Figure S9

A)


TgCDC50.3_Toxoplasma_gondii_ 0.3275
CDC50A_PF3D7_0719500_ 0.34738
CDC50B_PF3D7_1133300_ 0.37108
TgCDC50.1_Toxoplasma_gondii_ 0.25957
TgCDC50.2_Toxoplasma_gondii_ 0.25822
TgCDC50.4_Toxoplasma_gondii_ 0.38257
CDC50C_PF3D7_1029400_ 0.38867

B)

Alignment of *P. falciparum* CDC50s alongside Cdc50p and LEM3 from *S. cerevisiae and* cdc50a from *H. sapiens* showing the region surrounding the conserved Asn 180 (HsCdc50a) glycosylation site

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ScCdc50p     LTNFYQNHRRYVQSFDTKQILGEPIKKDDLDTSCSPIRSRED-KIIYPCGLIANSMFNDTFSQVLSGIDDTED-YNLTNKHISWSIDR-HRFKTTKYN  237
ScLem3       LEKFAANHRRYVLSFSEDQIRGEDAS5DATGINCKPLSKNADGKIYYPCGLIANSMFNDTFPLQLTNVGDTSNNYSLTNKGINWESDK-KRYKKTKYN  279
HsCDC50a     LSNFYQNHRRYVKSRDDSQLNGDSSALLNPSKECEPYRRNED-KPIAPCGAIANSMFNDTLELFLIGNDSYPIPIALKKKGIAWWTDKNVKFRNPPGG  220
PfCDC50A     I5NFYQNHKKYLVSKSHNQLMGTVYTKDNEVSQCGPITKNHEGKILHPCGLIARSIFNDTFSVYMDRELHNMIKLDESKEGITWYSDYNKFKNPSDSE  332
PfCDC50B     V5GMQQNHYKFVSGMKKEQLNGNIFLKKEELEECYPLITFSE5KLLHPCGIFPWNVFTDSYIFYDKEPDEVPFPTPLPLK5ITIKYYRQFYKNPSPQN  229
PfCDC50C     VSNFYINFKTFLSDESHSLVNEKIPKKKKKNQKCHISDLKPE3KKIFPCGLVSAAIFNDKIALSKNSVNYDIDKFPILH3FLTYMKKHKQFTNYKIWI  335
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C)

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ATP8A1   EEVRTIFINQP---QLTKFCNNHVSTAKYNIITFLPRFLYSQFRRAANSFFLFIALL-QQIPDVSPTGRYTTLVPLLFILAVAAIKEIIEDIKRHKADNAVNKKQTQVLRN--GAWE   144
Drs2p    GEPRVIHINDSLANSSFGYSDNHISTTKYNFATFLPKFLFQEFSKYANLFFLCTSAI-QQVPHVSPTNRYTTIGTLLVVLIVSAMKECIEDIKRANSDKELNNSTAEIFSEAHDDFV   295
PfATP2   KNEDDKDVKININGENKRTCNNSVITSKYTVFNFIFLNMYEQFHKISNVYFFFIGIL-QVIPQFTNG-IPTVFFPLLIVLTANAIKDAFEDWNRHKTDKIENNRMCYGIVSEEEKKI   131
PfATP7   AENRIKEEDLNIDIIYGKKHKNEIRTAKYKLYSFLPLIVFFQFLRLGNLYFLSISML-QLIPEITDS2MPTYLIPLVFIIVVAMIKEFFEDWQRHKSDNEENSKKTMVFVQGELKEK   156
