

Table 1: *P. falciparum* putative transport proteins: proteins that share sequence similarities with known or putative transport proteins and/or conserved domains of transport protein families.

GENE PRODUCT ^a	CH ^b	ANNOTATION ^c	SIZE ^d	TMD ^e	CLOSEST BLASTP HOMOLOGUE ^f	E ^g	CONSERVED DOMAIN MATCH ^h	PUTATIVE FUNCTION ⁱ
MAJOR FACILITATOR SUPERFAMILY (TC 2.A.1)								
PFL0170w	12	Hypothetical protein	1250	12	Although PFL0170w does not have a sequence homologue in the current databases, it does display some structural similarity to the MFS proteins.	-	Pfam00083 0.028 (p)	Transporter
SUGAR PORTER FAMILY (TC 2.A.1.1; PFAM00083)								
PFB0210c	2	Monosaccharide transporter, putative	504	12	<i>T. gondii</i> facilitative glucose transporter (21630202; 1.7e ⁻⁸⁶ to Pfam00083).	1.3e ⁻¹⁰⁵	Pfam00083 7.5e ⁻⁹²	Hexose transporter 1 (PfHT1; [46])
PFI0955w	9	Sugar transporter, putative	476	11/12	PFB0210c PfHT1 (23613713).	3e ⁻²⁸	Pfam00083 8e ⁻¹²	Sugar transporter
PFI0785c	9	Transporter, putative	1379	11/13	<i>C. parvum</i> putative MFS protein (46229527; 7e ⁻⁰⁵ to Pfam00083).	4e ⁻⁴⁰	Pfam00083 1e ⁻⁰⁵	Sugar transporter
DRUG:H⁺ ANTIporter-1 FAMILY (TC 2.A.1.2; COG2814)								
PFB0275w	2	Membrane transporter Hypothetical protein, conserved	565	11	<i>A. thaliana</i> putative transporter (15234530; 1e ⁻¹¹⁹ to KOG1330 and 6e ⁻⁰⁷ to COG2814).	9e ⁻⁵⁹	KOG1330 2e ⁻²⁵ COG2814 25e ⁻⁰⁹	Metabolite/drug transporter
PF11_0059*	11	Hypothetical protein	417	9	<i>P. luminescens</i> putative multidrug resistance transporter (36787367; 3e ⁻¹⁴ to COG2814)	9.9e ⁻⁰⁴	Pfam00083 0.002 (p)	Metabolite/drug transporter
PF14_0260	14	Hypothetical protein	809	12/11	PFB0275w (23593282).	4.6e ⁻²²	COG2814 8e ⁻⁰⁴	Metabolite/drug transporter
PF14_0387	14	Hypothetical protein	582	12	<i>G. violaceus</i> putative tetracycline resistance protein (37521059; 8e ⁻⁰⁹ to COG2814).	3e ⁻⁰⁷	COG2814 1e ⁻¹¹	Metabolite/drug transporter
FullPhat								
PFE0825w	5	Transporter, putative	440	10/11	<i>M. musculus</i> putative organic cation transporter (6679180; 1e ⁻⁰⁵ to KOG2615).	2.1e ⁻²³	KOG2615 0.003 (p)	Metabolite/drug transporter
MONOCARBOXYLATE PORTER FAMILY (TC 2.A.1.13; KOG2504, PFAMB252, PFAMB1302)/ OXALATE:FORMATE ANTIporter FAMILY (TC 2.A.1.11; KOG2504, PFAMB252)								
