA synthetase	MRVSASGQKLR	Protein Terminal Acetyl@N-term; Oxidation(R)@2; Phospho(S)@6; Deamidated (Q)@8
Chaperonin containing TCP-1 delta subunit	AVAHPTAK	Protein Terminal Acetyl@N-term
T-complex protein 1 epsilon subunit, putative	MNIAIDEYGQPFVILR	Protein Terminal Acetyl@N-term
DnaJ homolog	FFSSGFPFDSMGGQQARR	Protein Terminal Acetyl@N-term; Oxidation(P)@7; Oxidation(M)@11; Deamidated(Q)@15
Proteasome 26S regulatory subunit, putative	TAEDKKAVSIQVPVKDVDDK	Protein Terminal Acetyl@N-term; Oxidation(K)@6; Phospho(S)@9
Ubiquitin-activating enzyme e1	QNKTPPLKK	Protein Terminal Acetyl@N-term; Phospho(T)@4; Oxidation(P)@6; Oxidation (K)@9
Hypothetical protein	ASTEEVSQER	Protein Terminal Acetyl@N-term
Hypothetical protein	MTKKPTFYARIGK	Protein Terminal Acetyl@N-term; Phospho(T)@2; Oxidation(K)@3; Oxidation (K)@13
Ribosomal protein S4, putative	GKGIKKHLK	Protein Terminal Acetyl@N-term
Translation elongation factor 1 beta-related	ASNASLLNVK	Protein Terminal Acetyl@N-term
Translation elongation factor 1 beta-related	ASNASLLNVK	Protein Terminal Acetyl@N-term; Phospho(S)@5; Oxidation(N)@8
Translation elongation factor 1 beta-related	ASNASLLNVK	Protein Terminal Acetyl@N-term; Phospho(S)@5
DNA-directed RNA polymerase III subunit	MVTNLGLMVTNLGLK	Protein Terminal Acetyl@N-term; Phospho(T)@10; Deamidated(N)@11
18hrs - treated		

HSP70	LEATLHPTQTVFDVKRLIGRK	Oxidation(H)@6; Oxidation(P)@7; Deamidated(R)@20; Ubiquitination GG(K)@21
HSP70	LEKMKEIAQSFLGKPVK	Ubiquitination GG(K)@3; Oxidation(K)@14; Oxidation(P)@15
HSP70	SLLPYEIVNNQGKPNIK	Deamidated(N)@10; Deamidated(Q)@11; Deamidated(N)@15; Ubiquitination GG(K)@17
Endoplasmin homolog precursor	DMVNDPNYDSVKVEETDDPNKK	Oxidation(P)@19; Ubiquitination GG(K)@22
Endoplasmin homolog precursor	EITKKLSEPSTYK	Oxidation(K)@5; Oxidation(P)@9; Ubiquitination GG(K)@13
Endoplasmin homolog precursor	KDNNVDNESNDK	Ubiquitination GG(K)@1; Deamidated(N)@3; Oxidation(N)@7; Deamidated (N)@10
Glyceraldehyde-3-phosphate dehydrogenase, putative	AGRCALSNIIPASTGAAKAVGKVLPELNGK	Carbamidomethyl(C)@4; Oxidation(P)@11; Ubiquitination GG(K)@22; Oxidation (P)@25
Glyceraldehyde-3-phosphate dehydrogenase, putative	PELNGKLTGVAFRVPIGTVSVVDLVCR	Deamidated(N)@4; Ubiquitination GG(K)@6; Deamidated(R)@13; Carbamidomethyl(C)@26
L-lactate dehydrogenase	PKNKIIGLGGVLDTSR	Ubiquitination GG(K)@2; Oxidation(K)@4
Translation elongation factor EF-1, subunit alpha	RSGKVVEENPK	Oxidation(R)@1; Ubiquitination GG(K)@4; Deamidated(N)@9
Phosphoglycerate kinase	VKANKEDVEK	Ubiquitination GG(K)@10
Phosphoglycerate kinase	GNKLSISDLKDI	Deamidated(N)@2; Ubiquitination GG(K)@3
Phosphoglycerate kinase	IDNIVISPGYGNPMLNDKKDK	Oxidation(N)@3; Dioxidation(P)@8; Deamidated(N)@16; Ubiquitination GG(K)@21
Merozoite surface protein 1 precursor	FNNNFNKDVVDKIFSAR	Deamidated(N)@6; Val->Leu@10; Ubiquitination GG(K)@12; Deamidated(R)@17
Merozoite surface protein 1 precursor	FRVLSKIDGKLNDNLHLGK	Oxidation(K)@6; Ubiquitination GG(K)@10; Deamidated(N)@12; Oxidation(H)@16
Merozoite surface protein 1 precursor	KLVFGYRKPLDNIK	Oxidation(K)@1; Oxidation(F)@4; Carbamyl(R)@7; Ubiquitination GG(K)@14
Merozoite surface protein 1 precursor	LSDLKAIDDK	Oxidation(K)@5; Ubiquitination GG(K)@10

Merozoite surface protein 1 precursor	NPPPANSGNTPNTLLDK	Oxidation(N)@9; Oxidation(P)@11; Ubiquitination GG(K)@17
Merozoite surface protein 1 precursor	QKKNKKGCIYTYNIYIYTYVFNSIMK	Gln->pyro-Glu@N-term; Carbamidomethyl(C)@8; Oxidation(Y)@19; Deamidated (N)@22; Ubiquitination GG(K)@26
Merozoite surface protein 1 precursor	SLFQKEKMVLNEEEITTK	Deamidated(Q)@4; Ubiquitination GG(K)@5; Dioxidation(K)@7; Oxidation(M)@8
Cell division cycle protein 48	LQQSPKVSINKTDK	Deamidated(Q)@3; Ubiquitination GG(K)@14
Cell division cycle protein 48	GSSLGDGSGAGDRVMNQLLTEIDGVGPKK	Deamidated(N)@16; Phospho(T)@20; Ubiquitination GG(K)@29
Cell division cycle protein 48	IMKYNISSIWLNK	Oxidation(K)@3; Dioxidation(Y)@4; Deamidated(N)@5; Ubiquitination GG(K)@13
Cell division cycle protein 48	NYENGINDKNDENNKNDK	Oxidation(K)@9; Ubiquitination GG(K)@18
14-3-3 protein	EMSKANVHNKNVAATYRK	Deamidated(R)@17; Ubiquitination GG(K)@18
HSP70	IINEPTAAALAFGLEK	Oxidation(F)@12; Ubiquitination GG(K)@16
HSP70	IINEPTAAALAFGLEK	Oxidation(F)@12; Ubiquitination GG(K)@16
HSP70	RQAITNPENTVYATKR	Oxidation(P)@7; Ubiquitination GG(K)@15
S-adenosylmethionine synthetase, putative	IKDLSHEK	Ubiquitination GG(K)@2
S-adenosylmethionine synthetase, putative	LNPSGKFVLGGPAADAGL	Ubiquitination GG(K)@6
PyRhopH2	KCHNVIGNIRNTFSNK	Ubiquitination GG(K)@1; Carbamidomethyl(C)@2; Oxidation(N)@8; Oxidation(K) @16
PyRhopH2	YYESVSIYIRLKKVFNGIPAFLDKNCRK	Deamidated(N)@16; Oxidation(D)@23; Carbamidomethyl(C)@26; Ubiquitination GG(K)@28
Rhoptry-associated protein, putative	FKDINPLF	Ubiquitination GG(K)@2; Oxidation(D)@3; Oxidation(P)@6; Oxidation(F)@8

