

Product datasheet for **SC200251**

ATP5ME (NM_007100) Human 3' UTR Clone

Product data:

Product Type:	3' UTR Clones
Product Name:	ATP5ME (NM_007100) Human 3' UTR Clone
Vector:	pMirTarget (PS100062)
Symbol:	ATP5ME
Synonyms:	ATP5I; ATP5K
ACCN:	NM_007100
Insert Size:	94 bp
Insert Sequence:	>SC200251 3'UTR clone of NM_007100 The sequence shown below is from the reference sequence of NM_007100. The complete sequence of this clone may contain minor differences, such as SNPs. Blue=Stop Codon Red=Cloning site GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAAGCCAAGAAGGGCGGAAAGATCGCCGTG TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC TTGGCAGAAGATGACAGCATATTAAGTGAAGTGACCCCTGCGACCCACTCTTTGGACCAGCAGCGGATGA ATAAAGCTTCCTGTGTTGTGTGATA ACGCGTAAGCGGCCGCGCATCTAGATTGAAGAAAATGACCGACCAAGCGACGCCCAACCTGCCATCA CGAGATTCGATTCCACCGCCGCTTCTATGAAAGG
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.
RefSeq:	<u>NM_007100.4</u>



[View online »](#)

Summary:

Mitochondrial ATP synthase catalyzes ATP synthesis, utilizing an electrochemical gradient of protons across the inner membrane during oxidative phosphorylation. It is composed of two linked multi-subunit complexes: the soluble catalytic core, F1, and the membrane-spanning component, Fo, which comprises the proton channel. The F1 complex consists of 5 different subunits (alpha, beta, gamma, delta, and epsilon) assembled in a ratio of 3 alpha, 3 beta, and a single representative of the other 3. The Fo seems to have nine subunits (a, b, c, d, e, f, g, F6 and 8). This gene encodes the e subunit of the Fo complex. Alternative splicing results in multiple transcript variants.[provided by RefSeq, Jun 2010]

Locus ID:

521

MW:

3.4