

PfAtg7 MKKKFEEENKPSYILKHNNEFKIDISYFTQLHEHKINIKLQSNYVNLCSSTYVNKIKL 60
 ScAtg7 ----MSSSERVLSYAPAFKS---FLDTSFFQELSRRLKLDVVKLDSTCQPLTVNLDLHNIK 53

PfAtg7 GFKYKLLNRYLIEFAHPFIHVRTIEINKKSLFKYENFDNEDEKNNMEPNDCCTKIENERN 120
 ScAtg7 SADQVPL-----FLTNRSEKHNKRRTNEVP----- 79

PfAtg7 HINNINDGNKKVQKIWIYIMNRYRNNYLGVLLNFNTELEFLKCNKDDHINYTLEPLKCYIN 180
 ScAtg7 -----LQGSIFNFNVLDEFKNLDK--QLFLHQRALECWED 112

PfAtg7 NEKNDICKDMNLYIHDNIYDDTFWEYKENCLTVLEKINKYVILSFFDLKKYICYYSIANP 240
 ScAtg7 G-----IKDINKCVSFVIISFADLKKYRFYYWLGVP 143

PfAtg7 IIKPKDNYKLIKLNSTRYFFYIDSKYVYINTENRHINIIDIFYLSYKIDDYFNMYKMLFN 300
 ScAtg7 CFQRP-----S 149

PfAtg7 TNIFLLKFDNIPLHTMNNQDYDEYINKLYTNIIECEEDQKSKKEFYQINSFYKLFYELK 360
 ScAtg7 STVLHVRPEPSLKGLFSKCQKWFVNVYSKWVCILDADDEIVN----- 191

PfAtg7 LNDISQNSYHPMGNKSFNNHYNSSMLHKNYDMVILPINALSELKEDIKNSKDKILRYI 420
 ScAtg7 -----YDKCIRKTKVLAIRDSTMENVPSALTKNFLSVLQYD 229

PfAtg7 KKDFFDLYICFIDINYIFNSLSWDFRNLLYCLTLKYKLYDFQIDVLAFRDISLLRQQYVG 480
 ScAtg7 VPDLDIDFKLLIIRQ----- 243

PfAtg7 TFKSQEGFIWSYPKVMKRGSIINPRNYNDEDKNNNDNNYDDKNNNDNNYDDSHNNNYDD 540
 ScAtg7 -----

PfAtg7 KNNNDNNYDDSHNNNYEDSHNNNYDDSDLHKDIDMDKDKNNSFHYNPINCLSHQDVSFC 600
 ScAtg7 -----

PfAtg7 SVTKMCKVNYNSIKDCKNDWRDDLNEYSHDMNPIHEDIHSSSQYENMSVNNYKKN 660
 ScAtg7 -----NEGSFALNATFASIDPQSSSNPDMKVS----- 271

PfAtg7 RNIKHNHNNIYHNHLVKYILNSSLFQVTPDKVHFYIDNGSNYVDINLNGKKDDSLNKQD 720
 ScAtg7 -----

PfAtg7 IHILEKKKEGDTCIINSYLKSFSEDEKKNDCIDVSSNLGFSINIRKEDNHFTTRVKYKDEE 780
 ScAtg7 -----

PfAtg7 MDVLHISEGDEENENMNNATNNINNNIKNYKTFCCDNKVYDILCGWKYYEDKKEKKS 840
 ScAtg7 -----GWERNVQGLAPR- 284

PfAtg7 IISIIINLNDNFINKDTIQRISLELNLIKWKILKDLKFEHIKKLKLILIGLGTLCMVAR 900
 ScAtg7 ---VVDLSSLDPKIAADQSVDLNLKLMKWRILPDLNLDIIKNTKVLLLGAGTLGCYVSR 341

PfAtg7 NCVSWGIIQHYTFVDNSRVFSNISRQYLYTLEDAEKYGNIGEYKCVAAKKNLLKICPDLN 960
 ScAtg7 ALIAGWRKIITFVDNGTVSYSNPVRQALYNFEDCGKP-----KAELAASLKRIFPLMD 395

PfAtg7 ITAKVMDIPMPGHLNLYNENLEDTINELDNLINNHDVVFLLTDSKESRYFPCLMIAEKQY 1020
 ScAtg7 ATGVKLSIPMIGHKLVNEEAQHKDFDRRALIKEHDIIIFLLVDSRESRWLPSLLSNIENK 455

PfAtg7 NSLQELQESVNHNNNNNNNNSSSSSSGSKFRKGDVNLCEENMITHEYIENIKCTKIM 1080
 ScAtg7 T----- 456

PfAtg7 DKSLNNILLYEQNNIYKSLNNIHMVDRYQEIFYNNILTSVKRLCKMPPLGITVAISFDS 1140
 ScAtg7 -----VINALGFDS 466

PfAtg7 FVVLRHYSYLYFKG---ACYFCNDMHCPSDLSYRTLDEKCTVTRCGISNISSSIATELL 1196
 ScAtg7 YLVMRHGNRDEQSSKQLGCYFCHDVVAPTDSLTDRTLDQMCTVTRPGVAMMASSLAVELM 526

PfAtg7 LALQHPHYFFAPHIDRDQYIYNYDNMNMQKNSDISNIFTSCLGATPHIMNFNLANFTI 1256
 ScAtg7 TSLLQT-----KYSGSETTVLGDIPHQIRGFLHNFSI 558

PfAtg7 KKIFCEPFKCMCCSERVILKYQEDKMDFIRNVIRDSSILERITNMDQLKVEEN---DV 1312
 ScAtg7 LKLETPAYEHCPACSPKVI EAF TDLGWEFVKKALEHPLYLEEISGLSVIKQEVERLGNDV 618

PfAtg7 IILE----- 1316
 ScAtg7 FEWEDESDEIA 630

Figure S7. Alignment of Atg7 proteins. The sequences of yeast (ScAtg7) and *P. falciparum* (PfAtg7) were aligned using the Clustal W2 program. Conserved residues are shown in red, the ATP-binding pockets are underlined, and the catalytic cysteine residues are highlighted with black background.