PFB0465c	2	Membrane transporter Hypothetical protein	457	12/11	<i>C. briggsae</i> hypothetical protein (39587811; 4e ⁻³³ to KOG2504, 3.5e ⁻⁰⁹ to PfamB252 and 4.7e ⁻⁰⁶ to PfamB1302).	1e ⁻³⁴	PfamB252 2.8e ⁻³⁸ KOG2504 2e ⁻¹⁶	Monocarboxylate transporter
PFI1295c	9	Membrane transporter, putative	612	11/12	PFB0465c (16804992).	6e ⁻³⁰	KOG2504 2e ⁻⁰⁹ PfamB252 8.3e ⁻⁰⁸	Monocarboxylate transporter
GeneFinder								
PEPTIDE-ACETYL-COENZYME A TRANSPORTER FAMILY (TC 2.A.1.25; KOG3574)								
PF10_0360	10	Hypothetical protein	~579	9/11	<i>A. gambiae</i> hypothetical protein (31199731; 4e ⁻¹⁵³ to KOG3574). Chr10.gen_231 appears to contain ORFs for 3 different proteins, amino acid residues 1644-2222 were used in our analysis.	1e ⁻⁶¹	KOG3574 3e ⁻⁶⁹	Acetyl-CoA transporter
GeneFinder								
GLYCOSIDE-PENTOSIDE-HEXURONIDE:CATION SYMPORTER FAMILY (TC 2.A.2; COG2211)[§]								
PFE1455w	5	Sugar transporter, putative	548	12	<i>C. aurantiacus</i> hypothetical protein (22972266; 4e ⁻⁹⁰ to COG2211).	9e ⁻²⁰	COG2211 1e ⁻³⁰	Sugar: cation symporter
ORGANO ANION TRANSPORTER FAMILY (TC 2.A.60; Pfam03132, KOG3626)[§]								
MAL6P1.283	6	Hypothetical protein	853	12	<i>A. thaliana</i> hypothetical protein (4314370; 7e ⁻¹⁰⁷ to KOG1330 and 3e ⁻¹¹ to KOG3626).	1.9e ⁻⁰⁸	Pfam03132 7.8e ⁻⁰⁵ KOG1330 1e ⁻⁰⁷	Organic anion transporter
FOLATE-BIOPTERIN TRANSPORTER FAMILY (TC 2.A.71; PFAM03092)[§]								
MAL8P1.13	8	Integral membrane protein, conserved	505	12	PF11_0172 (23508363).	8e ⁻⁵⁰	Pfam03092 3.9e ⁻³⁵	Folate/biopterin transporter
PF10_0215	10	Hypothetical protein	629	12/11	<i>T. elongatus</i> hypothetical protein (22297560; 2.8e ⁻¹⁶⁴ to Pfam03092).	6e ⁻⁰⁴	Pfam03092 0.079 (p)	Metabolite/vitamin transporter
GlimmerM								
PF11_0172	11	Hypothetical protein, conserved	455	11	<i>C. parvum</i> putative biopterin transporter (32398782; 4.2e ⁻⁵⁶ to Pfam03092).	7e ⁻⁹⁵	Pfam03092 7.8e ⁻⁴⁴	Folate/biopterin transporter
NOVEL PUTATIVE TRANSPORTER FAMILY								
PFA0240w	1	Hypothetical protein	711	12/11	PFA0245w (23613408).	4.9e ⁻⁵⁹	No matches	Transporter
PFA0245w	1	Hypothetical protein	577	12	PF11_0310 (23508501).	2e ⁻²⁸	KOG0569 0.008 (p)	Transporter
PFC0530w	3	Hypothetical protein	579	12/11	PFA0245w (23613408).	3.5e ⁻⁰⁷	No matches	Transporter
PFI0720w	9	Hypothetical protein	516	11	PFA0245w (23613408).	5e ⁻¹⁵	No matches	Transporter
PF11_0310	11	Hypothetical protein	609	12	PFA0240w (23513407).	1.1e ⁻³⁴	No matches	Transporter