HECT domain Ubiquitin ligase E3 (putative)	KNIDGLNNISGNGRIK	Ubiquitination GG(K)@1; Oxidation(D)@4; Oxidation(N)@7
HECT domain Ubiquitin ligase E3 (putative)	MNNMNILNNPNFKTK	Deamidated(N)@11; Ubiquitination GG(K)@15
HECT domain Ubiquitin ligase E3 (putative)	IPKNNGSNKPSVHMKFTEMNEK	Ubiquitination GG(K)@3; Oxidation(M)@14
HECT domain Ubiquitin ligase E3 (putative)	EPSMYNSMKMNASLLVHY	Glu->pyro-Glu@N-term; Ubiquitination GG(K)@9; Oxidation(N)@11; Oxidation (H)@17
HECT domain Ubiquitin ligase E3 (putative)	KTLMNNDNDK	Ubiquitination GG(K)@1
HECT domain Ubiquitin ligase E3 (putative)	MIMSVLIK	Ubiquitination GG(K)@8
HECT domain Ubiquitin ligase E3 (putative)	NKKVMNTNSSGR	Deamidated(N)@1; Ubiquitination GG(K)@3
60S acidic ribosomal protein	KLQNIGGGVAAAPAGAAAVETAEAKKEDK	Ubiquitination GG(K)@1; Deamidated(Q)@3; Deamidated(N)@4
Dynein beta chain	CKPQEIAYEK	Carbamidomethyl(C)@1; Ubiquitination GG(K)@2
Dynein beta chain	CKPQEIAYEK	Carbamidomethyl(C)@1; Ubiquitination GG(K)@2
Dynein beta chain	CKPQEIAYEK	Carbamidomethyl(C)@1; Ubiquitination GG(K)@2
Dynein beta chain	CKPQEIAYEK	Carbamidomethyl(C)@1; Ubiquitination GG(K)@2
Dynein beta chain	CKPQEIAYEK	Carbamidomethyl(C)@1; Ubiquitination GG(K)@2
Dynein beta chain	CKPQEIAYEK	Carbamidomethyl(C)@1; Ubiquitination GG(K)@2
Dynein beta chain	CKPQEIAYEK	Carbamidomethyl(C)@1; Ubiquitination GG(K)@2
Dynein beta chain	KRFKTILK	Ubiquitination GG(K)@8
Dynein beta chain	KSNADRNGEKKDISK	Ubiquitination GG(K)@1
Dynein beta chain	LSKKINTCYSLLY	Ubiquitination GG(K)@3; Carbamidomethyl(C)@8
Conserved hypothetical protein	KEQERKRK	Oxidation(K)@1; Ubiquitination GG(K)@8

Conserved hypothetical protein	RKGLRAFDNIKIMK	Oxidation(N)@9; Oxidation(K)@11; Ubiquitination GG(K)@14
Plasmepsin 2 precursor (Aspartic hemoglobinase II)	SNSTFDGLNIDNSK	Oxidation(N)@2; Oxidation(D)@6; Ubiquitination GG(K)@14
Conserved hypothetical protein	VHGYSIKSLDSLK	Oxidation(H)@2; Oxidation(D)@10; Ubiquitination GG(K)@13
Ubiquitin	LRGGAIEPSLAQLAQK	Deamidated(R)@2; Oxidation(P)@8; Ubiquitination GG(K)@16
Ubiquitin	LRGGAIEPSLAQLAQK	Deamidated(R)@2; Oxidation(P)@8; Ubiquitination GG(K)@16
26S proteasome subunit	KVAEILLK	Ubiquitination GG(K)@8
26s protease regulatory subunit s10b (p44) (conserved atpase domain protein 44)	LEGKIEYEK	Ubiquitination GG(K)@4
Probable mitochondrial import receptor subunit tom40 homolog	KINNNIDCKLNFNTYAK	Carbamidomethyl(C)@8; Ubiquitination GG(K)@17
Probable mitochondrial import receptor subunit tom40 homolog	KINNNIDCKLNFNTYAK	Ubiquitination GG(K)@1; Carbamidomethyl(C)@8
PFG377 protein	GKLYLFEK	Ubiquitination LRGG(K)@8
PFG377 protein	MGDNQNQVGSILEK	Ubiquitination GG(K)@14
Conserved hypothetical protein	KNDLLFYTNYLCFIYK	Oxidation(D)@3; Carbamidomethyl(C)@12; Ubiquitination GG(K)@16
Conserved hypothetical protein	NTNKNKNTNKNKNKNK	Ubiquitination GG(K)@4; Deamidated(N)@13; Deamidated(N)@15
SET-domain protein, putative	GDKDKGDILCDNKKMK	Ubiquitination GG(K)@5; Carbamidomethyl(C)@10; Oxidation(K)@13; Oxidation(M)@15
SET-domain protein, putative	MNNIMNSQQKKENDFK	Ubiquitination GG(K)@10; Deamidated(N)@13; Oxidation(F)@15; Dioxidation(K)@16
SET-domain protein, putative	SKKNTQKKKDHVNDVKINQNNSNNK	Deamidated(Q)@6; Oxidation(D)@14; Ubiquitination GG(K)@25

Chain A, Crystal Structure Of Nucleosome Assembly Protein	GPIYDKRREALVGNGEAKIGTPNLPEF	Ubiquitination GG(K)@6; Deamidated(R)@8; Oxidation(K)@18
von Willebrand factor type A domain, putative	NVVLDTKLK	Ubiquitination GG(K)@7
Protein disulfide isomerase related protein, putative	NAKIAKIDATVEQR	Ubiquitination GG(K)@6
High molecular weight rhoptry protein 3	MKFLDKEQRLFFTYNFGDVEPQGK	Protein Terminal Carbamyl@N-term; Ubiquitination GG(K)@2; Oxidation(P)@21; Deamidated(Q)@22
Chloroquine resistance marker protein	LKRVNTKIKSK	Carbamidomethyl@N-term; Ubiquitination GG(K)@2; Oxidation(R)@3; Oxidation(K)@7
Conserved hypothetical protein	IVEKNNNTNDVNIVFK	Oxidation(D)@10; Oxidation(N)@12; Oxidation(F)@15; Ubiquitination GG(K)@16
Conserved hypothetical protein	IKRDKIKMEK	Ubiquitination GG(K)@2; Dioxidation(K)@10
Conserved hypothetical protein	THDLITNESIMYKNNEIYDK	Ubiquitination GG(K)@13; Oxidation(D)@19; Oxidation(K)@20
Tetratricopeptide repeat family protein, putative	LKCKEMLQK	Carbamidomethyl(C)@3; Oxidation(M)@6; Ubiquitination GG(K)@9
Hypothetical protein	KMLCNISFNSKRK	Carbamidomethyl(C)@4; Deamidated(N)@9; Ubiquitination GG(K)@11
Eukaryotic translation initiation factor 3 subunit 10	SGKPENEKKR	Ubiquitination GG(K)@3; Deamidated(N)@6
Erythrocyte membrane protein 1 (PfEMP1)	LKNGPCKNESEENK	Carbamidomethyl(C)@6; Ubiquitination GG(K)@7; Deamidated(N)@8; Oxidation(N)@13; Oxidation(K)@14
Hypothetical protein	RIGNRKVYNK	Oxidation(N)@9; Ubiquitination GG(K)@10
CCAAT-box DNA binding protein subunit B, putative	KTDNFNNNNVYEYLNPLK	Deamidated(N)@4; Oxidation(Y)@11; Ubiquitination GG(K)@18
CCAAT-box DNA binding protein subunit B, putative	NNQNIKNYQNIKNYQNIK	Deamidated(N)@16; Ubiquitination GG(K)@18

