about the Cytoplasm-to-vacuole targetingpathway Cytoplasm-to-vacuole targetingis a constitutive and specific form of autophagy that uses autophagosomal-like vesicles for selective transport of hydrolases aminopeptidase Iand alpha-mannosidaseto the vacuole. Unlike autophagy, which is primarily a catabolic process, Cvt is a biosynthetic process. Like autophagosomes, Cvt vesicles form at a structure known as the phagophore assembly site. The PAS structure generates an isolation membrane, which expands and eventually fuses along the edges to complete vesicle formation. At the vacuole, the outer membrane of the Cvt vesicle fuses with the vacuolar membrane, the vesicle is degraded, and the cargos are released and processed into their mature forms by vacuolar peptidases. The Cvt pathway has not been observed outside of yeast, and enzymes specifically involved in this pathway are not well conserved in other organisms.about ATG11 ATG11 encodes a phosphoprotein that is the adapter protein required for cargo loading in pexophagy and the cytoplasm-to-vacuole targetingpathway. Atg11p directs receptor-bound cargoto the PAS through direct interactions with the receptor protein Atg19p. Atg11p dissociates from the Cvt complex and is recycled at some unknown point before vesicle completion. Atg11p is also required for the recruitment of other proteins to the PAS during Cvt vesicle formation and for Atg9p anterograde transport from the mitochondria to the PAS. Atg11p also self-associates, in a manner negatively regulated by the Atg1p kinase, but the function of these homo-dimers/homo-oligomers are yet unknown. atg11 mutant strains are defective in Cvt vesicle formation and sporulation, and have shortened telomeres. ATG11 homologs have been identified in all yeast species and most filamentous fungi studied to date, but no ATG11 ortholog has yet been identified in higher eukaryotes.about autophagy nomenclature The initial identification of factors involved in autophagy was carried out by several independent labs, which led to a proliferation of nomenclature for the genes and gene products involved. The differing gene name acronyms from these groups included APG, AUT, CVT, GSA, PAG, PAZ, and PDD. A concerted effort was made in 2003 by the scientists working in the field to unify the nomenclature for these genes, and \"AuTophaGy-related\" genes are now denoted by the letters ATG. In addition to the ATG gene names that have been assigned to S. cerevisiae proteins and their orthologs, several ATG gene names, including ATG25, ATG28, and ATG30, have been used to designate proteins in other ascomycete yeast species for which there is no identifiable equivalent in S. cerevisiae.