

Product datasheet for **SC207218**

ATP6V1E1 (NM_001039366) Human 3' UTR Clone

Product data:

Product Type: 3' UTR Clones
Product Name: ATP6V1E1 (NM_001039366) Human 3' UTR Clone
Vector: pMirTarget (PS100062)
Symbol: ATP6V1E1
Synonyms: ARCL2C; ATP6E; ATP6E2; ATP6V1E; P31; Vma4
ACCN: NM_001039366
Insert Size: 568 bp
Insert Sequence: >SC207218 3'UTR clone of NM_001039366
The sequence shown below is from the reference sequence of NM_001039366. The complete sequence of this clone may contain minor differences, such as SNPs.
Blue=Stop Codon **Red**=Cloning site

```
GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAAGCCAAGAAGGGCGGAAAGATCGCCGTG
TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC
GCAAAATGCCAACAGGAAGTTTTGGACTAAGCCTTCAGGAGGTGGAGCTCGTCGTCAGCTCTCCTGCTG
TGATGTGGAAGCTTCTGATATTTGAAGAAACACGAATGTCTCTGTAGCTTCTTCACTGCCCCAGTA
TTGCTCTGTATTTATCAGCGATGCCCTCTGTCACTCATGCCTTGCCTAATTGTTCAACAATGGTGGAAA
GCTTCATGTAATATGATCAGGACCCACCTCCAGTTCTTCTGAAAGTGTGACAGTGTCCAGCCGGTTCTG
CAGCACTAGGGGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
AGGTGATGATTTGGTGTGGCCCTGCAGTCCCACTCTTGAGGCTTAAGGCGCATGTGGCACACCAC
TCCTTCCAGCAGTAGTCGCTTTACTGTTACCTGTTTAGGCCTAGAAGTTTTCCCTCATCTGTAATGTG
ATTTAAAATCTAAGCCATGAATATGCTTTATTTATTTAAAAGAGTTATGCGGATTTAATGTGATTTCTAG
TGTAAGGCACTACAAA
ACGCGTAAGCGGCCGCGCATCTAGATTGAAGAAAATGACCGACCAAGCGACGCCCAACCTGCCATCA
CGAGATTTGATTCCACCGCCGCTTCTATGAAAGG
```

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 µg 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_001039366.1](#)

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