

```

PfAtg8      MPS---LKDEVSFENRVAETHKIRSKYPNRIPVVCERAN-RSNLP IIEKKKFLVPMNMLV 56
ScAtg8      MKST--FKSEYPF EK RKAESER IADR FKNRIPV ICEKAE-KSDIPEIDKRKYLVPADLTV 57
HLC3B       MPSEKTFKQRRTFEQRVEDVRLIREQHPTKIPV I IERYKGEKQLPVLDTKTKFLVPDHVNM 60

PfAtg8      GEFKFIHQHINQSAYGSNMKLFRETIYLFVN-NIVPKTGLLMQDL YEMYKDE DGYLYM 115
ScAtg8      GQFVYVIRKRIMLPP-----EKAIFIFVN-DTLPPTAALMSAIYQEHKDKDGF LYV 107
HLC3B       SELIKIIRRLQLNAN-----QAFFLLVNGHSMVSVSTPISEVYESEKDE DGF LYM 111

PfAtg8      EYSCESCLG----- 124
ScAtg8      TYSGENTFGR----- 117
HLC3B       VYASQETFGMKLSV 125

```

Figure S5. Alignment of Atg8 proteins. The *P. falciparum* (PfAtg8), yeast (ScAtg8), and human light chain 3B (HLC3B) proteins were aligned using the Clustal W2 program. Conserved residues are shown in red. ScAtg8 and LC3B are cleaved immediately after the C-terminus Gly residue (highlighted) by Atg4, and the exposed Gly residue is conjugated to PE. This Gly residue is positionally conserved in PfAtg8, and is also the last C-terminus residue, thereby bypassing the processing step.