ZINC (Zn²⁺)-IRON (Fe²⁺) PERMEASE FAMILY (TC 2.A.5; KOG1558)							
MAL6P1.94	6	Transporter protein, putative	361	8	<i>D. melanogaster</i> hypothetical protein (24586056; 1e ⁻⁵⁸ to KOG1558).	1e ⁻¹⁰	KOG1558 1e ⁻¹³ Zn ²⁺ or Fe ²⁺ permease
RESISTANCE-NODULATION-CELL DIVISION SUPERFAMILY (TC 2.A.6; COG1033)							
EUKARYOTIC (PUTATIVE) STEROL TRANSPORTER FAMILY (TC 2.A.6.6; KOG1934)							
PFA0375c	1	Patched family protein, putative	1470	12	<i>C. parvum</i> putative patched family protein (46227691; 3e ⁻⁵⁶ to KOG1934).	1e ⁻³⁸	KOG1934 2e ⁻⁴¹ Lipid/sterol:H ⁺ symporter
DRUG/METABOLITE TRANSPORTER SUPERFAMILY (TC 2.A.7; PFAM00892, KOG3912)							
PF07_0070	7	Transporter/permease protein, putative	322	9	<i>G. lamblia</i> hypothetical protein (29247301; 4e ⁻⁰⁷ to KOG3912).	9e ⁻²⁰	KOG3912 3e ⁻⁰⁴ Drug/metabolite transporter Pfam00892 0.008 (p)
PFE0785c	5	Hypothetical protein	456	10	<i>D. discoideum</i> putative GDP-fucose: GMP antiporter (28828290; 5e ⁻⁶² to KOG1442).	2e ⁻⁰⁴	No matches Drug/metabolite transporter
TRIOSE-PHOSPHATE TRANSPORTER FAMILY (TC 2.A.7.9; KOG1441, KOG1443)							
PFE0410w*	5	Triose- or hexose-P _i ; P _i antiporter, putative	342	9	<i>P. sativum</i> chloroplast triose-P _i ; P _i antiporter (117290; 2e ⁻⁴⁶ to KOG1441).	1e ⁻⁴⁷	KOG1441 4e ⁻²⁹ Triose- or hexose-P _i ;P _i antiporter
PFE1510c*	5	Phosphoenolpyruvate: P _i antiporter, putative	524	7/8	PFE0410w (2361306).	3e ⁻⁴⁴	KOG1441 1e ⁻³⁰ Phosphoenolpyruvate:P _i antiporter
PFL0890c	12	Hypothetical protein	491	10	<i>S. bicolor</i> putative phosphoenolpyruvate: phosphate antiporter (18481711; 7e ⁻⁴⁰ to KOG1441).	5e ⁻¹³	KOG1443 6e ⁻⁰⁶ Triose- or hexose-P _i ;P _i antiporter
GDP-MANNOSE: GMP ANTIPORTER FAMILY (TC 2.A.7.13; KOG1442)							
PFB0535w gi:7494384	2	Probable multiple-TM membrane protein Hypothetical protein	311	7/8	<i>R. norvegicus</i> putative GDP-fucose: GMP antiporter (34856560; 1e ⁻¹³⁶ to KOG1442).	2e ⁻¹⁶	KOG1442 9e ⁻⁰⁸ GDP-fucose:GMP antiporter
UDP-N-ACETYL GLUCOSAMINE: UMP ANTIPORTER FAMILY (TC 2.A.7.10; KOG2234)							
PFE0260w	5	Hypothetical protein	611	9/10	<i>R. norvegicus</i> putative NDP-sugar: NMP antiporter (34859909; 8e ⁻¹⁰⁴ to KOG2234).	3e ⁻¹⁰	KOG2234 4e ⁻¹¹ UDP-N-acetyl glucosamine:UMP antiporter
UDP-GALACTOSE: UMP ANTIPORTER FAMILY (TC 2.A.7.11; KOG1581)							
