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PfAtg3          MSDQINVKHKIGDTCRKLYSYFKTVNNTSTFIQNGTLTPSEFVDSGDFLVYKFKTWEWQE 60
ScAtg3          ---------MIRSTLSSWREYLTPITHKSTFLTTGQITPEEFVQAGDYLCHMFPTWKWNE 51

PfAtg3          ADKDR-VVPYLPENKQFLITKNVPCKQRIKDLNNIVHDLKIVDNDWLLPSYEEDNNPTDI 119
ScAtg3          ESSDISYRDFLPKNKQFLIIRKVPCDKRAEQC------VEVEGPDVIMKGFAEDGDEDDV 105

PfAtg3          YEYLPNSEYTINDKNVQNVQNIYNYEEEEEDDNCDEAIDINNFYMENNLIKEHDPASINS 179
ScAtg3          LEYIGSETEHVQSTPAGGTK--------------DSSIDDIDELIQDMEIKEED-ENDDT 150

PfAtg3          TSCYSKNMLHDNLMKIRTYDVSITYDKYYQTPRIWLFGYNENGDPLKSEEIFEDILSDYS 239
ScAtg3          EEFNAKGGLAKDMAQERYYDLYIAYSTSYRVPKMYIVGFNSNGSPLSPEQMFEDISADYR 210

PfAtg3          YKTVTYDPHPCTG--VMTASIHPCKHA-----------------------EAILNVVNNW 274
ScAtg3          TKTATIEKLPFYKNSVLSVSIHPCKHANVMKILLDKVRVVRQRRRKELQEEQELDGVGDW 270

PfAtg3          ISEEKEP----RHDLYLLFLLKFISGVIPTIEYDFTTDIEIPRDSNAGL 319
ScAtg3          EDLQDDIDDSLRVDQYLIVFLKFITSVTPSIQHDYTMEGW--------- 310
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Figure S8. Sequence alignment of Atg3 proteins. The sequences of yeast (ScAtg3) and *P. falciparum* (PfAtg3) were aligned using the Clustal W2 program. Conserved residues are shown in red, the predicted catalytic cysteine residues are highlighted, and the Atg8 family interacting motifs (AIM) are underlined.