CCAAT-box DNA binding protein subunit B, putative	SKSKCKSKKEK	Ubiquitination GG(K)@2; Carbamidomethyl(C)@5; Phospho(S)@7
Pvstp1	GDNINKGDNINKGDNINK	Oxidation(K)@6; Deamidated(N)@11; Deamidated(N)@17; Ubiquitination GG(K)@18
Pvstp1	GDNINKGDNINKGDNINK	Oxidation(K)@6; Deamidated(N)@11; Deamidated(N)@17; Ubiquitination GG(K)@18
6-phosphofructokinase	AYRSLKIALQK	Oxidation(Y)@2; Deamidated(R)@3; Oxidation(K)@6; Ubiquitination GG(K)@11
6-phosphofructokinase	DTKSGDKNAANKGGADGLVK	Ubiquitination GG(K)@20
Conserved hypothetical protein	ICLDLILK	Carbamidomethyl(C)@2; Ubiquitination GG(K)@8
Conserved hypothetical protein	SATYLLKIEIEK	Methyl(T)@3; Ubiquitination GG(K)@12
Conserved hypothetical protein	KINQRKSYMIQENDQHMKYLLNK	Deamidated(N)@13; Oxidation(Y)@19; Oxidation(N)@22; Ubiquitination GG(K)@23
Conserved hypothetical protein	MSGKDIMNISSNLDK	Oxidation(M)@7; Deamidated(N)@12; Ubiquitination GG(K)@15
Hypothetical protein	KNILINQCEIK	Oxidation(N)@2; Deamidated(N)@6; Carbamidomethyl(C)@8; Ubiquitination GG(K)@11
Key		
	Proteins (Set 1) implicated in alpha,beta unsaturated sequiterpene lactone induced cell growth inhibition*	
	Set 1 PTMs not observed in corresponding comparative group	
	Corresponding peptide sequence to above, unmodified	
	Set 1 PTMs observed in corresponding comparative group	
	Set 1 protein peptide sequences not detected in corresponding comparative group	
*PTMs implicated are the acetylation/methylation of histones, ubiquitination and subsequent degradation of histone deacetylase by the proteomsome, and carboxy-terminal cleavage of alpha-tubulin		

Table 15: Cleavage of alpha tubulin C-terminal tyrosine residue by tubulin carboxypeptidase

Annotation	**Sequence**	**Modifications**
6hrs - untreated		
N/A		
6hrs - treated		
N/A		
18hrs - untreated		
-		
18hrs - treated		
Tubulin alpha	EDEGYEAD	Oxidation(Y)@5

Key		
	Proteins (Set 1) implicated in alpha,beta unsaturated sequiterpene lactone induced cell growth inhibition*	
	Set 1 PTMs not observed in corresponding comparative group	
	Corresponding peptide sequence to above, unmodified	
	Set 1 PTMs observed in corresponding comparative group	
	Set 1 protein peptide sequences not detected in corresponding comparative group	
*PTMs implicated are the acetylation/methylation of histones, ubiquitination and subsequent degradation of histone deacetylase by the proteomsome, and carboxy-terminal cleavage of alpha-tubulin		

Table 16: Detected phosphorylation sites (An addition of a phosphate (PO_4) group, to a protein or other organic molecule

Annotation	Sequence	Modifications
6hrs - untreated		
EMP1	MARPSGSAGGGAGGKKEDESAK	Protein Terminal Acetyl@N-term; Oxidation(P)@4; Phospho(S)@5; Phospho(S)@7
EMP1	MARPSGSAGGGAGGKKEDESAK	Protein Terminal Acetyl@N-term; Oxidation(R)@3; Phospho(S)@5
EMP1	ARPSGSAGGGAGGK	Protein Terminal Acetyl@N-term; Deamidated(R)@2; Phospho(S)@4
EMP1	ARPSGSAGGGAGGK	Protein Terminal Acetyl@N-term; Deamidated(R)@2; Phospho(S)@6
EMP1	MARPSGSAGGGAGGKKEDESAK	Protein Terminal Acetyl@N-term; Oxidation(P)@4; Phospho(S)@5; Phospho(S)@7
EMP1	MARPSGSAGGGAGGKKEDESAK	Protein Terminal Acetyl@N-term; Oxidation(R)@3; Phospho(S)@5
EMP1	ARPSGSAGGGAGGK	Protein Terminal Acetyl@N-term; Deamidated(R)@2; Phospho(S)@4
EMP1	ARPSGSAGGGAGGK	Protein Terminal Acetyl@N-term; Deamidated(R)@2; Phospho(S)@6
EMP1	MARPSGSAGGGAGGKKEDESAK	Protein Terminal Acetyl@N-term; Oxidation(P)@4; Phospho(S)@5; Phospho(S)@7
Transcription factor with AP2 domain(s) (putative)	KERKKVSK	Protein Terminal Acetyl@N-term; Deamidated(R)@3; Phospho(S)@7; Carbamyl(K)@8
14-3-3 protein	SKANVHNKNVAATYRKK	Protein Terminal Acetyl@N-term; Oxidation(K)@8; Deamidated(N)@9; Phospho(T)@13
Transcription factor with AP2 domain(s) (putative)	KERKKVSK	Protein Terminal Acetyl@N-term; Deamidated(R)@3; Phospho(S)@7; Carbamyl(K)@8
Histone H2A	MSAKGKTGRK	Protein Terminal Acetyl@N-term; Phospho(S)@2; Oxidation(K)@6; Phospho(T)@7
Histone H2A	MSAKGKTGRKKASKGTSNSAK	Protein Terminal Acetyl@N-term; Phospho(T)@7; Oxidation(K)@14; Phospho(S)@19
Histone H2A	MSAKGKTGRK	Protein Terminal Acetyl@N-term; Phospho(S)@2; Oxidation(K)@6; Phospho(T)@7
Hypothetical protein - function unknown	SSIRPELK	Protein Terminal Acetyl@N-term; Phospho(S)@2; Oxidation(K)@8
Tubulin alpha	MFSAVGGGTGSGF	Protein Terminal Acetyl@N-term; Phospho(S)@3; Phospho(S)@11; Oxidation(F)@13
Hypothetical protein - function unknown	SSIRPELK	Protein Terminal Acetyl@N-term; Phospho(S)@2; Oxidation(K)@8
Tubulin alpha	FSAVGGGTGSGFGCLMLERLSVDYGKKSK	Protein Terminal Acetyl@N-term; Phospho(S)@2; Carbamidomethyl(C)@14
Histone H4	MSGRGKGGKGLGKGGAK	Protein Terminal Acetyl@N-term; Phospho(S)@2; Oxidation(K)@13; Carbamyl(K)@17
Histone H4	MSGRGKGGKGLGKGGAK	Protein Terminal Acetyl@N-term; Phospho(S)@2; Oxidation(K)@13; Carbamyl(K)@17