TgATP2A  LPEEREWRVTLNGPQLLPACGNRVVTSKYTLWNFPFKNFWEQLHRISNMYFFFIGFL-QCIPQISGT2LPTIGMPLSVVLICNGVKDAVEDYRRHQADDVENGQICQLVGRGPPPAS   132
TgATP2B  SPPLEDWVVRVGGTQEMKTASNAVVTSKYTVWNFVVKNLWEQFHKVSNVYFVVICCL-QMIPQISTT2VPTLALPLSIVLVVNAAKDAFEDWQRHRSDRIENGQVTHCIAMAPDRAA   124
ATP8B1   EQPH-FMNTKFLCIKESKYANNAIKTYKYNAFTFIPMNLFEQFKRAANLYFLALLIL-QAVPQISTLAWYTTLVPLLVVLGVTAIKDLVDDVARHKMDKEINNRTCEVIKD--GRFK   187
Dnf1     QELRTVYYNMPL5NPIMQYPRNKIRTTKYTPLTFLPKNILFQFHNFANVYFLVLIIL-GAFQIFGVTNPGLSAVPLVVIVIITAIKDAIEDSRRTVLDLEVNNTKTHIL109DCKFA   394
PfGCα    WDFRKIQINPTETDELISFPSNKICSKNYGKYSFIFKGLYEQFLRLPNIWFLLISLL6QNLKHSNYMYYSSSFFLLLFFICVSIIKNIYEDSRRSNIDYQINNRLCHMLDGPNSQLK   184
TgGC     WSLRKITINPTDKDDLRRFPSNAIYTHRYSAMTFIFKNLWEQFHRVINWWFLVMAII-QAIPQLHYNPNHAWSTALPFAIVLVF3KDAFTDLGRRERDRVLNQRVCCIVDGHTPQLR   223

ATP8A1   IVHWEKVAVGEIVKVTNGEHLPADLISLSSSEPQAMCYIETSNLDGETNLKIRQGLPATSDIK-DVDSLMRISGRIECESPNRHLYDFVGNIRLDGH-GTVPLGADQILLRGAQLRN   259
Drs2p    EKRWIDIRVGDIIRVKSEEPIPADTIILSSSEPEGLCYIETANLDGETNLKIKQSRVETAKFI-DVKTLKNMNGKVVSEQPNSSLYTYEGTMTLNDR--QIPLSPDQMILRGATLRN   409
PfATP2   KKRWKDIKAGDIILCRRSEFFCADILLLCTSHKNGIAFVETSSLDGETNLKVKEANTFLFNILGNDRNSAIDNVK6LSDKPNKDLSTMYGTIYFE82YIRIPFDEKQFVLRGCKLKN   395
PfATP7   --KWADVKDGDVVKIFSYEYFPADLIVLNCSNKKGIVNIETKNVDGESNVKQKYCLPDISKYFSDDKTAGFCRIELISERPNDNIFDYKGYMILP236KFVQITIDNLVLRGTSLVN   504
TgATP2A  50PWESVELGDIVVCFRDDFFPADLLLLASADPNGVAFIETAGLDGEGNMKVKQLQKDLALWIGHQPHAANLSAS6AASPPAALLAAL3GTLSGSLC--CDPVNIDNMLLRGCRLRN   366
TgATP2B  56QWKDVQVGDVILCLKNDCFPADMVLLATSDTRGGAFVETASLDGETNLKLKQTHRVTFEWLGSFLPLAVCYLL6RCQVPNRDLNTYEGVLELD33QVDAALSVQQLLLRGCRLRN   331
ATP8B1   VAKWKEIQVGDVIRLKKNDFVPADILLLSSSEPNSLCYVETAELDGETNLKFKMSLEITDQYLQREDTLATFDGFIECEEPNNRLDKFTGTLFWRNT--SFPLDADKILLRGCVIRN   302
Dnf1     KNYWKGVKVGDIVRIHNNDEIPADIILLSTSDTDGACYVETKNLDGETNLKVRQSLKCTNTIR-TSKDIARTKFWIESEGPHSNLYTYQGNMKWRN5IRNEPITINNVLLRGCTLRN   514
