

## **Product datasheet for SC204569**

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## ATP1A4 (NM\_001001734) Human 3' UTR Clone

**Product data:** 

**Product Type:** 3' UTR Clones

Product Name: ATP1A4 (NM\_001001734) Human 3' UTR Clone

**Vector:** pMirTarget (PS100062)

Symbol: ATP1A4

**Synonyms:** ATP1A1; ATP1AL2 **ACCN:** NM 001001734

**Insert Size:** 311 bp

Insert Sequence: >SC204569 3'UTR clone of NM\_001001734

The sequence shown below is from the reference sequence of NM\_001001734. The complete

sequence of this clone may contain minor differences, such as SNPs.

Blue=Stop Codon Red=Cloning site

GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG

TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC

CGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGG

Restriction Sites: Sgfl-Mlul

**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.

**RefSeg:** NM 001001734.2







**Summary:** 

The protein encoded by this gene belongs to the family of P-type cation transport ATPases, and to the subfamily of Na+/K+ -ATPases. Na+/K+ -ATPase is an integral membrane protein responsible for establishing and maintaining the electrochemical gradients of Na and K ions across the plasma membrane. These gradients are essential for osmoregulation, for sodium-coupled transport of a variety of organic and inorganic molecules, and for electrical excitability of nerve and muscle. This enzyme is composed of two subunits, a large catalytic subunit (alpha) and a smaller glycoprotein subunit (beta). The catalytic subunit of Na+/K+ - ATPase is encoded by multiple genes. This gene encodes an alpha 4 subunit. Alternatively spliced transcript variants encoding different isoforms have been identified. [provided by RefSeq, Jul 2008]

**Locus ID:** 480 **MW:** 11.6