PfEMP1	GTGSSTPSVPK	Protein Terminal Acetyl@N-term; Phospho(T)@2
6hr treated		
Hypothetical protein - function unknown	MSLKNSK	Protein Terminal Acetyl@N-term; Oxidation(N)@5; Phospho(S)@6
Hypothetical protein - function unknown	MSSKSDR	Protein Terminal Acetyl@N-term; Phospho(S)@5; Oxidation(R)@7
Phosphoglycerate kinase	LGNKLSISDLK	Protein Terminal Acetyl@N-term; Oxidation(K)@4; Phospho(S)@8; Oxidation(D)@9
HSP70	ASLNKKNIVK	Protein Terminal Acetyl@N-term; Phospho(S)@2; Deamidated(N)@4; Oxidation(K)@10
PfEMP1	EPHGGSGGGGDVIDHQSAKHLL	Protein Terminal Acetyl@N-term; Oxidation(H)@15; Phospho(S)@17
PfEMP1	MARPGSGGGGSSQDAK	Protein Terminal Acetyl@N-term; Deamidated(R)@3; Phospho(S)@12
12hr untreated		
histone h2b	QVHPDTGISR	Phospho(S)@9
actin, putative	SVFPSIVGRPK	Phospho(S)@1; Oxidation(F)@3; Ser->Glu@5
polyubiquitin-like protein	MQIFVKTLTGKTITL	Oxidation(M)@1; Phospho(T)@9; Oxidation(K)@11; Phospho(T)@14
60S Acidic ribosomal protein P2	LQNIGGGVAAAPAGAAAVETAEAK	Phospho(T)@20; Glu->His@22
histone h2a	AKGKTGRKKASK	Dioxidation(K)@2; Oxidation(K)@8; Phospho(S)@11
thioredoxin	ENITSMPTFK	Phospho(T)@8
hypothetical protein	IFPGLACRCTK	Carbamidomethyl(C)@7; Carbamidomethyl(C)@9; Phospho(T)@10
hypothetical protein	AEASKEQSK	Phospho(S)@8
actin depolymerizing factor	ESSNSRDR	Phospho(S)@2; Oxidation(R)@8
heat shock 70 kDa protein	AKGSKPNLPESNI	Phospho(S)@4; Deamidated(N)@12
hypothetical protein	GDNKKGTPGAK	Deamidated(N)@3; Oxidation(K)@4; Phospho(T)@7
plasmepsin I	KDLSIGSVDPVVVELKNQNK	Phospho(S)@7; Oxidation(N)@17
hypothetical protein	DINTPQNNNKK	Phospho(T)@4
heat shock protein 86	ADADKSDKTVK	Dehydrated(D)@4; Oxidation(K)@5; Phospho(S)@6
40S ribosomal protein S14	ETLVRITGGMKVK	Phospho(T)@2
endoplasmin homolog	ALIDVISDTLK	Oxidation(D)@4; Phospho(T)@9; Oxidation(K)@11
Cyclophilin	IGSRGGDITNGNGSGGESIYGR	Phospho(S)@3; Oxidation(D)@7; Oxidation(N)@10
merozoite capping protein 1	QLAENTVLDESIQK	Oxidation(N)@5; Phospho(T)@6; Phospho(S)@11
rhoptry-associated protein	NKLSEINNIISGDFLSTLK	Oxidation(N)@7; Oxidation(N)@8; Oxidation(D)@13; Phospho(T)@17

40S ribosomal protein S15/S19, putative	GVDLDKLLDLSQDELIK	Leu->Val@8; Phospho(S)@11; Deamidated(Q)@12
ribosomal protein L14	LCLIEYGPYAGK	Carbamidomethyl(C)@2; Oxidation(P)@8; Phospho(Y)@9
heat shock protein 70	QATKDAGAIAGLNVLR	Phospho(T)@3; Oxidation(D)@5;
small GTPase Rab11	QKKQATKNDDNLSIQPRGK	Oxidation(K)@3; Phospho(T)@6; Deamidated(Q)@15
alpha-tubulin	DVNAAVATIKTKR	Oxidation(N)@3; Phospho(T)@11; Deamidated(R)@13
protein disulfide isomerase	TDEKKVEYDEK	Phospho(T)@1; Oxidation(D)@2; Oxidation(Y)@8; Oxidation(K)@11
thioredoxin peroxidase 1	GGIGNIQHTLISDITK	Oxidation(N)@5; Oxidation(H)@8; Phospho(S)@12; Phospho(T)@15
hypothetical protein	RNYISSGGLEATK	Carbamyl(R)@1; Phospho(S)@5
histone H2A variant	VGSTAAVYAAAILEYLTAEVLELAGNATKDLKVKR	Phospho(T)@4; Oxidation(D)@30; Oxidation(R)@35
exported protein 2	AATSALTTVI	Phospho(T)@8
hypothetical protein	NKSFLK	Phospho(S)@3
Ribosomal protein family L5	ILAEAKSK	Phospho(S)@7
hypothetical protein	QVQAEMGQIDSDK	Deamidated(Q)@1; Phospho(S)@11
spermidine synthase	MTHVPMTVSK	Oxidation(P)@5; Oxidation(M)@6; Phospho(S)@9; Oxidation(K)@10
acid phosphatase	DTKGQILNAKYFKQFIKNER	Phospho(T)@2; Oxidation(F)@15; Oxidation(K)@17
adenosine deaminase, putative	VSESQELIDLVK	Phospho(S)@4
rhoptry-associated protein 1	TEVSKKTFSGIGFNLTEKEAK	Phospho(T)@7; Oxidation(N)@14; Oxidation(K)@18; Oxidation(K)@21
erythrocyte binding antigen 175	VIKTYTK	Phospho(T)@4
pre-mRNA splicing factor, putative	RPTSYKSSLSLKVDNIPVR	Phospho(S)@4; Oxidation(P)@17; Oxidation(R)@19
polyadenylate-binding protein	DPSLRKSGTGNIFVK	Oxidation(P)@2; Phospho(T)@9; Oxidation(K)@15
elongation factor 2	AGIISSKNAGDAR	Phospho(S)@6; Deamidated(N)@8
coatomer delta subunit, putative	SKNFRINTIYPLLK	Deamidated(N)@3; Phospho(T)@8
hypothetical protein	PIILSLHKFR	Phospho(S)@5; Oxidation(R)@10
hypothetical protein	KSKIININSIININTSEK	Phospho(S)@2; Deamidated(N)@12; Dioxidation(K)@18
diacylglycerol kinase	NNSTKVSNSSKK	Phospho(T)@4; Oxidation(K)@5; Deamidated(N)@8
hypothetical protein	KIFTLGKSGR	Oxidation(K)@1; Oxidation(F)@3; Phospho(S)@8; Oxidation(R)@10
heat shock protein 101, putate	VSKKKYNKLIK	Phospho(S)@2; Dioxidation(K)@4
hypothetical protein	DIYGDVIIIKRMFSSHTSK	Oxidation(D)@5; Deamidated(R)@11; Phospho(T)@17; Oxidation(K)@19
QF122 antigen	KANKNNTTEGNEKNKGSNNK	Phospho(T)@7; Deamidated(N)@14; Oxidation(K)@20
conserved Plasmodium protein	NITKINTLNSNTK	Phospho(T)@3; Deamidated(N)@11; Phospho(T)@12