PfGCα    AVRWMELSVGSIIRLIENEQVPADILLLSCNNSEGVVYIETSLLNGETNLNKKYCVNETRNET-SIYAISNIRGRIVCEKPNSNMESFNGSLKLDAHPRATSLSINNVIFKGSHIKN   300
TgGC     LLQWQGVRVGNILRLTDGEEVPADIVVLATSNTDGVAYVETSKLDGETNLKFKQGVKETRGES-SPLSIAGIRGRVVCEKPCAVMDAFTGSLKLDAHPRATPLDIVNFIQRGSHIRN   339

ATP8A1   TQWVHGIVVYTGHDTKLMQNSTSPPLKLSNVERITNVQILILFCILIAMSLVCSVGSAIWNRRHSG-KDWYLNLNY-GGASNF-GLNFLTFIILFNNLIPISLLVTLEVVKFTQAYF   373
Drs2p    TAWIFGLVIFTGHETKLLRNATATPIKRTAVEKIINRQIIALFTVLIVLILISSIGNVIMSTADAK-HLSYLYLEGTNKAGLF-FKDFLTFWILFSNLVPISLFVTVELIKYYQAFM   524
PfATP2   TDWIMGIVIYVGRETKIQMNSSKSIKKTSKLEILTNKMTIIIWVIQMIICLISAYYNAIIVSSSRKNRFRYLPF3KAKKPYIVGIISFFSWVVITGNFVPISLIVTMSFVKVVQAYF   514
PfATP7   TKWIYGLVINTGNRTKLMKNAS2SRQKWSRLEFVYGNHVIVLIICQVFISLIVAIAGVLWMRRKGYTL-WYLNLDQTSDSLKTFFITIGSMVLLFGSFIPVDLLLIWEVVRLLQGYL   621
TgATP2A  TDWIVGLAVYTGDNTKIQLNSGPPRSKRSRVERLSGRMIVGIAVLQAIMCTATAIASTVLWYSPSSPL3TYLHN3RSLPGFLFWLIQALTCVVLTANLIPISLILQTTFVQAIQASM   487
TgATP2B  TEWILGLVVYTGQETKIQMNSSTPPRKSSRVERLTNRLTLSIWFVQTLLCLSVSVGHTVLLFDPTAKARTYLTA2NSEGPVVFCILNFFTWMVLTCNLVPISLVLQMGMVKALQSLF   449
ATP8B1   TDFCHGLVIFAGADTKIMKNSGKTRFKRTKIDYLMNYMVYTIFVVLILLSAGLAIGHAYWEAQVGN-SSWYLYDGEDDTPSYRGFLIFWGYIIVLNTMVPISLYVSVEVIRLGQSHF   418
Dnf1     TKWAMGVVMFTGGDTKIMLNSGITPTKKSRISRELNFSVVINFVLLFILCFVSGIANGVYYDKKGRSRFSYEFGTIAGSAATNGFVSFWVAVILYQSLVPISLYISVEIIKTAQAAF   631
PfGCα    TEYIFGVILYTGNDTKIMKNISNNKHKLGYVNKELN--SYTIIGLIFTFICVFISVLFKWTEDDKFRNGSHFFLITVKDN---ICESIVKYTLLYSNIIPISILISVDLISILQSIL   412
TgGC     TEWLYGVVIYTGEDTRIQKNAAPPGFKRPHIEKDINTYLFISFFIVFLTILISVMSKWSVQERDSGDTGVTDA25GSRDLLQNPWMSILRFLAVYAPVLPLSLPLILDVVYLLQSVL   479
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                 P-domain        Phosphorylation site                  N-domain
