

Product datasheet for **MC229464**

Atp2b2 (NM_009723) Mouse Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: Atp2b2 (NM_009723) Mouse Untagged Clone
Tag: Tag Free
Symbol: Atp2b2
Synonyms: D6Abb2e; dfw; Gena300; jog; PMCA2; Tmy; wms; wri
Vector: pCMV6-Entry (PS100001)
E. coli Selection: Kanamycin (25 ug/mL)
Cell Selection: Neomycin
Fully Sequenced ORF: >MC229464 representing NM_009723
Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCC**CGGATCGCC**

ATGGGTGACATGACCAACAGCGACTTTTACTCCAAAACCAAAGAAATGAGTCGAGCCATGGGGCGGAGT
TCGGGTGCACCATGGAGGAGCTGCGCTCCCTCATGGAGCTGCGGGGCACCGAGGCTGTGGTCAAGATCAA
GGAGACGTATGGGGACACTGAAGCCATCTGCCGGCGCCTCAAACCTCGCCTGTTGAAGGTTTACCAGGC
ACTGCTCCAGACTTGAAAAGAGGAAACAGATTTTGGGCAAACTTCATACCTCAAAGAAACCAAAAA
CCTTCCTGCAGCTGGTGTGGGAAGCGCTACAGGACGTGACACTTATCATCCTGGAGATCGCGGCCATCAT
CTCCCTGGGACTGTCTTCTACCAACCCACGGGAGAGCAATGAAGGATGTGCCACGGCCAGGGTGGG
GCAGAGGATGAAGGTGAAGCAGAAGCAGGCTGGATTGAGGGGGCTGCCATCCTGTGTGTCAGTCATCTGTG
TGGTCTGGTACAGCCTTCAATGACTGGAGTAAGGAGAAACAGTTCGGGGCCTGCAGAGCCGAATTGA
GCAGGAGCAGAAGTTCAGTGTGGTCCGGGCCGGCCAGGTGGTTCAGATCCCTGTGGCCGAGATCGTGGT
GGGGACATTGCCAGATCAAATATGGTGACCTTCTCCCGCTGATGGCCTTTTCCAGGGAAATGACC
TCAAATGATGAAAGCTCACTCACAGGGGAATCTGACCAGGTGCGCAAGTCTGTGGATAAGGACCCCAT
GTTGCTGTGAGGAACCCATGTGATGGAGGGCTCAGGACGGATGGTGGTTACTGCTGTGGGTGTAACCT
CAGACTGGCATCATATTTACCCTGCTTGGGGCTGGTGGTGAAGAGGAAGAGAAGAAAGACAAAAAGCCA
AGCAGCAGGATGGGGCAGCTGCCATGGAGATGCAGCCTCTGAAGAGTGCAGAGGGCGCGCATGCAGATGA
CAAGAAGAAAGCCAACATGCACAAGAAAGAGAAGTCGGTGCTTCAGGGCAAGCTCACAAACTGGCTGTG
CAGATAGGCAAGGCGGGCCTGGTGTGTCGGCCATCACAGTATCATCCTGGTACTTACTTCCCGTGG
ACACCTTCGTGGTCAACAAGAAGCCATGGCTGACGGAATGCACACCCGTCTACGTACAGTACTTTGTCAA
GTTCTTCATCATTGGTGTGACGGTGTGGTGGTCGCTGTGCCGAGGGCCTCCCTCTGGCTGCACCATC
TACTGGCCTATTCTGTGAAGAAAATGATGAAGGACAACAACCTGGTACGCCACCTGGATGCCTGTGAGA
CCATGGGCAATGCCACAGCCATCTGCTCAGACAAGACAGGAACGCTGACCACCAACCGCATGACCGTGGT
CCAGGCCATGTGCGGTGACGTCCACTACAAGGAGATCCCCGATCCAGCTCCATCAATGCCAAGACGCTG
GAGCTGCTGGTCAACGCCATTGCCATCAACAGCGCCTACACCACCAAGATCCTTCCCCAGAAAAAGAGG



[View online >](#)