kinesin-like protein, putative	SISSSVKFLSSKERYNNNQKRK	Phospho(S)@4; Oxidation(F)@8; Oxidation(N)@16; Deamidated(N)@17
DNA-directed RNA polymerase 1, subunit 2	GTFFQDVKVLTPR	Deamidated(Q)@5; Phospho(T)@11; Deamidated(R)@13
hypothetical protein	MGIKRMYQKIPATILVLK	Dioxidation(P)@11; Phospho(T)@13
erythrocyte membrane protein 1 (PfEMP1	VSNGATGKK	Phospho(S)@2; Oxidation(K)@8
hypothetical protein	QPLLRRHSTAILNHNISNLKTKISNVKDKNDK	Phospho(S)@8; Oxidation(H)@14; Deamidated(N)@15; Oxidation(N)@25
conserved Plasmodium protein	LDSDIESPR	Phospho(S)@3
conserved Plasmodium protein	SHIKNIGANLISSFK	Phospho(S)@13
hypothetical protein	AAHIMVASLASSLALATCK	Oxidation(M)@5; Phospho(T)@17; Carbamidomethyl(C)@18
hypothetical protein	IVNSSDCK	Phospho(S)@5; Carbamidomethyl(C)@7
conserved Plasmodium protein	EIKSNEYYENVESNEELDFLFKDMRKNL	Glu->pyro-Glu@N-term; Phospho(S)@4; Oxidation(M)@24
NOT family protein, putative	KKTKLNSK	Deamidated(N)@6; Phospho(S)@7; Oxidation(K)@8
hypothetical protein	MKHADASK	Oxidation(H)@3; Phospho(S)@7; Oxidation(K)@8
hypothetical protein	ITYLIDIVLKIKSNTVNK	Phospho(T)@2; Phospho(T)@15; Deamidated(N)@17
dynein heavy chain, putative	GRKIFNDFLCSNILKYNLK	Oxidation(F)@8; Carbamidomethyl(C)@10; Phospho(S)@11; Oxidation(K)@19
SET-domain protein	INNSKINKGRKGINKK	Deamidated(N)@3; Phospho(S)@4; Oxidation(K)@11
conserved Plasmodium protein	FGKSVLSGILEGINR	Phospho(S)@7
hypothetical protein	VTSNLLASYSNER	Phospho(S)@8; Deamidated(N)@11
12 hr treated		
hypothetical protein	SGRGKGGKGLGKGGAK	Phospho(S)@1; Deamidated(R)@3; Formyl(K)@12
60S ribosomal protein P1, putative	MSITSDNILK	Phospho(S)@2
glyceraldehyde-3-phosphate dehydrogenase	SKGGKDWRAGRCALSNIIPASTGAAKAVGK	Phospho(S)@1; Oxidation(K)@2; Carbamidomethyl(C)@12; Dioxidation(K)@26
Enolase	LTAAIGKDVQIVGDDLLVTNPTR	Phospho(D)@15; Phospho(T)@19
hypothetical protein	IIDVVYNASNNELVRTK	Deamidated(N)@7; Phospho(S)@9; Deamidated(N)@11
heat shock protein	ITPSYVSFVDGERKVGEAAK	Phospho(S)@4; Oxidation(F)@8; Phospho(K)@20
hypothetical protein	GGNRGGSRSGFRGGRGGFRGGR	Oxidation(R)@8; Phospho(S)@9; Oxidation(F)@11; Oxidation(R)@19
heat shock 70 kda protein	NRGKDLSK	Oxidation(K)@4; Oxidation(D)@5; Phospho(S)@7
actin depolymerizing factor	KIEGVNVLTSVIESAQDVAD	Carbamyl(K)@1; Phospho(T)@9

REX2	LAEIFSSGK	Phospho(S)@7; Oxidation(K)@9
thioredoxin, putative	TYTKMVFIKVDVDEVSEVTEK	Phospho(T)@1; Phospho(T)@19
hypothetical protein	SNLLSRFTR	Phospho(S)@1; Oxidation(N)@2; Oxidation(R)@6; Oxidation(F)@7
hypothetical protein	IKDSKRKMQR	Phospho(S)@4
hypothetical protein	TIEVITK	Phospho(T)@6
Chain A, Structure Of Gtp-Bound	VIILGDSGVGK	Phospho(S)@7; Phospho(K)@11
rhoptry-associated protein 3	DLSLSSILR	Phospho(S)@3
histone H2A	VLGLGKGGKGKTGSGKTKKAPLSRASR	Deamidated(R)@24; Phospho(S)@26; Oxidation(R)@27
heat shock protein 70	AMTKDNNLLGK	Phospho(T)@3; Deamidated(N)@7
hypothetical protein	NPSQSGPYR	Deamidated(N)@1; Phospho(S)@5; Oxidation(P)@7; Deamidated(R)@9
40S ribosomal protein S12	AVFDNVTAIQK	Phospho(T)@7; Deamidated(Q)@10
40S ribosomal protein S12	SIPYIHPDVKVNDTVR	Oxidation(P)@7; Deamidated(N)@12; Oxidation(D)@13; Phospho(T)@14
beta3 proteasome subunit	LGANTFTTVSTKFSK	Oxidation(N)@4; Oxidation(F)@6; Phospho(T)@11
hypothetical protein	KSSQVGK	Phospho(S)@3; Oxidation(K)@7
ribosomal protein 113	TNTNPKKGPLHLR	Phospho(T)@3; Oxidation(N)@4
40s ribosomal protein	WTPGMLTNQIIQKFTEPR	Phospho(T)@2; Phospho(T)@7; Phospho(T)@15
hypothetical protein	SNNNSTHSKK	Phospho(T)@6
Plasmodium exported protein	SKQRRNEALR	Phospho(S)@1; Oxidation(K)@2; Oxidation(N)@6
hypothetical protein	VVALTGSGTSAESNIPSFR	Phospho(S)@6; Deamidated(R)@18; Dehydrated(S)@21
hypothetical protein	IIKGDSMTR	Phospho(S)@6; Carbamyl(M)@7
thioredoxin-related protein	SGASKVAKK	Phospho(S)@1
hypothetical protein	TNKTNK	Phospho(T)@1; Oxidation(N)@2; Oxidation(N)@5
knob-associated histidine-rich protein	EASTSKGATK	Phospho(S)@5; Phospho(T)@9
Ribosomal protein family L5	DVGITRTTTGNR	Phospho(T)@5; Deamidated(R)@6
conserved protein	SSTSTQK	Phospho(T)@5
hypothetical protein	TIVSASR	Phospho(S)@6; Oxidation(R)@7
HAP protein	LTSKAGTISGIFSK	Phospho(T)@7; Phospho(S)@13
plasmepsin 2	ILKTIKTHK	Oxidation(K)@3; Phospho(T)@4; Phospho(T)@7
adenosine deaminase, putative	LTDIYIDYTVVEDLAKHAVFNK	Phospho(T)@9; Oxidation(N)@21; Oxidation(K)@22

