

Supplemental Figure S4

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ScAtg9 1 MERDEYQLPNSHGKMFFLSRHQGLQDEVNPSLNSQEMSNFPLPDIERGSSLLHSTNSREEDVDENLRVQSSQDTTE
PpAtg9 1 -----MRENNTFLSRQGLQ-----NIVENPLFADSVLYQNOQAY

ScAtg9 81 EEDEVDEEQVAVAPQISQGLQGDHQLNSVTSKENVLETEKSNLERLVEGSTDDSVPKVQGLSEEEDNFEINNDGFDD
PpAtg9 44 YDN-----ASDYSSEE-----S--KPR--TS-RQTSNLHHTDHSG

ScAtg9 161 DTLFQSKKIHRSSKKNTIEDGKRLPFRHILQNNRPQRDTQKLFTSNAENHQFKSANNGPRNINGNKKHGTVYG
PpAtg9 80 NDPFNMNDNSSRNSSSFHYNN-----TD-----QEDDNPLLELQDSSLNRKLDNSDFQSFAKKTEN

ScAtg9 241 SATQPRTGSPLNNTNRFFKLPLLRKNELSNISVNNEPDSNTSVERALQQKANVENLDHFLDYSYLQNGFY
PpAtg9 142 QIPKIQLPKKEDYP-TSHRQ-----DENNQNGTKSVKKQHFDPMKALMMSNVNLDFLHQWYVYTQNGFN

ScAtg9 321 QIEERLNICHLVVVYSYNGQVDYGLPTS-----NRVDIIDKCYSI-TPTFWFWF
PpAtg9 218 CMMNKFTSLFVVHVMLFFMGCQDYLMDNRV-----YQFQVKIDKCYSIG-FFPQLITWFF

ScAtg9 384 FVLRIVLYPVQRSQNEFYDISDELOQWQNVQQLRYDQ-NATANVVEKAQEDAHDANRI
PpAtg9 284 KQLCKIVQLFLVKDMLQFMLLSDDELOQESQLVYQWLEDKNINSVQNTHTSERKMARDANRI

ScAtg9 462 MRRNYIALYNDIANGSLPIPF-RTNVDTNTEWNNHCVMGFVN-SQFIKOSIRS--QSFTRESTQRFML
PpAtg9 364 RRRNYIALYNKSIDINDLQKVQLFNTQNNNALEDYFQSQNIPALSR-NRHTSTSIKREIE

ScAtg9 538 APFNILAPLWTFVLYFFYNENKTQPSIGAROVPIAWFFRENSIVIFKKRISESTILANKYDQFPKK
PpAtg9 442 CHINIVLAPLSIVFNYLKFYDEKTNPADSRRYSPTARKLREFNLPHIFNRLNSTSNKYNOPPKKT

ScAtg9 618 TNDLFKFYGTCSFVAHALVYDENFLNFELSDRSVFYHLGAINGCNHIQEYNVFDPETKSVEYCH
PpAtg9 522 TALLKFIMFISOSIVQVYLVIVLDPEFLNFELPGSVLFYVSLGAIFICRNSIPDTVFDPESRITSQFTH

ScAtg9 698 YLFKSWEQNHRESRLSFOKLNRSVELRELSLMEDFVLQSSAQHIVDFFRENSVDGLGYVCQAMENN
PpAtg9 602 YLFKSWEQNHRESRLSFOKLNRSVELRELSLMEDFVLQSSAQHIVDFFRENSVDGLGYVCQAMENN

ScAtg9 778 KNIDGQTHSMDESLEKKIANGSHLNSRRS-----KPTADHSDKDLNNKMLQSVVFMDDVE
PpAtg9 682 NNOHNQNGNANVHQNGNGNGVPSAKKSKVPNPN-----RPTKPSMRDENDDKMKSVHFRESG

ScAtg9 841 NGNHTGKYCPARKKQPNNEODFLNNKYSWRKQFQGQKPEFRICKHAQFQNISPAIVQN-PKNDNNNNQD
PpAtg9 747 NDLVHQQANRSIISTEIPTSD-----DNDNSNILG-RQQNVATTRRNSIQNGLIYNG-QNRLSIGEAK

ScAtg9 920 DEKMTNNAKKNDNGNDHEVTSFLDSQFPNHVIDHNCLSNYNG-----
PpAtg9 819 NVGSNPASCTRKLGYFEANGFHNGPLHENQFADKNERSTSD-----

ScAtg9 974 -----NGINKOVLCVKEYKKSDVR-----
PpAtg9 869 -----SDVNKVDKISQHKA-----

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Fig. S4. Amino acid alignment of Atg9 proteins. The amino acid sequences of Atg9 from *S. cerevisiae* and *P. pastoris* were aligned using the ClustalW program (<http://www.ch.embnet.org/software/ClustalW.html>). Amino acid identities and similarities are highlighted in black and gray, respectively. PpAtg9 is 31.8% identical to ScAtg9. The 8 putative transmembrane domains (underlined) were identified with the Tmpred program (http://www.ch.embnet.org/software/TMPRED_form.html).