VMA1 encodes the A subunit of the yeast V-ATPase V1 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 Forgac 1999, Graham and Stevens 1999, Kane 1999and Stevens and Forgac 1997. The A subunitof the V-ATPase contains the catalytic nucleotide binding sites. The vma1 null mutant is viable but is calcium-sensitive, lacks vacuolar-ATPase activity, and is defective in vacuolar acidification and assembly of the remaining V1 subunits. Extensive mutational analysis of Vma1p has identified amino acid residues important for ATP binding and hydrolysis. Vma1p homologs have been identified in many organisms including S. pombe; cDNAs encoding A subunit homologs have been identified in cotton and can complement the vma11 null mutant. VMA1 also encodes the site-specific endonuclease PI-SceI, which cleaves VMA1 sequences that lack the endonuclease-coding portion to initiate homing, which introduces the endonuclease-coding sequence into the DNA. The V-ATPase A subunit and PI-SceI are produced as a single primary translation product that undergoes a self-catalyzed \"protein splicing\" reaction to release the endonuclease. The protein splicing activity resides in the endonuclease segment, and has been well characterized. The substrate specificity and molecular mechanism of PI-SceI DNA cleavage have also been examined in detail; recent studies include Duan et al. 1997, Hu et al. 1999, Christ et al. 1999, and Hu et al. 2000.