conserved Plasmodium protein	LNNIIKYKTNK	Oxidation(K)@8; Phospho(T)@9; Oxidation(K)@11
Rifin	SNQAAEAAVAAGKAAETAEK	Phospho(S)@1; Deamidated(N)@2; Oxidation(K)@13; Oxidation(K)@20
pre-mRNA splicing factor, putative	KNKNESSSDVLSKHSSAYR	Phospho(K)@3; Oxidation(N)@4; Phospho(S)@6; Oxidation(H)@14
TCP-1/cpn60 chaperonin family	LTNGQIRLTLSSIDGTEK	Phospho(T)@2; Oxidation(R)@7
phosphoglucomutase, putative	NSRTKLAIVYSPMHGIGRK	Oxidation(N)@1; Phospho(S)@2; Phospho(S)@11; Oxidation(P)@12
heat shock protein 101	TSGTSYRGEFETRMK	Phospho(T)@4; Oxidation(F)@10; Dioxidation(R)@13; Oxidation(M)@14
hypothetical protein	NTPSSSGLVK	Phospho(T)@2; Oxidation(K)@10
S-adenosylmethionine synthetase	TQITIEYK	Phospho(T)@4; Oxidation(Y)@7
conserved hypothetical protein	NSSSGNGK	Phospho(S)@2; Deamidated(N)@6
conserved Plasmodium protein	TLTNFALLQNR	Phospho(T)@1; Deamidated(N)@4; Oxidation(R)@11
tudor staphylococcal nuclease	IQKKNIWSLEK	Oxidation(K)@3; Oxidation(N)@5; Phospho(S)@8; Oxidation(K)@11
leucine aminopeptidase	TIEVGNTDAEGRLTLADALVYAEK	Phospho(T)@1; Oxidation(N)@6
hypothetical protein	YDFMNETNELKVGRNVINYK	Deamidated(N)@5; Phospho(T)@7; Oxidation(N)@8; Deamidated(N)@18
conserved Plasmodium protein	AGSELTRK	Phospho(S)@3
Helicase	DTLMADFKKGISK	Phospho(S)@12
conserved Plasmodium protein	KTIDANISR	Phospho(S)@8
inositol phosphatase, putative	ELFTSLKR	Phospho(S)@5
hypothetical protein	SSSIGLKLTK	Oxidation(K)@7; Phospho(T)@9; Oxidation(K)@10
hypothetical protein	YSNTSSSIGSFSK	Oxidation(Y)@1; Phospho(S)@2; Oxidation(F)@11
hypothetical protein	KGNSSKLR	Phospho(S)@5
ring-infected erythrocyte surface antigen	LSKRIESLR	Phospho(S)@2
18 hr untreated		
HSP70	ASAKGSKPNLPESNI	Protein Terminal Acetyl@N-term; Phospho(S)@6
HSP70	MASAKGSKPNLPESNIAIGIDLGTTYSCVGVWR	Protein Terminal Acetyl@N-term; Phospho(S)@3; Dioxidation(Y)@26; Carbamidomethyl(C)@28; Oxidation(W)@32
Phosphoglycerate kinase	KSSVVSLF	Protein Terminal Acetyl@N-term; Phospho(S)@6

Phosphoglycerate kinase	LGNKLSISDLKDIKNK	Protein Terminal Acetyl@N-term; Phospho(S)@6; Phospho(S)@8; Phospho(K)@16
Glyceraldehyde-3-phosphate dehydrogenase, putative	AVTKLGINGFGRIGR	Protein Terminal Acetyl@N-term; Phospho(T)@3; Deamidated(R)@15
Glyceraldehyde-3-phosphate dehydrogenase, putative	AVTKLGINGFGRIGR	Protein Terminal Acetyl@N-term; Phospho(T)@3; Oxidation(K)@4; Dioxidation(R)@12
Cell division cycle protein 48 (putative)	EDNTDKKALVDENNGENK	Protein Terminal Acetyl@N-term; Phospho(T)@4; Deamidated(N)@14; Oxidation(N)@17
Enolase	AHVITRINAR	Protein Terminal Acetyl@N-term; Phospho(T)@5; Dioxidation(R)@6; Deamidated(N)@8
HSP60 (putative)	MVKQVAANTNDK	Protein Terminal Acetyl@N-term; Phospho(T)@9; Carbamyl(K)@12
HSP70	MYTTPTSINLKTK	Protein Terminal Acetyl@N-term; Phospho(T)@3; Phospho(S)@7; Phospho(T)@12
Erythrocyte membrane protein 3	ATIKKYHIRGR	Protein Terminal Acetyl@N-term; Phospho(T)@2; Oxidation(K)@4; Oxidation(Y)@6
Elongation factor 1-gamma (putative)	ISKNINKTK	Protein Terminal Acetyl@N-term; Phospho(S)@2; Oxidation(N)@4; Phospho(T)@8
Hypothetical PIESP2 erythrocyte surface protein	GKRSYPKSGHK	Protein Terminal Acetyl@N-term; Carbamyl(K)@7; Phospho(S)@8; Oxidation(H)@10
Lysyl-tRNA synthetase	MRVSASGQKLR	Protein Terminal Acetyl@N-term; Phospho(S)@4; Oxidation(K)@9
Lysyl-tRNA synthetase	MRVSASGQKLR	Protein Terminal Acetyl@N-term; Oxidation(R)@2; Phospho(S)@6; Deamidated(Q)@8
Ubiquitin-activating enzyme e1	QNKTPPLKK	Protein Terminal Acetyl@N-term; Phospho(T)@4; Oxidation(P)@6; Oxidation(K)@9
DNA/RNA-binding protein	MTKKPTFYARIGK	Protein Terminal Acetyl@N-term; Phospho(T)@2; Oxidation(K)@3; Oxidation(K)@13
Translation elongation factor 1 beta-related	ASNASLLNVK	Protein Terminal Acetyl@N-term; Phospho(S)@5; Oxidation(N)@8
Translation elongation factor 1 beta-related	ASNASLLNVK	Protein Terminal Acetyl@N-term; Phospho(S)@5
Hypothetical protein	MVTNLGLMVTNLGLK	Protein Terminal Acetyl@N-term; Phospho(T)@10; Deamidated(N)@11
Endoplasmin homolog precursor	SVTNPKDLELTNSIK	Phospho(T)@3; Oxidation(N)@4; Methyl(K)@15
Endoplasmin homolog precursor	EGKKNKETLR	Phospho(T)@8; Methyl(L)@9
Endoplasmin homolog precursor	SFELTEEEKKKEQQMQK	Phospho(S)@1; Methyl(E)@8; Oxidation(K)@11; Oxidation(M)@15
Endoplasmin homolog precursor	EKNILSITDTGIGMTKVDLINNLGTIAK	Glu->pyro-Glu@N-term; Oxidation(N)@3; Phospho(S)@6; Methyl(K)@16
Molecular chaperone of HSP90 family	ELISNAADALEK	Methyl(E)@1; Phospho(S)@4; Oxidation(N)@5
Molecular chaperone of HSP90 family	ELISNAADALEK	Phospho(S)@4; Methyl(E)@11; Oxidation(K)@12
Endoplasmin homolog precursor	EQLQQNKILKAVSKR	Methyl(E)@1; Phospho(S)@13
Heat-shock protein	YSAYLVADHVVVISK	Phospho(S)@2; Methyl(D)@8; Oxidation(H)@9; Oxidation(K)@15
Heat-shock protein	DKIRYESITDTQKL	Oxidation(R)@4; Phospho(T)@9; Trimethyl(K)@13