ATP8A1   INWDLDMHYEPTDTAAMARTSNLNEELGQVKYIFSDKTGTLTCNVMQFKKCTIAGVAYGHVPEPEDYGCSPDEWQNSQFGDEK—TFSDSSLLENLQN---NHPTAPIICEFLTMMAV  486
Drs2p    IGSDLDLYYEKTDTPTVVRTSSLVEELGQIEYIFSDKTGTLTRNIMEFKSCSIAGHCYIDKI-PEDKTATVE--DGIEVGYR---KFDDLKKKLNDP---SDEDSPIINDFLTLLAT  632
PfATP2   ISCDKNMIHKV113NAVPRTSSLIEELGQIEYIFSDKTGTLTCNIMEFRKCAINGISYGKGLTEIKRNILKKKNLEIPVEPTMKFKKKTPHVNIIDNDIINH7NHVNLINFFLHLAI  747
PfATP7   INWDNDMYSEKTGRHALSKAGQLLEEMGNVTHIYSDKTGTLTQNVMQLQNIGLG2GTYGFYDFSNIKENITKSRHWGSQDPMDPVLEEYENEENVYSNVN159VQDQIYFLLLVLSL  895
TgATP2A  INSRRVGSSPD272EIVARTSDLNEELGQVSYVFSDKTGTLTENMMEFRKCCIQGIRYGDEVEGEKVRLTQSGGREGLPQEREAPHVKVGDPTLRAALSDPD2MHSHIIDFFLHLAV  874
TgATP2B  IAQDESMFFHP402GAWPRTSDLNEELGQVSYIFSDKTGTMTSNVMEFRKCCVRGLSYGQGLTEVRRQALRRLGLPVPADPLPPPDEPTTPQVQMVDSALRH8MHPYLVDFFLHLAI  972
ATP8B1   INWDLQMYYAEKDTPAKARTTTLNEQLGQIHYIFSDKTGTLTQNIMTFKKCCINGQIYGDHRDASQHNHNK--IEQVDFSWNTYADGKLAFYDHYLIEQIQSGKEPEVRQFFFLLAV  533
Dnf1     IYGDVLLYNAKLDYPCTPKSWNISDDLGQVEYIFSDKTGTLTQNVMEFKKCTINGVSYGRAYTEALAGLRKRQGIDVETEG31VTFVSKEFVRDLKGASGEVQQRCC-EHFMLALAL  776
PfGCα    IENDNHISTFE311WGLCLNSNMHGDLGNVDFIFTDKTGTLTNNNMTFNMCSIAGKTYGSK352KQNFPRPKSFRLNMNSSSVKGRCDFNDTKIYNDLNSQSWRGYYIDEFFKCMTL 1184
TgGC     IEGDIHIRGGG270WAEVHTPALNPNLGQVDFIFTDKTGTITENDMTFSMCSVAGKIYGMA396YDNIDFPTGFRETPMEGQIRRNCDFYDASIFTDLARKDLRSHRINEFIKCMAL 1256

                                         N-domain                          Adenine-binding
ATP8A1   CHTAVPEREGDKIIYQAASPDEGALVRAAKQLNFVFTGRTPDSV--IIDSLGQEERYELLNVLEFTSARKRMSVIVRTPSGKLRLYCKGADTVIYDRLAETSK-YKEITLKHLEQFA  600
Drs2p    CHTVIPEF2DGSIKYQAASPDEGALVQGGADLGYKFIIRKPNSVTVLLEETGEEKEYQLLNICEFNSTRKRMSAIFRFPDGSIKLFCKGADTVILERLDDEANQYVEATMRHLEDYA  750
PfATP2   NHAVICEK2EGVTTYSSSSPDEEALVNAAKHFDITFLYRREGKY--GISIFGKIYEIDTLATIEFTSKRKMSSVICRIP103IMLFCKGAGSIILKKLAK-RTDVDEITIEHMETYA  962
