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PfAtg18      MVSLRLDNNRYISFNQDYGCLCMANEKGFKIYNTNPFQTYSRDLTDRNKNGLYLAEMLY 60
ScAtg18      MSDSSPTIN-FINFNQTGTCSISLGTSGFKIFNCEPFGKFYSEDSG-----GYAIVEMLF 54

PfAtg18      RCNILAITGNKNDKKGKWKAKNVLIWDDRQMRREIAKLTFSSNIIGVRLLEIIVVILEYK 120
ScAtg18      STSLLALVG-IGDQPALSPR-RLRIINTKKHSICEVTFPTSILSVKMNKSRLLVLLQEQ 112

PfAtg18      LCIYRLKDIILLETLNTSKNVSGLCCLSNIDKNIIIAYLSPIKGRVNIHIFEINSSENIH 180
ScAtg18      IYIYDINTMRLLHTIETNPNPRGLMAMSPSVANSYLVYPSPK-----VINSEIKAH 164

PfAtg18      EELPYIN-----FKT----- 190
ScAtg18      ATTNNITLSVGGNTETSFKRDQQDAGHSDISDLQYSSFTKRDDADPTSSNGGNSIIKN 224

PfAtg18      -----NLS-----IYAHDNSIGCINLSDGKLLVTSSTKGTIIRLFNTFDGTLLEF 237
ScAtg18      GDVIVFNLETLQPTMVEAHKGEIAAMAISFDGTLMATASDKGTIIRVFDIETGDKIYQF 284

PfAtg18      RRGTKNAKILSLNISEDNNWLCLTSSRNTVHVFSIYKKRPLRKVDIICK----- 287
ScAtg18      RRGTYATRIYSISFSEDSQYLAVTGSSKTVHIFKLG-HSMSNKLSDSDSNMEEAAADDS 343

PfAtg18      -GKNVSPPALLNYE-----KESKNKKSSLKCLLPCHPY 319
ScAtg18      SLDTTSIDALSDEENPTRLAREPYVDASRKTMGRMIRYSSQKLSRRAARTLGQIFPIKVT 403

PfAtg18      LNSEWS--FASYKLPGKK-----ISSICA-----FVND 345
ScAtg18      SLESSRHFASLKLPVETNSHVMTISSIGSPIDIDTSEYPELFETGNSASTESYHEPVMK 463

PfAtg18      QNCIIVICSNGIIYKLRFNEHIGGDMFKISSHSFD-- 380
ScAtg18      MVPIRVVSSDGYLYNFVMDPERGGDCLILSQYSILMD 500

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**Figure S4.** Alignment of the yeast Atg18 (ScAtg18) and its putative *P. falciparum* homolog (PfAtg18) was performed using the Clustal W2 program. The conserved residues are in red font, WD40 repeat domains are shaded, Atg8-family interacting motifs (AIM) are underlined. Both the proteins contain the FRRGT motif (boxed) that has been shown to be essential for binding of ScAtg18 to PtdIns3P and PtdIns(3,5)P2.