PF11_0141	11	UDP-galactose transporter, putative	343	8/9	<i>R. prolixus</i> putative UDP-galactose: UMP antiporter (33518713; 8e ⁻⁴⁸ to KOG1581).	3e ⁻³³	KOG1581 3e ⁻³⁶ UDP-galactose:UMP antiporter
10 TMS DRUG/METABOLITE EXPORTER FAMILY (TC 2.A.7.3; COG0697, PFAM00892, KOG3912)							
PF07_0064	7	Hypothetical protein	434	9/10	<i>B. anthracis</i> putative transporter (30260969; 3e ⁻⁰⁸ to Pfam00892).	2e ⁻¹³	COG0697 1e ⁻⁰⁸ Drug/metabolite exporter
MAL7P1.27	7	Chloroquine resistance transporter, putative	424	10	<i>C. parvum</i> putative transporter (32399066; Pfam00892 0.049 (p)).	1e ⁻²⁵	KOG3912 4e ⁻⁰⁴ Chloroquine resistance transporter (PfCRT; [17, 19])
AMINO ACID/AUXIN PERMEASE FAMILY (TC 2.A.18; PFAM01490)							
MAL6P1.133	6	Transmembrane amino acid transporter protein, putative	606	9/11	<i>S. pombe</i> putative amino acid transporter (3367790; 1.2e ⁻⁶⁷ to Pfam01490).	6e ⁻¹³	Pfam01490 2e ⁻¹⁶ Amino acid transporter
PFL0420w	12	Hypothetical protein	1564	10/11	<i>D. discoideum</i> hypothetical protein (28828536; 3e ⁻⁰⁴ to Pfam01490).	3e ⁻²⁸	Pfam01490 7e ⁻¹¹ Amino acid transporter
PFL1515c*	12	Hypothetical protein	1936	9/10	PFL0420w (23496616).	2.1e ⁻⁵²	Pfam01490 4e ⁻⁰⁴ Amino acid transporter
Ca²⁺: CATION ANTIPORTER FAMILY (TC 2.A.19; KOG1397)							
MAL6P1.38	6	Calcium antiporter, putative	441	11/10	<i>N. crassa</i> putative Ca ²⁺ :H ⁺ antiporter (32413763; 3e ⁻⁸⁶ to KOG1397).	2e ⁻⁷³	KOG1397 3e ⁻⁶⁵ Ca ²⁺ :H ⁺ antiporter
INORGANIC PHOSPHATE TRANSPORTER FAMILY (TC 2.A.20; PFAM01384)							
MAL13P1.206	13	Phosphate transporter, putative	687	10/11	<i>T. chui</i> high affinity phosphate transporter (28569257; 7.2e ⁻¹⁴³ to Pfam01384).	1.7e ⁻⁹⁵	Pfam01384 1.4e ⁻¹¹⁴ Na ⁺ -dependent P _i transporter [†]
NEUROTRANSMITTER:Na⁺ SYMPORTER FAMILY (TC 2.A.22; PFAM00209, KOG3660)							
PFB0435c gi:16804986	2	Predicted amine transporter Hypothetical protein	1138	14/11	<i>D. melanogaster</i> hypothetical protein (24661428; 1e ⁻¹⁶³ to KOG3660).	9e ⁻¹⁶	KOG3660 4e ⁻²⁵ Pfam00209 2e ⁻⁰⁷ Amino acid transporter
PFE0775c	5	Hypothetical protein	960	14/15	PFB0435c (7494357).	3.5e ⁻²⁰	No matches Amino acid transporter
PF11_0334 GlimmerM	11	Hypothetical protein	1439	15/14	<i>H. sapien</i> GABA transporter (4507039; 0.0 to Pfam00209).	6e ⁻⁰⁶	Pfam00209 1.3e ⁻⁰⁵ Amino acid transporter