PfATP7   CHSAMIR35QTQPQYDASSPDELALISTSLYLGCEFVNRPNLTT58MINNKG44LSFEILDVFAFDNVRKRMSLIVKNEKKEIFMLVKGADTSVLKLASKNQENIVDHVEHQLHAFA 1143
TgATP2A  NHSALAEH3TGHLCYSANSPDERAFVCAARHFGVTFRARTPFGV--ELNVLGRTVHVDILASFPFESRRRRSSVLCQIS122VVLLTKGADMVILPRLRRRA51RRKAMETALEAYA 1160
TgATP2B  NHAVVLET2FGMTRYSASSPDEGALVYGARHFGIEFLGQTPSGL--EVSVLGRKLHVRVLASVEFSSKRKRSSMLCEIRY16IVLFTKGADTVILPLLKQ--RREETQMLNTMEEYA 1101
ATP8B1   CHTVMVDRTDGQLNYQAASPDEGALVNAARNFGFAFLARTQNTI--TISELGTERTYNVLAILDFNSDRKRMSIIVRTPEGNIKLYCKGADTVIYERLHR-MNPTKQETQDALDIFA  647
Dnf1     CHSVLVEA4PKKLDLKAQSPDEAALVATARDVGFSFVGKTKKGL--IIEMQGIQKEFEILNILEFNSSRKRMSCIVKIPGL7ALLICKGADSIIYSRLSRQSG5ILEKTALHLEQYA  904
PfGCα    CHAVTP386FDAIKYQSSSLDEECLIYSSSFLGYRLVLRNKNTM--CIEIDGSFNKWTIIGVNEFTNRRGKMSIVVK-PDS4SILYVKGSDSSILSLLNLK140RYRRLEKQLRKFS 1821
TgGC     CNTVVP396VSIIKYQASSPDEECLVSAASHMGYTLVSRTNNYA--ILNINGQERRWQIIGVNEFTQKRGRMSIVVRPQEW3SILYVKGADVAMLDLLSTS231DIALVEQHLRKFS 1994

                                 N-domain                                      P-domain   TGD motif
ATP8A1   TEGLRTLCFAVAEISESDFQEWRAVYQRASTSVQNRLLKLEESYELIEKNLQLLGATAIEDKLQDQVPETIETLMKADIKIWILTGDKQETAINIGHSCKLLKKNMGMIVINEGSLD  717
Drs2p    SEGLRTLCLAMRDISEGEYEEWNSIYNEAATTLDNRAEKLDEAANLIEKNLILIGATAIEDKLQDGVPETIHTLQEAGIKIWVLTGDRQETAINIGMSCRLLSEDMNLLIINEETRD  867
PfATP2   DEGLRTLCIAQRELSEESFAEWYHLYKEASLSIKDREEKLESVAEYIENDLILQGITGIEDKLQEGVSSTIEDLRMAGIHIWMLTGDKIETAMNIGIAANLIDNYSEQFIYTEEYIE 1079
PfATP7   TSGLRTLVLGYKYLTENEFSDMYRNHINARKKSE2KEEYLQEFYEEAENNLIIIGCTGIDDKLQDDVPQVIQDLRDAGMTICVLTGDKLETAINIGHSINILNKQTYNAIFTETDPT 1261
TgATP2A  GEGLRTLCIAKRTIDEEEFARWYKEYQKEHTSRT2KEERLYQLAERLEVDLELQGVTAVEDRLQQDVAMTIVKLRQAGIHVWMLTGDKTETALNVGISTFLVARDTRLSRYLWNGRE 1278
TgATP2B  ADGLRTLCIAKREVDTDEFFTWFQAYQQAERATVGRQEQIEAVAERLEVQLELQGITGVEDKLQAGVADTIEKLRAAGIKVWMLTGDKVETAINIGFATSLLTREMTQRTYVWEELD 1218
ATP8B1   NETLRTLCLCYKEIEEKEFTEWNKKFMAASVASTNRDEALDKVYEEIEKDLILLGATAIEDKLQDGVPETISKLAKADIKIWVLTGDKKETAENIGFACELLTEDTTICYEGDINSL  764
