

Ortholog Group	OG5_165036	OG5_131021	OG5_133717	OG5_129101	OG5_137339	OG5_156754	OG5_194975	OG5_195812	OG5_150032	OG5_195806	OG5_eten ETH_00036600	No orthologs				
Ave % Identity	41.8	37.7	34.1	34.1	36.7	40	59.7	71.3	32.8	64.7	N/A	N/A				
	GeneID	Notes	GeneID	Notes	GeneID	Notes	GeneID	Notes	GeneID	Notes	GeneID	Notes	GeneID	Notes	GeneID	Notes
Toxoplasma																
<i>T. gondii</i> GT-1	TgPL1: TgGT1_232600 SP	TgPL2: TgGT1_231370 TM	TgPL3: TgGT1_305140	TgGT1_212130 DUF3336, 2 TM	TgGT1_254420	TgGT1_273730										
<i>T. gondii</i> ME49	TgPL1: TgME49_232600 SP	TgPL2: TgME49_231370 TM	TgPL3: TgME49_305140	TgME49_212130 DUF3336, 2 TM	TgME49_254420	TgME49_273730										
<i>T. gondii</i> VEG	TgPL1: TgVEG_232600 SP	TgPL2: TgVEG_231370 TM	TgPL3: TgVEG_305140	TgVEG_212130 DUF3336, 2 TM	TgVEG_254420	TgVEG_273730										
Plasmodium																
<i>P. falciparum</i> 3D7		PF3D7_1358000 SP TM	PF3D7_0218600	DUF3336, 2 TM	PF3D7_0924000 DUF3336, 2 TM	PF3D7_0209100										
<i>P. berghei</i> ANKA		PBANKA_1134300 SP TM	PBANKA_0315300 2 TM	PBANKA_0824900 DUF3336, TM	PBANKA_0306200											
<i>P. knowlesi</i> H		PKNH_1113500 TM	PKNH_0402300 2 TM	PKNH_0722000 DUF3336, TM	PKNH_0412000											
<i>P. vivax</i> P01		PVP01_1113900 TM	PVP01_0406400	DUF3336, TM	PVP01_0415700											
<i>P. yoelii</i> yoelii 17X		PY17X_1135800 SP TM	PY17X_0315800 2 TM	PY17X_0828200 DUF3336, TM	PY17X_0306800											
Cryptosporidium																
<i>C. parvum</i> Iowa II	Cgd8_3870 SP, TM			cgd7_2630	cgd2_4050 SP, DUF3336, 3 TM		Cgd1_3610 SP, TM	cgd8_4130 SP, TM	Cpd7_3390 SP	cgd8_3880 SP						
<i>C. muris</i> RN66	CMU_005760 SP			CMU_034720	CMU_002900 SP, DUF3336, 3 TM		CMU_019990 SP	CMU_005500 SP	CMU_015650, CMU_023390 SP	CMU_005750 SP					CMU_015640 TM, no orthologs	
<i>C. hominis</i> UdeA01	CHUDEA8_3870 SP			CHUDEA7_2630	CHUDEA2_4050 SP, DUF3336, 3 TM		CHUDEA1_3610 SP, TM	CHUDEA8_4130 SP, TM	CHUDEA7_3390	CHUDEA8_3880 SP						
Hammondia																
<i>H. hammondi</i> H.H.34	HHA_232600	HHA_231370 TM	HHA_305140	HHA_212130 DUF3336, 2 TM	HHA_254420	HHA_273730										
Eimeria																
<i>E. acervulina</i> Houghton	EAH_00017960 SP	EAH_00014460		EAH_00063930												EAH_00023330 no orthologs
<i>E. tenella</i> Houghton		ETH_000158335		ETH_00043390	ETH_00013220 SP	ETH_00022375	ETH_00021090 TM									EAH_00028580 SP, no orthologs
<i>E. necatrix</i> Houghton		ENH_00076700		ENH_00047220 SP		ENH_00071370	ENH_00082450									ENH_00036600
<i>E. maxima</i> Weybridge		EMWEY_00030960		EMWEY_00044720	EMWEY_00032800	EMWEY_00041260	EMWEY_00048650 TM									ENH_00054670 SP, TM
Neospora																
<i>N. caninum</i> Liverpool	NCLIV_032560	NCLIV_031630 SP		NCLIV_049240 DUF3336, 2 TM	NCLIV_008710	NCLIV_033980										
Sarcocystis																
<i>S. neurona</i> SO SH1		SRCN_2315 SP, 2 TM		SRCN_5319 2 TM												
<i>S. neurona</i> SN3		SN3_01100885		SN3_01100200 DUF3336, 2 TM		SN3_00101735 SP										SN3_00301105 no orthologs
Cyclospora																
<i>C. cayetanensis</i> CHN_HEN01	cyc_03366 SP	cyc_07282 SP	cyc_05125	cyc_02282 DUF3336	cyc_08887	cyc_07751										

Table. S1. Classification of Apicomplexan PLPs by ortholog group in *Toxoplasma*, *Plasmodium*, *Cryptosporidium*, *Hammondia*, *Eimeria*, *Neospora*, *Sarcocystis*, and *Cyclospora* represented by commonly studied species in each genus. The GeneID and name, if one has been assigned, is given along with any other annotated protein features for each PLP such as signal peptides (SP) or transmembrane domains (TM) under notes. The last column contains PLPs that did not fall into any ortholog groups. *The *C. muris* genome contains two PLPs in the same ortholog group, but CMU_015650 does not contain a SP and CMU_023390 does.