MONOVALENT CATION:H⁺ ANTIPORTER-1 FAMILY (TC 2.A.36; Pfam00999)								
PF13_0019	13	Na ⁺ :H ⁺ exchanger, putative	1920	14	C. parvum putative Na⁺:H⁺ antiporter (32398656; 1.4e ⁻⁴⁸ to Pfam00999).	2e ⁻⁶⁴	Pfam00999 3e ⁻²⁸	Na ⁺ :H ⁺ antiporter
FORMATE-NITRITE TRANSPORTER FAMILY (TC 2.A.44; COG2116)								
PFC0725c	3	Transporter, putative	309	6/7	B. anthracis putative formate-nitrite transporter (21401706; 2e ⁻⁵⁰ to COG2116).	5e ⁻²⁵	COG2116 4e ⁻³⁵	Formate-nitrite transporter
SULPHATE PERMEASE FAMILY (TC 2.A.53; COG0659)								
PF14_0679	14	Sulphate transporter, putative	664	11	V. cholerae putative sulphate permease (9656576; 7e ⁻⁹⁰ to COG0659).	7.2e ⁻⁶⁶	COG0659 7e ⁻³⁷	Inorganic anion exchanger
METAL ION (Mn²⁺-IRON) TRANSPORTER FAMILY (TC 2.A.55; KOG1291)								
PFE1185w	5	Transporter, putative	684	11	A. thaliana NRAMP metal ion transporter 4 (15240711; 2e ⁻¹⁶⁹ to KOG1291).	9e ⁻⁵²	KOG1291 5e ⁻⁵⁹	Divalent cation (metal) :H ⁺ symporter
EQUILIBRATIVE NUCLEOSIDE TRANSPORTER FAMILY (TC 2.A.57; KOG1479)								
PFA0160c	1	Integral membrane protein	460	11	MAL8P1.32 (23612771) shares limited similarity in sequence with PFA0160c and is a structural homolog of this protein.	0.38	No matches	Nucleoside transporter
MAL8P1.32	8	Nucleoside transporter, putative	585	10/11	PF13_0252 PFENT1 (7688921).	4e ⁻¹²	No matches	Nucleoside transporter
PF13_0252	13	Nucleoside transporter 1	422	9/10	T. gondii putative adenosine transporter (6062551; 2e ⁻¹¹ to KOG1479).	3.1e ⁻¹¹	KOG1479 2e ⁻⁰⁵	Nucleoside transporter 1 (PFENT1; [62, 63])
PF14_0662	14	Hypothetical protein	437	11	The D. melanogaster hypothetical protein (24580625; 5e ⁻⁷⁸ to KOG1479) shares limited similarity in sequence with PF14_0662 and is a structural homolog of this protein.	0.037	KOG1479 3e ⁻¹¹	Nucleoside transporter
MULTI ANTIMICROBIAL EXTRUSION (MATE) FAMILY (TC 2.A.66.1; COG0534)								
PFB0580w	2	Hypothetical protein	1224	11/10	A. fumigatus putative multidrug:Na⁺ antiporter (21627817; 1e ⁻⁶⁰ to COG0534).	7e ⁻⁰⁸	COG0534 6e ⁻⁰⁷	MATE antiporter
VOLTAGE-GATED ION CHANNEL SUPERFAMILY (TC 1.A.1; KOG1420, KOG4390)								
PFL1315w	12	Hypothetical protein	1979	8/10	Nostoc sp putative ion transporter (17232125; 3e ⁻¹⁵ to KOG4390 and 4e ⁻⁰⁸ to KOG1420).	5e ⁻¹⁸	KOG1420 4e ⁻⁰⁹	K ⁺ channel
PF14_0342*	14	Hypothetical protein	1898	5/12	PFL1315w (AAN36349).	2.2e ⁻⁵⁸	No matches	Ion channel
PF14_0622	14	Hypothetical protein	1495	9/11	Nostoc sp putative ion transporter (17232125).	3e ⁻⁰⁸	KOG1420 3e ⁻⁰⁶	K ⁺ channel
ATP-BINDING CASSETTE (ABC) SUPERFAMILY (TC 3.A.1; KOG0059, COG1129)								