Dnf1     TEGLRTLCIAQRELSWSEYEKWNEKYDIAAASLANREDELEVVADSIERELILLGGTAIEDRLQDGVPDCIELLAEAGIKLWVLTGDKVETAINIGFSCNLLNNEMELLVIKTTGDD 1021
PfGCα    VKGLRSMIFAFRYLSEEETIKYKRMYDDACSSIYNKEQRLEKVAEEFERDLIYLGITGVKNGLQEKVPKTIDILNQSGIRIWMLTGDNVEYSLHVSFLCKFLNKHTKIFHAALENSN 1938
TgGC     LQGLRTMALACRYLTQEETETYKRLYTDACASVYCRAERLEEVAEDMERDLEYLGITGVRDKLQEQVPETLQLMMEAGIRVWMVTGDNVEYALHICHSCRLLTSRTRIFHAALEFSG 2111
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                                                   P-domain                Phosphate-binding/ Mg2+ coordination
ATP8A1   GTRETLSRH----------CTTLGDALRKENDFALIIDGKTLKYALTFGVRQYFLDLALSCKAVICCRVSPLQKSEVVEMVKKQVKVVTLAIGDGANDVSMIQTAHVGVGISGNEGL  824
Drs2p    DTERNLLEK-------INALNEHQLSTHDMNTLALVIDGKSLGFALEPELEDYLLTVAKLCKAVICCRVSPLQKALVVKMVKRKSSSLLLAIGDGANDVSMIQAAHVGVGISGMEGM  977
PfATP2   45NFIKNFFCAKNKSGLLLNPDKYNMLINTLNYVLVVDGSVIDLLLSEKMERKFFYLADKCSSVICGRVSPYQKGAIVSSANRLLNKITLAIGDGANDRNMINTANIGIGIRGQEGV 1239
PfATP7   85NSFLESSESFCHNNNEMDKTKGKEKVHYSQFSITITGEALDVIMK-DLKIKFYTLARSASTLIACRVTPKQKSLLVKENSAFNP2TSLAIGDGANDVGMILMANVGVGIAGKEGL 1463
PfATP2A  33KWSGHPRREAEDSRAETGSEGGDQAVREPPEALIVDGEALTFLFE2ERQCAFIRLCCACRAVICCRLAPHQKGAVVSLVKKTTQKVTLAIGDGSNDCNMLLQAHIGVGIRGNEGN 1427
TgATP2B  10EAQEMSILAKHQGKSGRGEAKGSPGRERQAHALVVDGEALQQMLEPDMEQLFVSVCTNCVTVICSRVTPHQKGAVVSLIKRHLQKITLAIGDGANDCNMIQSADIGIGLKGEEGM 1343
ATP8B1   LHARMENQRNRGGVYAKFAPPVQESFFPPGGNRALIITGSWLNEIL37QRQKNFVDLACECSAVICCRVTPKQKAMVVDLVKRYKKAITLAIGDGANDVNMIKTAHIGVGISGQEGM  916
Dnf1     VKEFGSEPSEIVDALLSKYLKEYF16EFPKGNYAIVIDGDALKLALY2DIRRKFLLLCKNCRAVLCCRVSPSQKAAVVKLVKDSLDVMTLAIGDGSNDVAMIQSADVGIGIAGEEGR 1153
PfGCα    AKKLKREGMALYELF-----QLEKEEKKPYENLCLLVNGRNLQTFLN2DLQTHFLNMACTCDVVIACRITAKQKAFLVQLIKNRLY3NTLAIGDGANDIAMIQEANIGVSIMTSDCI 2053
