

Recombinant Human ATP4A protein, His-tagged

Cat. No. ATP4A-19H **Lot. No.** (See product label)

SPECIFICATION

Product Overview	Recombinant Human ATP4A(Leu798~Gly896) fused with His tag at N-terminal was expressed in E. coli.
Species	Human
Source	E.coli
ProteinLength	798-896 a.a.
Description	The protein encoded by this gene belongs to a family of P-type cation-transporting ATPases. The gastric H⁺, K⁺-ATPase is a heterodimer consisting of a high molecular weight catalytic alpha subunit and a smaller but heavily glycosylated beta subunit. This enzyme is a proton pump that catalyzes the hydrolysis of ATP coupled with the exchange of H(+) and K(+) ions across the plasma membrane. It is also responsible for gastric acid secretion. This gene encodes a catalytic alpha subunit of the gastric H⁺, K⁺-ATPase.
Form	Supplied as lyophilized form in PBS, pH7.4, containing 5% trehalose, 0.01% sarcosyl.
Molecular Mass	12.7kDa
AA Sequence	MGHHHHHHSG SEF-LTPYLIY ITVSVPLPLG CITILFIELC TDIFPSVSLA YEKAESDIMH LRPRNPKRDR LVNEPLAAYS YFQIGAIQSF AGFTDYFTAM AQEGWFPLLC VG

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Endotoxin	<1.0EU per 1g (determined by the LAL method)
Purity	> 95%
Applications	SDS-PAGE; WB; ELISA; IP.
Storage	Avoid repeated freeze/thaw cycles. Store at 2-8 centigrade for one month. Aliquot and store at -80 centigrade for 12 months.
Reconstitution	Reconstitute in sterile PBS, pH7.2-pH7.4.

GENE INFORMATION

Gene Name	ATP4A ATPase, H+/K+ exchanging, alpha polypeptide [Homo sapiens]
Official Symbol	ATP4A
Synonyms	ATP6A
Gene ID	495
mRNA Refseq	NM_000704.2
Protein Refseq	NP_000695
MIM	137216
UniProt ID	P20648
Chromosome Location	19q13.1

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Pathway	Collecting duct acid secretion, organism-specific biosystem;Collecting duct acid secretion, conserved biosystem;Gastric acid secretion, organism-specific biosystem;Gastric acid secretion, conserved biosystem;Ion channel transport, organism-specific biosystem;Ion transport by P-type ATPases, organism-specific biosystem;Oxidative phosphorylation, organism-specific biosystem;
Function	ATP binding;hydrogen:potassium-exchanging ATPase activity;magnesium ion binding;protein heterodimerization activity;

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