PFC0875w	3	Hypothetical protein	3032	12/14	D. discoideum putative ABC transporter (19110836; 1e ⁻⁶⁵ to KOG0059).	4.5e ⁻¹⁶	COG1129 6e ⁻¹⁴	ABC transporter
MHC PEPTIDE TRANSPORTER (TAP) FAMILY (TC 3.A.1.209 (DPL); KOG0058)								
PFC0125w*. [‡]	3	ABC transporter, putative	1365	6	C. tepidum putative ABC transporter (21674321; 1e ⁻¹⁰⁵ to KOG0058).	3e ⁻²²	KOG0058 4e ⁻²³	ABC transporter (TAP family)
PF11_0466*	11	Transport protein, putative	872	8	D. rerio putative TAP protein (26788076; 7e ⁻¹⁴² to KOG0058).	9e ⁻³²	KOG0058 7e ⁻³⁷	ABC transporter (TAP family)
PFL0495c [‡]	12	ABC transporter, putative	855	5/6	H. sapien putative MDR/TAP protein (9961244; 0.0 to KOG0058).	1e ⁻⁴⁵	KOG0058 8e ⁻⁶⁷	ABC transporter (TAP family)
MULTIDRUG RESISTANCE EXPORTER (MDR) FAMILY (TC 3.A.1.201 (DPL); KOG0055)								
PFE1150w	5	Multidrug resistance protein	1419	11	R. norvegicus putative multidrug/pheromone exporter Mdr1a (25453402; 0.0 to KOG0055).	e ⁻¹⁵⁴	KOG0055 0.0	Multidrug resistance protein (MDR family) (PfMDR1; [124, 125])
PF13_0218 [‡]	13	ABC transporter, putative	925	4/6	S. histriomuscorum putative ABC transporter (13346110; 2e ⁻¹⁴⁰ to KOG0055).	3e ⁻²¹	KOG0055 2e ⁻²²	ABC transporter (MDR family)
HEAVY METAL TRANSPORTER (HMT) FAMILY (TC 3.A.1.210 (DPL); KOG0056, KOG0057)								
PF13_0271*. [‡]	13	ABC transporter, putative	1049	5/6	A. thaliana putative ABC transporter (15237155; 0.0 to KOG0057).	7e ⁻⁵⁹	KOG0057 2e ⁻⁴¹	ABC transporter (HMT family)
PF14_0455	14	Multidrug resistance protein 2	1024	10/11	C. elegans ABC transporter required for heavy metal detoxification (25150042; 0.0 to KOG0056).	e ⁻¹¹²	KOG0056 4e ⁻¹⁰⁹	Multidrug resistance protein 2 (HMT family) (PfMDR2; [126])
CONJUGATE TRANSPORTER (CT) FAMILY (TC 3.A.1.208 (OAD); KOG0054)								
PFA0590w	1	ABC transporter, putative	1822	11/13	PFL1410c (23508976).	e ⁻¹⁶⁰	KOG0054 4e ⁻⁴⁵	ABC transporter (CT family) (PfMRP; [127])
PFL1410c	12	Hypothetical protein	2108	11/17	PFA0590w (23613477).	e ⁻¹⁶⁴	KOG0054 2e ⁻²²	ABC transporter (CT family)
EYE PIGMENT PRECURSOR TRANSPORTER (EPP) FAMILY (TC 3.A.1.204 (EPD); KOG0061)								
PF14_0244 [‡]	14	ABC transporter, putative	660	6	A. thaliana putative ABC transporter (18415230; 3e ⁻¹³¹ to KOG0061).	4e ⁻⁷¹	KOG0061 2e ⁻⁵⁹	ABC transporter (EPP family)
P-TYPE ATPASE (P-ATPASE) SUPERFAMILY (TC 3.A.3; KOG0202, KOG0204, KOG0206-10)								
PFA0310c	1	Calcium-transporting ATPase	1228	8/11	L. esculentum Ca²⁺-transporting P-type ATPase LCA1 (170378; 0.0 to KOG0202).	e ⁻¹⁵⁴	KOG0202 3e ⁻¹⁶⁹	SERCA-type Ca ²⁺ -transporting P-ATPase (PfATPase6; [128-130])

