

Product datasheet for **SC216918**

ATP1B2 (NM_001678) Human 3' UTR Clone

Product data:

Product Type:	3' UTR Clones
Product Name:	ATP1B2 (NM_001678) Human 3' UTR Clone
Vector:	pMirTarget (PS100062)
Symbol:	ATP1B2
Synonyms:	AMOG
ACCN:	NM_001678
Insert Size:	1905 bp



[View online »](#)

Insert Sequence: >SC216918 3'UTR clone of NM_001678
 The sequence shown below is from the reference sequence of NM_001678. The complete sequence of this clone may contain minor differences, such as SNPs.
 Blue=Stop Codon Red=Cloning site

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GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAAGCCAAGAAGGGCGGAAAGATCGCCGTG
TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC
GCCTTCAAACCTCCGCATCAACAAAACCTGAGGCCCTTCCCTCCCACCCCATCTCTCTCTGTGGATGCT
CCTGGAATGTCCCTGACCTGCCTGATCCCTCCCTCACCCACCCCAAAGGTATTTTTGATAACAGAGCT
ATGACTTGTCTGAGCCTCACATCCTTTTCTTGACTTCTCAACCCAGCCTGAAGTCCATTGCGGTTCCG
TCACTCGCTTTCCACCAACTTCTCCCAACCTCAGATCAGTCAGACAGGGAGCTGGGCTAAGATGGCC
ACGGAGGAGTTAGGAGCCTTTCTAGTTCTGGTTTAGCTGTGAGAGCTATCCACTCTCTGCCTGCATAT
CCCCTGAGAGTTATAGGAAGTGCCCACTGACCCACCCACCCACCTACACCCCGCCACACACACACAC
AAACGTGCACACGCGTCTCATTTGACCCTTTGCTTCCAGAGATGAATGTGGCACTCCCTCCTCCATT
CCTAAGCTCTGGCCACCGTCCCTTGATCTCTCATACTTTCTCCCTGTCTACACAGTCGCCATCTTGGTG
ACTTTGAATTTATCTGGCTCCTGGGCAGGTCTTCTCCTCTCTCCATCCCTATTCCCTCCTCTGAAATG
CACCCCTTTGTAATTGAGGACAAGGTGGTTCTGTGGCCTTTTCCCTCTTTGCTGGCACGTTCTGCTTCT
CACCTCTGGTACTCTGTGAGCTGGGAAATGAGGGACTGGAAGTGAAGCCTGTGTTGACCTTCTGGA
AAATCCTCTAGCAGCCCCGACTTCAGCAGTTTCTTTCTTTGTTTTTGGAGATGGAGTTTCGCTCTTG
TTGCCAGGCTGGAGTGAATGGTGAATCTCAGCTCACTGCAACTTCCGCATCCAGGTTCAAGCGAT
TCTCCCGCTCAGGTTCCCGAGTAGCTGGGACTACAGGCATGTGCCACCATGCCCGGCTAATTTCTTTC
TTTTTTTTTTTTTTTTTGCATTTTTTAGTAGAGATGGGGTTTTCTCCTTGTGGTCAAGCTGGTCTC
GAACTCCCGACCTCAGGTGATCCACCTGCCTCGGCTCCCAAAGTGTGGGATTACAGGCTGAGCCAC
CGCGCCCGCCTTCAGTTTCTTCTAGGCGGTTCTGTACCCCAAATAGCTGCTACCCAGAGGGCGGGG
TTGACCTAGGCTGAATATCCACTTTGTTTTATGGATGGCTCCCTTCCCCATTCCGCTTCCCAGAATA
TCCTTCAAGTTCACCTTCCCAGGGAGCTCTGGGGAGGGGCGGCCATTCTGGCTCCGTCGCCAGTGGCC
ACCTTGGAAACATCGGCTGGCTTTGGGACTATTCCACCTCCTTCCCCTGAGCCAGATCTGCCCCACC
ATCCTTCTCTGGCTTCTTTAGCAAGTATCAACTAATCACTAACTCCTTCTTCTCTGCTGATGCC
AGCCTGAAAATCCAAATCTAGCCTCTGAATGTCTTGGTCCATCTTCCAGACCCCTTTGCCTTAAA
AAAAAACAAAAACAAAAACAAAAAACCCATAATGCCACAGAAATGCAATGAGGGGCTCCTGCCT
CCTGCTCTGAATATTCTGTAGCTGTAGAGGCATTTTAAACCCTTTGCTCCTCCAGCATCCCTTCACTTCT
CATCCTCTCTAACCTCCTTTTTCTTTTTTAATGCTGCAGCCTCCACACTCCACCCACAGGTGGACCCT
TCCTTTTTCTCTAGCTGGATCTGTGTTTCTTCCCTTCGGGCCCCCATGTTTTCTGCACCCGCCCTAC
CATGGTCTCTCTGCAATTATTAATGCCTGTGTGAGATCTACTGTAAGAGAGGATTAAGTAAAAATA
AAATGAGAGCAATTATATATATAAATATATATACACAGA
AGCGGACCGACTTACGCGTAAGCGGCCCGGCATCTAGATTGGAAGAAAATGACCGACCAAGCGACGCC
CAACCTGCCATCACGAGATTTGATTCCACCGCCG
  
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Restriction Sites: Sgfl-RsrII

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.

RefSeq: [NM_001678.5](#)

Summary:

The protein encoded by this gene belongs to the family of Na⁺/K⁺ and H⁺/K⁺ ATPases beta chain proteins, 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 beta subunit regulates, through assembly of alpha/beta heterodimers, the number of sodium pumps transported to the plasma membrane. The glycoprotein subunit of Na⁺/K⁺ -ATPase is encoded by multiple genes. This gene encodes a beta 2 subunit. Two transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Dec 2014]

Locus ID:

482

MW:

68.4