GAGCCCTGCCCCGGCAGGTGGGCAACAAGACAGAGTGCAGCCTGCTGGGCTTTGTGCTGGACTTGAGGCA
 GGACTACGAGCCGGTGCAGCCAGATGCCAGAGGAGAAGCTGTATAAGGTGTACACCTCAACTCCGTG
 CGCAAGTCCATGAGCACCCTCATCAAGATGCCGACGAGAGCTTCCGCATGTACAGCAAGGGCGCCTCGG
 AGATTGTGCTCAAAAAGTGTGCAAGATCCTCAGTGGGGCAGGGGAAGCCCGTGTCTCCGGCCCCGAGA
 CAGGGATGAGATGGTTAAGAAGGTGATTGAGCCCATGGCTGTGACGGGCTCCGTACCATCTGCGTGGCC
 TATCGTGACTTCCCCAGCAGCCCTGAGCCTGACTGGGACAATGAGAATGACATTCTCAATGAACTCACGT
 GCATCTGCGTGGTGGGCATCGAAGACCCAGTACGACCTGAGGTCCCAGAAGCCATCCGCAAGTGCCAGCG
 GGCAGGTATCACAGTCCGCATGGTCACCGGTGACAATATCAACACAGCCCGGGCCATCGCCATCAAGTGT
 GGCATTATCCACCCTGGAGAGGACTTCTGTGCCTGGAAGGCAAAAGAATTCAATCGGAGGATTCCGAACG
 AGAAGGGGGAGATTGAGCAGGAGCGGATTGACAAGATCTGGCAAAGCTGAGGGTGTGGCTCGCTCCTC
 GCCCACGGATAAGCACACGCTGGTCAAAGGCATCATCGACAGTACACACTGAGCAGCGGCAGGTGGTG
 GCTGTGACAGGGGATGGGACCAACGACGGGCTGCTCTCAAGAAGGCAGATGTGGCTTCGCAATGGGCA
 TCGCAGGCACAGATGTGGCAAGGAGCCCTCAGACATCATCTGACAGATGACAACCTCAGCAGCATCGT
 CAAGGCAGTGATGTGGGCCGTAACGTCTATGACAGCATATCAAATTCCTGCAGTTCAGCTGACTGTC
 AACGTGGTGGCGGTGATCGTGGCCTTACGGGGCCTGCATTACACAGGACTCCCCTCTCAAGGCTGTGC
 AGATGCTCTGGGTGAACCTCATCATGGACACGTTTGCCTCCCTGGCCCTGGCCACAGAGCCACCTACGGA
 GACTCTGCTTCTGAGAAACCGTACGGTCGCAACAAGCCGCTCATCTCGAGGACCATGATGAAGAATC
 CTGGGCCACGCCGTCTACCAGCTCACCTCATCTTACCCTGCTCTTCTGGGTGAGAAGATGTTCCAGA
 TCGACAGCGGAAGGAACGCCCGCTGCACTCACCCCTCAGAGCACTACACCATCATCTTCAACACCTT
 CGTCATGATGCAGCTTTTCAACGAGATCAACGCCCGCAAGATCCACGGCGAGCGCAACGTCTTTGACGGG
 ATCTTCCGGAACCCATCTTCTGCACCATCGTTCTTGGCACTTTCGCCATCCAGATAGTGATCGTGCAGT
 TTGGCGGGAAGCCCTTCCAGCTGCTCCCCACTCCAGCTGGACCAGTGGATGTGGTGCATCTCATAGGCC
 GGGAGAGCTCGTCTGGGGCCAGGTGATCGCCACCATCCCTACCAGCAGGCTCAAGTTCCTGAAAGGGCA
 GGGCGTCTAACACAGAAGGAGGAGATCCCCGAGGAGGAGTTAAATGAGGATGTGGAAGAGATAGACCACG
 CAGAGCGGGAGCTTCGCGTGGCCAGATCCTGTGGTTCGGGGCCTGAATCGGATCCAGACACAGATCCG
 CGTCGTGAAGGCGTTCCGTAGCTCTCTCTATGAAGGGTTAGAAAAACCCGAGTCTCGAACCTCCATCCAT
 AACTTCATGGCTCATCTGAATTCGGATCGAAGATTCCAGCCCCACATCCCCCTCATCGATGACACCG
 ACCTGGAAGAAGATGCCGCGCTCAAGCAGAAGTCCAGCCCCCGTCTCGCTCAACAAGAACAATAGCGC
 CATCGACAGCGGGATCAACCTGACGACCGACAGCAAATCAGTACCTCTTCAAGTCCAGGGAGCCCC
 ATCCACAGCCTGGAGACGTCGCTTAG

ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
 ACAAGGATGACGACGATAAGGTTTAA

- Restriction Sites:** SgfI-MluI
- ACCN:** NM_009723
- Insert Size:** 3597 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).
- OTI Annotation:** Clone contains native stop codon, and expresses the complete ORF without any c-terminal tag.
- 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:

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: [NM_009723.5](#), [NP_033853.1](#)

RefSeq Size: 7111 bp

RefSeq ORF: 3597 bp

Locus ID: 11941

UniProt ID: [Q9R0K7](#)

Cytogenetics: 6 52.85 cM

Gene Summary: This magnesium-dependent enzyme catalyzes the hydrolysis of ATP coupled with the transport of calcium out of the cell. Plays a role in maintaining balance and hearing. [UniProtKB/Swiss-Prot Function]

Transcript Variant: This variant (1) differs in the 5' UTR and coding region, compared to variant 3. These differences result in a shorter protein (isoform 1), compared to isoform 2. Variants 1 and 2 encode the same protein (isoform 1). Sequence Note: This RefSeq record was created from transcript and genomic sequence data to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on transcript alignments.