Heat shock protein 86	IMKAQALRDNSMTSYMLSK	Phospho(T)@13; Oxidation(M)@16; Methyl(K)@19
HSP 70	KNRGKDLSKNSR	Oxidation(K)@1; Phospho(S)@8; Methyl(N)@10; Phospho(S)@11
HSP 70	NRGKDLSKNSRALRR	Oxidation(D)@5; Phospho(S)@7; Trimethyl(K)@8
HSP 70	NRGKDLSKNSRALRR	Methyl(D)@5; Phospho(S)@7; Deamidated(R)@11; Carbamyl(R)@15
HSP 70	PGNAPAGSGPTVEEV	Phospho(S)@8; Methyl(E)@14
Elongation factor 1 alpha	APSAVVSECKSVEMHK	Oxidation(P)@2; Phospho(S)@3; Carbamidomethyl(C)@9; Oxidation(K)@10; Methyl(K)@16
Elongation factor 1 alpha	FLNIDSKIDKRSGK	Phospho(S)@12; Methyl(K)@14
Elongation factor 1 alpha	APSAVVSECKSVEMHK	Oxidation(P)@2; Phospho(S)@3; Carbamidomethyl(C)@9; Oxidation(K)@10; Methyl(K)@16
Mature parasite-infected erythrocyte surface antigen	EDVNEKDTANKDK	Methyl(D)@2; Oxidation(N)@4; Phospho(T)@8; Oxidation(K)@13
Mature parasite-infected erythrocyte surface antigen	ITEESKDREGNK	Phospho(T)@2; Dimethyl(K)@12
Merozoite surface protein-1	KTIDQNKNADNEEGKK	Phospho(T)@2; Deamidated(N)@11; Dimethyl(K)@16
Merozoite surface protein-1	NPPPANSGNTPNTLLDKNK	Methyl(N)@6; Phospho(S)@7; Oxidation(P)@11
Merozoite surface protein-1	DQVVTGEAISVTMDNI	Oxidation(D)@1; Phospho(T)@5; Methyl(T)@12; Oxidation(M)@13
Merozoite surface protein-1	ITKLSDLKAIDDKIDLFK	Phospho(T)@2; Methyl(S)@5; Methyl(D)@6
Merozoite surface protein-1	KEAEIAETENTLENTK	Phospho(T)@8; Trimethyl(K)@16
Merozoite surface protein-1	KKEAEIAETENTLENTK	Oxidation(K)@2; Phospho(T)@16; Methyl(K)@17
Merozoite surface protein-1	KLLDKINEIKNPPPANSGNTPNTLLDK	Oxidation(N)@7; Phospho(T)@23; Methyl(D)@26; Oxidation(K)@27
Merozoite surface protein-1	KKEAEIAETENTLENTK	Oxidation(K)@2; Phospho(T)@16; Methyl(K)@17
Merozoite surface protein-1	TGLEADIKKLTEEIK	Methyl(T)@1; Oxidation(K)@9; Phospho(T)@11
Merozoite surface protein-1	VDVTPKSQDPTK	Oxidation(D)@9; Phospho(T)@11; Trimethyl(K)@12
Pyruvate kinase	QILEPNNVNLRSKK	Deamidated(Q)@1; Methyl(I)@2; Oxidation(R)@11; Phospho(S)@12
Pyruvate kinase	FKYKNSAAGASMQSAANITLR	Methyl(K)@4; Phospho(S)@11; Deamidated(R)@21
Pyruvate kinase	GVTCIKVGSFQGTDIVIR	Phospho(T)@3; Carbamidomethyl(C)@4; Methyl(K)@6; Oxidation(D)@14; Oxidation(R)@18
Pyruvate kinase	LIADGSVSCK	Phospho(S)@6; Methyl(S)@8; Carbamidomethyl(C)@9
HSP 70	CVKNTLLSEKSR	Carbamidomethyl(C)@1; Methyl(T)@5; Phospho(S)@11

HSP 70	IVRASNGDAWIEAQGK	Phospho(S)@5; Oxidation(N)@6; Methyl(D)@8
HSP 70	KQQITIQSSGGLSKEEIEK	Phospho(T)@5; Methyl(I)@6; Oxidation(K)@19
HSP 70	NTLLSEKSRSLCTSK	Methyl(E)@6; Oxidation(K)@7; Oxidation(R)@9; Carbamidomethyl(C)@12; Phospho(S)@14
HSP 70	QAITNPENTVYATKR	Methyl(Q)@1; Oxidation(Y)@11; Phospho(T)@13
HSP 70	RFIGRKYDEDATKK	Arg->Orn(R)@1; Methyl(E)@9; Oxidation(D)@10; Phospho(T)@12
HSP 70, homologue	TTPSVVAFTNDNQR	Phospho(S)@4; Methyl(R)@14
Chain A, Crystal Structure Of Phosphoglycerate Kinase	KGAITIVGGGDTASLVEQQNK	Phospho(T)@5; Methyl(E)@17; Oxidation(N)@20; Oxidation(K)@21
Para-aminobenzoicacid synthetase	EPSRISFNSIVQKEQYIENVRK	Deamidated(N)@8; Phospho(S)@9; Methyl(I)@10; Oxidation(Y)@16
Chain A, Crystal Structure Of Phosphoglycerate Kinase	ANKEDVEKFQNDLTK	Oxidation(K)@3; Methyl(E)@4; Phospho(T)@14
Phosphoglycerate kinase	ELPGVLALSN	Methyl(E)@1; Phospho(S)@9; Oxidation(N)@10
Phosphoglycerate kinase	ELPGVLALSN	Methyl(L)@2; Phospho(S)@9; Oxidation(N)@10
Para-aminobenzoicacid synthetase	NMISIGAGGAITIK	Phospho(S)@4; Phospho(T)@12; Methyl(I)@13; Oxidation(K)@14
Rhoptry-associated protein 1	KTFSGIGFNLTEKEAK	Phospho(T)@11; Trimethyl(K)@13
Rhoptry-associated protein 1	TDMLSLQNEESKIPNDKSANSKLATR	Phospho(T)@1; Oxidation(M)@3; Oxidation(P)@14; Methyl(D)@16
Actin	SYELPDGNIITVGNERF	Phospho(S)@1; Methyl(E)@3; Oxidation(R)@16; Oxidation(F)@17
Enolase (2-phosphoglycerate dehydratase)	TEQKKIDNLMVEELDGSK	Phospho(T)@1; Methyl(E)@2
Ornithine aminotransferase	ALSGGHYPISAILANDDVML	Phospho(S)@3; Oxidation(P)@8; Methyl(I)@9
RhopH2	QSLPIIDHVYHKDLKTLK	Phospho(S)@2; Trimethyl(K)@12; Oxidation(K)@18
RhopH2	QLMSAIRKYVTTLTK	Phospho(S)@4; Oxidation(Y)@9; Methyl(K)@15
HSP 60	APGFGEHRKALIHDIAVMTGAK	Deamidated(R)@8; Methyl(D)@14; Phospho(T)@19
HSP 60	FGSDARTAMLTGCNK	Phospho(S)@3; Oxidation(M)@9; Carbamidomethyl(C)@13; Dimethyl(K)@15
HSP 60	LDDPQVVSYLGK	Methyl(D)@2; Phospho(S)@8
Hypothetical protein	FVLGGPAADAGLTGRK	Methyl(D)@9; Phospho(T)@13
s-adenosylmethionine synthetase	KNYIFIFGEITTKAK	Phospho(T)@12; Methyl(K)@13; Oxidation(K)@15
Membrane-associated calcium-binding protein	QTRSDESSGVK	Oxidation(D)@5; Methyl(E)@6; Phospho(S)@8; Oxidation(K)@11
HSP 101	GALKLYNSLSK	Methyl(L)@5; Deamidated(N)@7; Phospho(S)@10

