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 ATG23 Atg23p function is essential for the Cvt pathway, but not for the related process of autophagy. An atg23 null mutant is defective for maturation of proaminopeptidase I, indicating a defect in Cvt pathway function, but can perform autophagy, albeit with reduced efficiency relative to wild-type cells. Atg23p is a peripheral membrane protein that localizes to the phagophore assembly siteas well as to non-PAS cytoplasmic sites, in both nutrient-rich and starvation conditions. Atg23p cycles between these locations and does not remain associated with the completed Cvt vesicle; rather, it is retrieved for reuse. Anterograde movement of Atg23p to the PAS requires Atg27p and Atg9p, and retrograde movement from the PAS requires the Atg1p-Atg13p complex. Atg23p is also required for similar cycling of Atg9p and Atg27p between these locations; moreover, the three proteins form a complex in which Atg23p and Atg27p both interact directly with Atg9p but not with each other. Atg23p is not widely conserved and appears to be found only in species closely related to S. cerevisiae.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.