PFL0590c	12	P-type ATPase, putative	1208	8	<i>M. barkeri</i> putative cation-transporting P-type ATPase (23051256; 0.0 to KOG0202).	e^{-125}	KOG0202	$4e^{-152}$	Non-SERCA-type Ca^{2+} -transporting P-ATPase (PfATPase4; [130, 131])
MAL13P1.246	13	Hypothetical protein	1828	9/11	<i>T. gondii</i> Ca^{2+} -transporting P-type ATPase (8100498; $5e^{-140}$ to KOG0204).	$1e^{-11}$	KOG0204	$6e^{-06}$	Cation-transporting P-ATPase
PFI0240c	9	E1-E2_ATPase/ hydrolase putative	2563	6/10	<i>C. parvum</i> putative Cu^{2+} -transporting P-type ATPase (10122140; $2e^{-36}$ to KOG0207).	$1e^{-29}$	KOG0207	$2e^{-28}$	Cu^{2+} -transporting P-ATPase (PfCuP-ATPase; [132])
PFE0195w	5	P-type ATPase, putative	2393	12/14	<i>C. parum</i> putative Ca^{2+} -transporting P-type ATPase (7021535; $5e^{-36}$ to KOG0208).	$2e^{-40}$	KOG0208	$2e^{-41}$	Cation-transporting P-ATPase (PfATPase3; [133])
PFE0805w*	5	Cation-transporting ATPase 1	2400	10/12	<i>M. musculus</i> putative cation-transporting P-type ATPase (31982093; 0.0 to KOG0208).	$4e^{-40}$	KOG0208	$3e^{-44}$	Cation-transporting P-ATPase (PfATPase1; [134])
PF07_0115*	7	Integral membrane protein, putative	1918	12/13	<i>A. gambiae</i> hypothetical protein (31223925; 0.0 to KOG0209).	$8e^{-56}$	KOG0209	$4e^{-62}$	Cation-transporting P-ATPase
PF11_0395	11	Guanylyl cyclase	4226	19/24	<i>A. thaliana</i> putative phospholipid-transporting P-type ATPase II (15222212; 0.0 to KOG0206).	$3e^{-60}$	KOG0206	$2e^{-80}$	Protein with aminophospholipid-transporting P-ATPase and guanylyl cyclase domains
PF13_0320	13	Guanylyl cyclase	3127	21/22	PF11_0395 (23508585).	$3e^{-53}$	KOG0206	$3e^{-23}$	Protein with aminophospholipid-transporting P-ATPase and guanylyl cyclase domains
PFC0840w	3	P-type ATPase, putative	1864	10/11	<i>A. gambiae</i> hypothetical protein (31206633; $4e^{-134}$ to KOG0206).	$2e^{-61}$	KOG0206	$4e^{-62}$	Aminophospholipid-transporting P-ATPase (PfATPase7; [135])
PFL0950c	12	P-type ATPase2	1555	10/11	<i>D. discoideum</i> hypothetical protein (28850447; 0.0 to KOG0206).	e^{-100}	KOG0206	$8e^{-134}$	Aminophospholipid-transporting P-ATPase (PfATPase2; [136])
PFL1125w	12	Phospholipid-transporting ATPase, putative	1618	10	<i>M. musculus</i> putative phospholipid-transporting P-type ATPase IIB (29839753; 0.0 to KOG0202).	e^{-114}	KOG0210	$3e^{-104}$	Aminophospholipid-transporting P-ATPase
PF14_0654	14	Hypothetical protein	1837	6/8	PFL1125w (23508919).	$4.8e^{-33}$	KOG0210	$4e^{-08}$	Aminophospholipid-transporting P-ATPase
H⁺-TRANSLOCATING PYROPHOSPHATASE FAMILY (TC 3.A.10; PFAM03030)									
PFL1700c	12	V-type H ⁺ -translocating inorganic pyrophosphatase	1044	16	<i>A. thaliana</i> vacuolar-type H ⁺ -translocating inorganic pyrophosphatase (6901676; 0.0 to Pfam03030).	$1.1e^{-226}$	Pfam03030	$9.2e^{-247}$	V-type K ⁺ -independent H ⁺ -translocating inorganic pyrophosphatase (PfVPP2; [23])
PF14_0541	14	V-type H ⁺ -translocating pyrophosphatase, putative	717	16/15	<i>T. gondii</i> H ⁺ -translocating inorganic pyrophosphatase 1 (6901676; 0.0 to Pfam03030).	0.0	Pfam03030	0.0	V-type K ⁺ -dependent H ⁺ -translocating inorganic pyrophosphatase (PfVPP1; [23])