HSP 101	GDVPKELQGYTVISLNFR	Methyl(Q)@8; Phospho(S)@14; Deamidated(N)@16
HSP 101	FEKTKKDKDGK	Methyl(K)@3; Phospho(T)@4
HSP 101	EQLKKYYEEYVITGER	Deamidated(Q)@2; Oxidation(K)@5; Methyl(E)@8; Phospho(T)@13
HSP 101	EPPIELQNSLKEAQQK	Phospho(S)@9; Methyl(E)@12
HSP 101	SNTIIIMTSNLGAELFKK	Methyl(S)@1; Oxidation(N)@2; Phospho(T)@3; Oxidation(K)@18
14-3-3 protein, putative	ANVHNKNVAATYR	Phospho(T)@11; Oxidation(Y)@12; Methyl(R)@13
14-3-3 protein, putative	ASWRIISSVEQKEMSK	Phospho(S)@2; Oxidation(W)@3; Methyl(E)@10; Deamidated(Q)@11
Phosphoribosylpyrophosphate synthetase	ESLNDLFNIKS	Deamidated(N)@4; Methyl(L)@6; Phospho(S)@11
Rhoptry-associated protein 2	RSSSLALVGTNNNDPIFAYCEK	Oxidation(R)@1; Phospho(S)@4; Carbamidomethyl(C)@20; Methyl(E)@21
Chaperonin cpn60, mitochondrial precursor	GILDSSINSPNYLSKHR	Methyl(D)@4; Phospho(S)@5; Oxidation(Y)@12
Chaperonin cpn60, mitochondrial precursor	RSPNNKNRLFINK	Phospho(S)@2; Oxidation(P)@3; Methyl(L)@9; Oxidation(K)@13
Hypothetical protein	LNALIPLQTALRTHAK	Deamidated(N)@2; Phospho(T)@9; Methyl(T)@13
Hypothetical protein	AGLKTIKTLK	Methyl(K)@7; Phospho(T)@8
Hypothetical protein	EVGIALLNVFTSKTYTNK	Methyl(I)@4; Phospho(T)@11
Hypothetical protein	IDMISNKIGLSNFK	Oxidation(M)@3; Phospho(S)@11; Dimethyl(K)@14
Hypothetical protein	NISKGLSHPILISANK	Oxidation(K)@4; Phospho(S)@7; Methyl(I)@12; Phospho(S)@13
Hypothetical protein	NISKGLSHPILISANK	Oxidation(N)@1; Phospho(S)@3; Methyl(S)@7; Phospho(S)@13
Hypothetical protein	NKLSRGSAIK	Methyl(N)@1; Oxidation(K)@2; Phospho(S)@4; Deamidated(R)@5
Hypothetical protein	TVSENSDK	Phospho(S)@6; Methyl(K)@8
Ring-infected erythrocyte surface antigen	THLKKSSKSAK	Phospho(T)@1; Methyl(L)@3; Phospho(S)@7
Vacuolar ATP synthase catalytic subunit a	GRLTYIAPDGSYTLKDK	Methyl(L)@3; Phospho(T)@4; Oxidation(D)@9
Vacuolar ATP synthase subunit A, putative	LAEMPADSGYPAYLGARLASFYER	Methyl(S)@8; Phospho(S)@20; Oxidation(R)@24
Karyopherin beta	EYISAIDNAIAALGDVVLM	Phospho(S)@4; Methyl(D)@7; Oxidation(D)@15
Karyopherin beta	DNSLKSLSIEALVTIPER	Phospho(S)@8; Phospho(T)@14; Dimethyl(R)@18
Karyopherin beta	EQAVTAIAVIAGVIEEDFLKYYSTVVPMMK	Glu->pyro-Glu@N-term; Deamidated(Q)@2; Phospho(T)@5; Methyl(T)@24

Tubulin alpha	DVNAAVATIKTK	Methyl(D)@1; Deamidated(N)@3; Phospho(T)@8; Oxidation(K)@12
Tubulin alpha	DVNAAVATIKTKRTI	Deamidated(N)@3; Methyl(T)@11; Oxidation(K)@12; Phospho(T)@14
Tubulin alpha	GDVVPKDVNAAVATIK	Oxidation(P)@5; Oxidation(D)@7; Methyl(N)@9; Phospho(T)@14
Tubulin alpha	QLFHPEQLISGKEDAANNFAR	Methyl(E)@6; Phospho(S)@10; Deamidated(N)@18
18hr treated		
T-complex protein beta subunit	TVTNDGATILKSVWLDNPVSK	Deamidated(N)@4; Phospho(S)@12; Methyl(K)@21
T-complex protein beta subunit	ILTPLNIEGTR	Phospho(T)@3; Oxidation(P)@4; Methyl(E)@8
Hypothetical protein	KNGGKDVSKNSK	Methyl(D)@6; Oxidation(K)@9; Phospho(S)@11
Hypothetical protein	KNGGKDVSKNSK	Methyl(D)@6; Oxidation(K)@9; Phospho(S)@11
Hypothetical protein	KKNGGKDVSK	Dioxidation(K)@2; Oxidation(K)@6; Methyl(D)@7; Phospho(S)@9
Hypothetical protein	KNGGKDVSKNSK	Deamidated(N)@2; Methyl(D)@6; Oxidation(K)@9; Phospho(S)@11
Stress-seventy subfamily A protein	EAQNNGPTVEEV	Glu->pyro-Glu@N-term; Methyl(N)@5; Phospho(T)@8
HSP 70, putative	IINEPTAAAIAYGLDK	Phospho(T)@6; Dimethyl(K)@16
Hypothetical protein	MLTKKNTLKNSLSNGISK	Phospho(S)@13; Methyl(K)@18
Hypothetical protein	NSLSNGISKR	Phospho(S)@8; Trimethyl(K)@9
Hypothetical protein	MLTKKNTLKNSLSNGISK	Phospho(S)@13; Methyl(K)@18
Hypothetical protein	NSLSNGISKR	Phospho(S)@8; Trimethyl(K)@9
Hypothetical protein	NSLSNGISKR	Phospho(S)@8; Trimethyl(K)@9
Hypothetical protein	SLDNKSDGPLK	Oxidation(K)@5; Phospho(S)@6; Methyl(L)@10
6-phosphofructokinase	AERQIPISIIGVPK	Methyl(E)@2; Phospho(S)@8
Cg4 protein	LGIDIGNDNSVVATINK	Methyl(N)@7; Phospho(T)@14
Cg4 protein	LTPTLVGFTEKER	Phospho(T)@4; Methyl(T)@9; Deamidated(R)@13
Early transcribed membrane protein 10.2	VKSKSSNGKSK	Oxidation(K)@4; Methyl(S)@6; Phospho(S)@10; Oxidation(K)@11
S-antigen	KSKNSIINMLIGMIR	Phospho(S)@2; Methyl(N)@4; Phospho(S)@5; Oxidation(M)@9
S-antigen	KSKNSIINMLIGMIR	Phospho(S)@2; Methyl(N)@4; Phospho(S)@5; Oxidation(M)@9
S-antigen	NKKSKNSIINMLIG	Phospho(S)@7; Oxidation(M)@11; Methyl(I)@13