TgGC     RKAKREGVMLYELFR------KARRLKRSDEHICLVVTGPNLRTFLN2DLQTYFLNMACCSDVVVAARVTPSQKAEMVRLVKKRLT3ITMAVGDGGNDVAMLQEAHVGVAIRGKDSA 2225

             P-domain                     TM5                                     TM6
ATP8A1   QAANSSDYSIAQFKYLKNLLMIHGAWNYNRVSKCILYCFYKNIVLYIIEIWFAFVNGFSGQILFERWCIGLYNVMFTAMPPLTLGIFERSCRKENMLKYPELYKTSQNALDFNTKVF  941
Drs2p    DAARSADIAVGQFKFLKKLLLVHGSWSYQRISVAILYSFYKNTALYMTQFWYVFANAFSGQSIMESWTMSFYNLFFTVWPPFVIGVFDQFVSSRLLERYPQLYKLGQKGQFFSVYIF 1094
PfATP2   QAFNSSDYGISQFRFLKNLLLVHGRLSYRRISKLVVYMFYKNMVLIFPLFIFGSISLYSGQKIYFEFLLHLFNVLFTAIPVVIHAVLDQDISLNTAMEKPNLYKLGIHHYYFNIRTF 1356
PfATP7   QAARSSDFTISEFKYLKKLLFVHGRESLRRNSFLVYFCIFRNVSFCLCSMILIFWTGYSAIDAWNPWTKQIINIAFTSLPVIFFVALDKQLPHNILLNNPLLY61YGTHYLFVYLLF 1644
TgATP2A  QAFNCSDFGVTQFRLLLPLLLVHGRWCYRRITTVILYIIYKNFLLVLPLVYFGFLCLFSGQRFYPEVLAQTYNPVLTAMPITLYGVLEQDIDERASLKFPQLYRLGQADSFLNLRTC 1544
TgATP2B  QAFNCSDYGLVQFRFLLPLLLTHGSWNYRRISKLVLYMFYKNLVLVLPMFFFGYISLFSGQKFYFEFLYQMYNVVFTAIPITLYGVFDQDVDKKLALKYPQLYRCGQIDLYLNLRVF 1460
ATP8B1   QAVMSSDYSFAQFRYLQRLLLVHGRWSYIRMCKFLRYFFYKNFAFTLVHFWYSFFNGYSAQTAYEDWFITLYNVLYTSLPVLLMGLLDQDVSDKLSLRFPGLYIVGQRDLLFNYKRF 1033
Dnf1     QAVMCSDYAIGQFRYLARLVLVHGRWSYKRLAEMIPEFFYKNMIFALALFWYGIYNDFDGSYLYEYTYMMFYNLAFTSLPVIFLGILDQDVNDTISLVVPQLYRVGIRKEWNQRKFL 1271
PfGCα    ISAGYSDYCIKKFCYLRKLLFIYGSKHLYTISIILYWNFFKNILLILPIFFYQAYASWSCVKIYPELLYTFFSIFWVFIPIIYYMFLQHNLNYDILYNIPLFYALSRRRYNMNCFKF 2170
TgGC     AA3AYADYSFTEFRFLQRLLFVHGRLSLMRVSTVILWSFFKSLCIGLPTFLFQPQAFWSAVEVYDPLLLMIVDFFWTTLPGIIHGYSDQDLPTHLLPSVPVLYTPGRRRLYFNGFRF 2344

                  TM7                                  TM8                              TM9
ATP8A1   WVHCLNGLFHSVILFWFPLKALQYGTAFGNGKTSDYLLLGNFVYTFVVITVCLKAGLETSYWTWF-SHIAIWGSIALWVVFFGIYSSLWPAIPMAPDMSGEAAML--FSSGVFWMGL 1055
Drs2p    WGWIINGFFHSAIVFIGTILIYRYGFALNMHGELADHWSWGVTVYTTSVIIVLGKAALVTNQWTKFTLIAIPGSLLFWLIFFPIYAS--IFPHANISREYYGVVKHTYGSGVFWLTL 1209
