

Product datasheet for **MC200323**

Atp6v1c2 (NM_133699) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Atp6v1c2 (NM_133699) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Atp6v1c2
Synonyms:	1110038G14Rik
Mammalian Cell Selection:	Neomycin
Vector:	PCMV6-Kan/Neo (PCMV6KN)
E. coli Selection:	Kanamycin (25 ug/mL)

Fully Sequenced ORF: >BC003810 sequence for NM_133699
 CCCACGCGTCCGATCGGAGAGCATCAGCCATGGCTCTGCGCTACCCCATGGCCGTGGGCCTCAACAAGGG
 CCACAAGGTGACGAAAAACGTCAGTAAGCCGAGACACAGCCGGCGCCTCACCAACACACC
 AAGTTTCGTGCGGGAGCCGGCCTTGCCTCCCGCGAGCCTCCCGCACGGTGTCCCGCGTGTCTTCTACA
 GCTCAGTCTTCCGTGCTCCTGTCTTGGTGCCTGTGCGGTAACAGATAACCGGAAGACTTCAAACATGT
 CTGAGTTTTGGCTTATTTTCGCCCCCTGGCGATAAGGAAAAATTTACAGGCTCTGAAAGGATGAACAATGT
 AACTTCAAAGTCTAACCTGTCCACAACACCAAGTTTGCATCCCAGACTTCAAGGTGGGGACTTTGGAT
 TCCCTTGTGGCCTCTCTGATGAGTTGGGAAACTCGATACCTTTGCTGAAAGCCTATAAAGAGAATGG
 CACAGAGTGTGGTGGAGGTATGGAAGATTCCAAGGGAAAGCACACGAGACCCTCTGGCTAACGGAGT
 TGACCTGACATCCTTCGTGACGCACTTCGAGTGGGACATGGCCAAATATCCCGCCAAGCAGCCACTGGT
 AGCGTGGTGGACACACTGGCCAAGCAACTGGCACAAATCGAGACAGACCTGAAGTCCCGGACAGCCGCT
 ACAGCGTTCTGAAGGCCAACCTGGAGAACTTGGAGAAGAGATCCACGGGGAACCTTCTACTCGGACACT
 GAGCGATATTGTGACGAAGGAACTTCGTACTTGATTCTGAATATCTCATAACCCCTCTGGTCATCGTC
 CCCAAGTCAAGCTTTGCACAGTGGCAGAAGACATATGAGTCCCTATCGGACATGGTGGTCCCTCGGTCAA
 CCAAATTGATCGCCGAGGACAACGAAGGTGGCCTCTTACGGTACTCTTCCGAAAAGTATCGAAGA
 TTTCAAAGTCAAAGCCAAAGAAAACAAGTTTATTGTCGGGAATTTTACTACGATGAAAAAGAAATAAA
 CGAGAAAGGGAGGAGATGACCAGTTGCTGTCTGATAAGAAACAACAGTATCCAACCTTCTGTGTTGCTC
 TAAAAAAGGGATCAGCCACCTACCGTGACCACAAGGTTAAGGTAGCCCCGCTAGGTAACCCTGCTAGGCC
 TGCTGCGGGGACAGCCGACAGAGACAGAGAGTGAAGGGGAGGGTGAAGGACCTGCTGCGCTGGCTC
 AAGGTGAACCTTACGCGAGGCCTTTATTGCCTGGATCCACATTAAGGCCCTGAGAGTGTGTTGGAGTCTG
 TGCTCAGGTATGGAAGTCCAGTGAACCTCCAGGCTGTGCTCCTACAGCCCCATAAAAAAGTCAAGCCCAA
 ACGCCTGAGAGAGGTGCTCAATTCTGTCTTCCGGCACCTGGATGAAGTGTGCTGCAGCAAGCATACTGGAT
 GCATCCGTGGAGATTCTGGACTGCAGCTCAGCAACCAGGACTATTTCCCTATGTGTAATCCATATCG
 ACCTCAGCCTTCTGACTAGGTGGCCAGCCTGTTTCACTGCAGCCTCAGACCTTGCCAGACAACCGAGTC
 CTGCAGGATTCTGACTCAGAAGATACTCACAGACGTTAGTTAGAGTGTATTTATTTTTTAAAGTTACAAT
 AAAGTGCTCAGTCTGAGAAAAAAAAAAAAAAAAA



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Restriction Sites:	RsrII-NotI
ACCN:	NM_133699
Insert Size:	1284 bp
OTI Disclaimer:	Our molecular clone sequence data has been matched to the reference identifier above as a point of reference. Note that the complete sequence of our molecular clones may differ from the sequence published for this corresponding reference, e.g., by representing an alternative RNA splicing form or single nucleotide polymorphism (SNP).
Components:	The ORF clone is ion-exchange column purified and shipped in a 2D barcoded Matrix tube containing 10ug of transfection-ready, dried plasmid DNA (reconstitute with 100 ul of water).
Reconstitution Method:	<ol style="list-style-type: none">1. Centrifuge at 5,000xg for 5min.2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.3. Close the tube and incubate for 10 minutes at room temperature.4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.5. Store the suspended plasmid at -20°C. The DNA is stable for at least one year from date of shipping when stored at -20°C.
RefSeq:	BC003810
RefSeq Size:	1713 bp
RefSeq ORF:	1284 bp
Locus ID:	68775
UniProt ID:	Q99L60
Cytogenetics:	12 A1.1
Gene Summary:	<p>Subunit of the peripheral V1 complex of vacuolar ATPase. Subunit C is necessary for the assembly of the catalytic sector of the enzyme and is likely to have a specific function in its catalytic activity. V-ATPase is responsible for acidifying a variety of intracellular compartments in eukaryotic cells.[UniProtKB/Swiss-Prot Function]</p> <p>Transcript Variant: This variant (2) lacks an alternate in-frame exon in the central coding region, compared to variant 1. The resulting isoform (2) lacks an internal segment, compared to isoform 1. Sequence Note: The RefSeq transcript and protein were derived from genomic sequence to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on alignments.</p>