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Product datasheet for SC207219

ATP6V1E1 (NM_001696) Human 3' UTR Clone

Product data:

Product Type:	3' UTR Clones
Product Name:	ATP6V1E1 (NM_001696) Human 3' UTR Clone
Vector:	pMirTarget (PS100062)
Symbol:	ATP6V1E1
Synonyms:	ARCL2C; ATP6E; ATP6E2; ATP6V1E; P31; Vma4
ACCN:	NM_001696
Insert Size:	568 bp
Insert Sequence:	>SC207219 3'UTR clone of NM_001696 The sequence shown below is from the reference sequence of NM_001696. The complete sequence of this clone may contain minor differences, such as SNPs. Blue=Stop Codon Red=Cloning site GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC GCAAATGCCAACAGGAAGTTTTTGGACTAAGCCTTCAGGAGGTGGAGCTCGTCGTCAGCTCTCCTGCTG TGATGTGGAAGCTTCTGATATTTGAAGAAACACGAATGTCTCTGTAGCTTCCTCTTCACTGCCCCAGTA TTGCTCTGTATTTATCAGCGATGCCCCTCTGTCACTCATGCCTTGCCTAATTGTTCACAATGGTGGAAA GCTTCATGTAATATGATCAGGACCCACCTCCAGTTCTTCTGAAAGTGTGACAGTGTCCAGCCGGTTCTG CAGCACTAGGGGAGGGGGCAGATGGTGGTTGCATGGGCTTCCTGGGTCTCCACTCTCCGTCTGGCCTAA AGGTGATGTATTTGGTGTTTGGCCCTGCAGTCCCCACTCTTGAGGCTTAAGGCGCATGTGGCACACCAC TCCTTCCAGCAGTAGTCGCTTTACTGTTACCTGTTTAGGCCTAGAAGTTTTCCCTCATCTGTAAATGTG ATTTAAAATCTAAGCCATGAATATGCTTTATTTATTAAAAGAGTTATGCGGATTTAATGTGATTTCTAG TGTAAGGCACTACAAA ACGCGTAAGCGGCCGCGGCATCTAGATTCGAAGAAAATGACCGACCAAGCGACGCCCAACCTGCCATCA CGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGG
Restriction Sites:	SgfI-MluI
OTI Disclaimer:	Our molecular clone sequence data has been matched to the sequence identifier above as a point of reference. Note that the complete sequence of this clone is largely the same as the reference sequence but may contain minor differences , e.g., single nucleotide polymorphisms (SNPs).
Components:	The cDNA clone is shipped in a 2-D bar-coded Matrix tube as 10 ug dried plasmid DNA. The package also includes 100 pmols of both the corresponding 5' and 3' vector primers in separate vials.

View online »

RefSeq: NM_001696.4

Summary: This gene encodes a component of vacuolar ATPase (V-ATPase), a multisubunit enzyme that mediates acidification of eukaryotic intracellular organelles. V-ATPase dependent organelle 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, three B, and two G subunits, as well as a C, D, E, F, and H subunit. The V1 domain contains the ATP catalytic site. This gene encodes alternate transcriptional splice variants, encoding different V1 domain E subunit isoforms. Pseudogenes for this gene have been found in the genome. [provided by RefSeq, Jul 2008]

Locus ID: 529

MW: 21.9