^a Italics indicate where an alternate gene model was used in place of the Gardner et al. (2002) [3] version. Gene products were assigned to a known transport family according to the official transporter classification system [10]. The Transport Commission (TC) number and examples of conserved domains of the family are shown in parentheses. Abbreviations are as follows: COG, clusters of orthologous groups of proteins from prokaryotes and unicellular eukaryotes [137]; KOG, clusters of orthologous groups of proteins from eukaryotes [138]; Pfam, protein families and domains [139]; DPL, drugs, peptides, lipids; OAD, organic anion conjugates, anions, drugs; EPD, eye pigment precursors and drugs.

^b Chromosome on which the gene is located.

^c For some chromosome 2 proteins the annotation given by Gardner et al. (2002) [3] differed from that of Gardner et al. (1998) [140], in which case the 2002 annotation is listed first and the 1998 second.

^d Amino acid residues.

^e Number of transmembrane domains predicted to be present in the protein. Each protein was analysed by the TMHMM2 and TMPRED programs and where the outputs from the two programs were dissimilar, the predicted number of transmembrane domains were tabulated as TMHMM2/Tmpred.

^f The (non-*P. yoelii*) protein that was retrieved with the highest sequence similarity to the *P. falciparum* protein in a BLASTP search of the NCBI non-redundant protein database. The NCBI (gi) accession number and the best match to a conserved domain for the retrieved protein are given in parentheses. Abbreviations are as follows: MFS, major facilitator superfamily; NRAMP, 'natural resistance-associated' macrophage protein.

^g The 'E' value is the expectation that the sequence similarity shared by the *P. falciparum* protein and the protein identified in the Table as its 'Closest BLAST homologue' arose by chance. An 'E' value $< 10^{-04}$ is considered to indicate a significant sequence similarity between the two proteins, consistent with their having a related biological function.

^h E value for the best conserved domain match to the *P. falciparum* protein. (p) indicates that the match is only putative as the E value is $= 10^{-03}$.

ⁱ Functions have been assigned (tentatively) on the basis of the specificity and transport mechanism (proven or postulated) of related proteins as well as similarities to conserved domains.

* These proteins are predicted to contain an apicoplast targeting signal ([14]; GO cellular component 'apicoplast (GO:0020011)'; PlasmoDB). None of the proteins presented in Tables 1-3 are predicted to be targeted to the mitochondria.

[§] These families are related to the MFS.

[†] R. Martin, K. Saliba, A. Bröer, C. McCarthy, M. Downie, R. Henry, R. Allen, S. Bröer and K. Kirk, manuscript in preparation.

[‡] These putative ABC transport proteins were not retrieved by the hydrophathy-based approach, but have been included to complete the overview of ABC transport proteins in *P. falciparum*.