PfATP2   ISWVMNSLFHGSVVFLIPLYFLSYYNIPTSDGIPYDIWTVGCATYFLTVLIVNFKILFET---YYLNILPISGIALSIFSFVLLVTAFSFMCVGSIHLLGT----------IVYLVQ 1460
PfATP7   AIWLATVETVIMLHFSTSQILYTHHVIAVNIVVVLMTNTWFFISHVVLWIELIATFFFWF---IISNTKFFLDIIGADELHGTFEKAHSSG--------------------NYYASL 1759
TgATP2A  ISWILLGVVHAAIIFVVGLYAFGYYIIPGPSGQPFDMWMVGTVMMAANCLVANLAILFYS---FSVSAVTWCGIAFSLFSCLVLFFAASTATVGGISTGAIFLLFKASPTICLYVLV 1658
TgATP2B  LKWMLNGVWQAIVIFVVPTFVFGCNAVPTTTGRTMDLWMVGTVMFMMNMIVVNIKVLLET---YYLTTIIWAGFYISLLACLLFVFLFSSWPGFAGSVLGCVFYLFIDAAACAVIAT 1574
ATP8B1   FVSLLHGVLTSMILFFIPLGAYLQTVGQDGE-APSDYQSFAVTIASALVITVNFQIGLDTSYWTFVNAFSIFGSIALYFGIMFDFHSAGIHVLFPSAFQFTGTASNALRQPYIWLTI 1149
Dnf1     WYM-LDGLYQSIICFFFPYLVYHKNMIVTSNGLGLDHRYFVGVYVTTIAVISCNTYVLLHQYRWDW----FSGLFIALSCLVVFAWTGIWSSAIASREFFKAAARIYGAPS-FWAVF 1382
PfGCα    LPWIFEAIFYSMIIYFFAYAALKENSHLNN-GEVITINTFGNICFIGCLLISILRLFLEGSLWSPSILITCFGCFLFVFFPSLLFICFAYLSNEYIREVFRQTFLWAPLYVLLILWF 2286
TgGC     ILWTVEGIIYSFLIFYLLQATWMDGNTFHD-GQVLGFHSYGILLLFGSLLQSNVRIILETSLWTPTFLFTTIVLCTIMFFPTVLLYSVTGWPRRYMELAGRVVFAWPMLYFLIPLWV 2460
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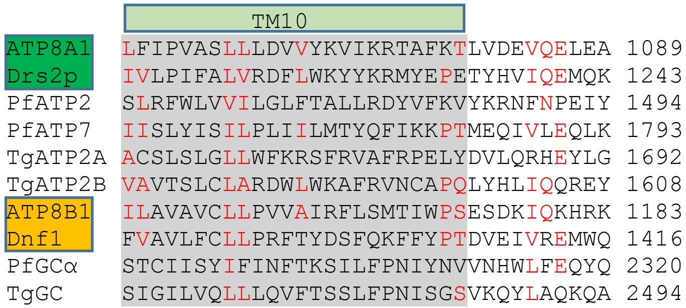

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           TM10
ATP8A1     LFIPVASLLLDVVYKVIKRTAFKTLVDEVQELEA 1089
Drs2p      IVLPIFALVRDFLWKYYKRMYEPETYHVIQEMQK 1243
PfATP2     SLRFWLVVILGLFTALLRDYVFKVYKRNFNPEIY 1494
PfATP7     IISLYISILPLIILMTYQFIKKPTMEQIVLEQLK 1793
TgATP2A    ACSLSLGLLWFKRSFRVAFRPELYDVLQRHEYLG 1692
TgATP2B    VAVTSLCLARDWLWKAFRVNCAPQLYHLIQQREY 1608
ATP8B1     ILAVAVCLLPVVAIRFLSMTIWPSESDKIQKHRK 1183
Dnf1       FVAVLFCLLPRFTYDSFQKFFYPTDVEIVREMWQ 1416
PfGCα      STCIISYIFINFTKSILFPNIYNVVNHWLFEQYQ 2320
TgGC       SIGILVQLLLQVFTSSLFPNISGSVKQYLAQKQA 2494
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