VMA16 encodes the c'' subunit of the yeast V-ATPase V0 domain. Vacuolar-ATPasesare ATP-dependent proton pumps that acidify intracellular vacuolar compartments. Vacuolar acidification is important for many cellular processes, including endocytosis, targeting of newly synthesized lysosomal enzymes, and other molecular targeting processes. The V-ATPase consists of two separable domains. The V1 domain has eight known subunits, is peripherally associated with the vacuolar membrane, and catalyzes ATP hydrolysis. The V0 domain is an integral membrane structure of five subunits, and transports protons across the membrane. The structure, function, and assembly of V-ATPases are reviewed in references 4, 6, 7 and 5. The V0 c, c', and c'' subunits are highly hydrophobic integral membrane proteolipids, and have similar amino acid sequences; all three are required for V-ATPase activity. The ppa1 null mutant is inviable in some strain backgrounds; in other strains it is viable but lacks vacuolar-ATPase activity, and is defective in vacuolar acidification. The remaining V-ATPase subunits do not assemble onto the vacuolar membrane in the absence of Vma16p. Point mutations have identified amino acid residues in Vma16p that are likely to be involved in proton transport. V-ATPases have been identified in numerous eukaryotes; c'' homologs have been identified in Arabidopsis, mouse and human. VMA16/YHR026W and IPP1/YBR011C have been refered to as PPA1 in the literature.