

## Product datasheet for PH312179

### ATP6V0A4 (NM\_020632) Human Mass Spec Standard

#### Product data:

Product Type:	Mass Spec Standards
Description:	ATP6V0A4 MS Standard C13 and N15-labeled recombinant protein (NP_065683)
Species:	Human
Expression Host:	HEK293
Expression cDNA Clone or AA Sequence:	RC212179
Predicted MW:	96.2 kDa
Protein Sequence:	>RC212179 representing NM_020632 Red=Cloning site Green=Tags(s)

MVSVFRSEEMCLSQLFLQVEAAAYCCVAELGELGLVQFKDLNMVNSFQRKFNVEVRRCESLERILRFLED  
EMQNEIVVQLLEKSPLTPLPREMITLETVLEKLEGELQEANQNQQALKQSFLELTELKYLKKTQDFET  
ETNLADDFFTEDTSGLLELKAVPAYMTGKLGFIAGVINRERMASFERLLWRICRGNVYLKFSMDAPLED  
PVTKEEIQKNIFIIFYQGEQLRQKIKKICDGFRAIVVPCPEPAVERREMLESVNVRELDLITVITQTESH  
RQRLLEAAANWHSWLKIVQKMKAVYHILNMCNIDVTQQCVIAEIWFPVADATRIKRALEQGMELSGSSM  
APIMTTVQSKTAPPTFNRTNKF TAGFQNIVDAYGVGSYREINPAPYTIITFPFLFAVMFGDCGHGTVMLL  
AALWMILNERRLLSQKTDNEIWNTFFHGRYLILLMGIFSIYTGLIYNDCFSKSLNIFGSSWSVQPMFRNG  
TWNTHVMEESLYLQLDPAIPGVYFGNPYPFGIDPIWNLASNKL TFLNSYKMKMSVILGIVQMVFVILSL  
FNHIYFRRTLNIILQFIPEMIFILCLFGYLVFMIIFKWCCFDVHVSQHAPSILIHFINMFLFNYSOSSNA  
PLYKHQQEVQSFVVMALISVPWMLLIKPFILRASHRKSQQLQASRIQEDATENIEGSSSPSSRSRQRTS  
ADTHGALDDHGEEFNFGDVFVHQAIHTIEYCLGCSINTASYLRLWALSLAHAQLSEVLWTMVMNSGLQTR  
GWGGIVGVFIIFAVFAVLTVAILLIMEGLSAFLHALRLHWVEFQNKFYVGDGYKFSFSPFKHILDGTAE

TRTRPLEQKLI SEEDLAANDILDYKDDDDKV

Tag:	C-Myc/DDK
Purity:	> 80% as determined by SDS-PAGE and Coomassie blue staining
Concentration:	>0.05 µg/µL as determined by microplate BCA method
Labeling Method:	Labeled with [U- <sup>13</sup> C <sub>6</sub> , <sup>15</sup> N <sub>4</sub> ]-L-Arginine and [U- <sup>13</sup> C <sub>6</sub> , <sup>15</sup> N <sub>2</sub> ]-L-Lysine
Buffer:	25 mM Tris-HCl, 100 mM glycine, pH 7.3
Storage:	Store at -80°C. Avoid repeated freeze-thaw cycles.
Stability:	Stable for 3 months from receipt of products under proper storage and handling conditions.
RefSeq:	<a href="#">NP_065683</a>



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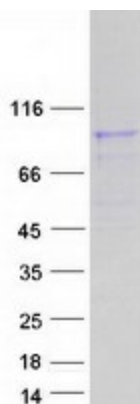
RefSeq Size:	3137
RefSeq ORF:	2520
Synonyms:	A4; ATP6N1B; ATP6N2; DRTA3; RDRTA2; RTA1C; RTADR; STV1; VPH1; VPP2
Locus ID:	50617
UniProt ID:	<a href="#">Q9HBG4</a> , <a href="#">A0A024R791</a>
Cytogenetics:	7q34

**Summary:** This gene encodes a component of vacuolar ATPase (V-ATPase), a multisubunit enzyme that mediates acidification of intracellular compartments of eukaryotic cells. V-ATPase dependent acidification is necessary for such intracellular processes as protein sorting, zymogen activation, receptor-mediated endocytosis, and synaptic vesicle proton gradient generation. V-ATPase is composed of a cytosolic V1 domain and a transmembrane V0 domain. The V1 domain consists of three A and three B subunits, two G subunits plus the C, D, E, F, and H subunits. The V1 domain contains the ATP catalytic site. The V0 domain consists of five different subunits: a, c, c', c'', and d. This gene is one of four genes in man and mouse that encode different isoforms of the a subunit. Alternatively spliced transcript variants encoding the same protein have been described. Mutations in this gene are associated with renal tubular acidosis associated with preserved hearing. [provided by RefSeq, Jul 2008]

**Protein Families:** Transmembrane

**Protein Pathways:** Epithelial cell signaling in Helicobacter pylori infection, Lysosome, Metabolic pathways, Oxidative phosphorylation, Vibrio cholerae infection

### Product images:



Coomassie blue staining of purified ATP6V0A4 protein (Cat# [TP312179]). The protein was produced from HEK293T cells transfected with ATP6V0A4 cDNA clone (Cat# [RC212179]) using MegaTran 2.0 (Cat# [TT210002]).