```
ScAtg4    MQRWLQLWKMDLVQKVSHGVFEGSSEEPAALMNHDYIVLGEVYPERDEESGAEQCEQDCR     60
PfAtg4    MSKEMKNFEDNQKKIEINSTIQEGKEEENKTLDEIKNVPVAINSNKINKKDNKYIKKKNS     60

ScAtg4    YRGEAVSDGFLSSLFGREISSYTKEFLLDVQSRVNFTYRTRFVPIARAPDGPSPLSLNLL
PfAtg4    KKTKNNFIHIKNKNVDDLYSYQNKSKYKILNYFNNFKYNFSIKRYFKILVNVSLLNYLPL    120

ScAtg4    VRTNPISTIEDYIANPDCFNTDI-------------------------------------     83
PfAtg4    NLRNISNKVYIFGLCLNLKNPDEmkiflilckskilftyrsnflirindnnlyrsnniml    180

PfAtg4    vdnnvsqsniftydnttynnsnitinnnnnnnsnitinnnnnnnnnssnitinnnisnlc
          innnnhtstsnttnssdnslpilcqeyehidqqdyliyiskkkkkkkklkkkkiyykqri
          inftdipehflkkiyfddkecfyinfkksskghndtytyqkqhsqeikenyslqnnkkkk
          skeeiygdtctyttsesnktiiylenskkcnsvdnkeiknkniskddmhyyreqkkkiik
          nksenntcdddlecfnnpdndrndpneemkkkkkkikinnnnnniieseatikniniiktk
          knslkilhsrskkhsvlkikkknknniiknnninikeylkyvnqnitksqiyekdkkyic    540

ScAtg4    ----GWGCMIRTGQSLLGNALQILHLGRDFRVNGNESLERESKFVNWFNDTPEAPFSLHN    199
PfAtg4    MSDNGWGCMIRVIQMVLANILIHFNISNRYVYFHNVNDYILYKNYINKLTTCTNKENKII    600

ScAtg4    FVSAGTELSDKRPG---------------------------------------------    213
PfAtg4    QIEEKTMNKDKEESiylnyknkdstkemvkheknnqcesnecnlnknasqnnkesdtlmi    660

PfAtg4    hpqsniingnnnninsnnnnnnnnnnsnnnnnsnnnnnnsssssttfsnsntylvpdsfkq
          eynkssiktdflqsdkqitlndtninesqgsdiynidnvenitnkynssdlhhcenynnf
          llnnknnnndsnseimhinnsliysilsefrdleqakysiqniiyemikykkiddnqieh    840

ScAtg4    ---EWFGPAATARSIQSLIYGFPECGIDDCI-----------------------------    241
PfAtg4    FVHDWLGPTSSAIIISNLINKKKVRFVKKNKmknnfrgtnihmdkniyiekeqkeltnyt    900

ScAtg4    --------------------------------------------------VSVSSGDIYE    251
PfAtg4    nnnkqiykllnqkeninisksddnikndkkkynkllflkekkkkkytffsVAFETGVIYN    960

ScAtg4    NEVEKVFAENPNSRILFLLGVKLGINAVNESYRESICGI—LSSTQSVGIAGGRPSSSLY    309
PfAtg4    NKVLKFFQIKQDIFIIIWICLKLGIDSLNVSKYKKSLLSCFLLKQFQGISSGNTNTSAHY   1020

ScAtg4    FFGYQGNEFLHFDPHIPQPAVEDSFVESCHTSKFGKLQLSEMDPSMLIGILIKGEKDWQQ    369
PfAtg4    FYSANDNGLFYLDPHIKCQNAFIDFNENISSQFFMHKVKFLPWEY--------------   1065

ScAtg4    WKLEVAESAIINVLAKRMDDFDVSCSMDDVESVSSNSMKKDASNNENLGVLEGDYVDIGA    429
PfAtg4    -------------LNSSLSLIFVVQSKDDYFNLIQNLKLIDSSLFEIYHEEPQYVYKNEL

ScAtg4    IFPHTTNTEDVDEYDCFQDIHCKKQKIVVMGNTHTVNANLTDYEVEGVLVEKETVGIHSP    489
PfAtg4    NYDTDDSGLVVL------------------------------------------------   1124

ScAtg4    IDEKC                                                          494
PfAtg4    -----
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Figure S6. Alignment of Atg4 proteins. The yeast (ScAtg4) and *P. falciparum* (PfAtg4) sequences were aligned using the Clustal W2 program. Shown are the conserved residues (red), and catalytic cysteine and histidine residues (highlighted). The inserts in PfAtg4 are shown in lower case.