ENA1 is the first member of a tandem array of genes encoding nearly, but not perfectly, identical P-Type ATPases. The reference strain, S288c, contains three genes in this cluster: ENA1, ENA2, and ENA5. Other Saccharomyces strains typically contain 4 or 5 genes.ENA1 is the most well characterized member of this cluster and is thought to encode the primary plasma membrane Na+-ATPase exporter in S. cerevisiae. Ena1p plays a critical role in the detoxification of Na+ ions and in maintaining ion homeostasis, making Ena1p a principal component of the cell's ability to survive high salt or alkaline conditions. Ena1p and Ena2p both transport Li+ ions, but with differing efficiencies, and have been shown to export K+ ions concomitantly with Na+, at some salt concentrations.Although basal levels of ENA1 expression are very low, it is rapidly induced in response to osmotic, saline, and alkaline stresses. Transcriptional regulation of ENA1 is complex and is independently mediated by multiple signaling pathwaysincluding the HOG1 pathway, the Calcineurin pathway, the TOR pathway, the RIM101 pathway, and the glucose repression pathway.Ena1p-Ena5p are closely related to Pmr1p, the Golgi membrane Ca2+-ATPase. Mutations in the human homolog of Pmr1p, ATP2C1, cause the acantholytic skin condition Hailey-Hailey disease.