

## **Product datasheet for MC205835**

## Atp5e (NM 025983) Mouse Untagged Clone

**Product data:** 

**Product Type:** Expression Plasmids

**Product Name:** Atp5e (NM 025983) Mouse Untagged Clone

Tag: Tag Free Symbol: Atp5e

**Synonyms:** 2410043G19Rik; ATPE; AV000645

Mammalian Cell

Selection:

Neomycin

Vector: PCMV6-Kan/Neo (PCMV6KN)

E. coli Selection: Kanamycin (25 ug/mL)

Fully Sequenced ORF: >BC024339

**Restriction Sites:** RsrII-NotI ACCN: NM\_025983

**Insert Size:** 159 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).



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**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.

**Note:** Plasmids are not sterile. For experiments where strict sterility is required, filtration with

0.22um filter is required.

**RefSeq:** <u>BC024339</u>, <u>AAH24339</u>

 RefSeq Size:
 425 bp

 RefSeq ORF:
 159 bp

 Locus ID:
 67126

 UniProt ID:
 P56382

 Cytogenetics:
 2 H4

Gene Summary: Mitochondrial membrane ATP synthase (F(1)F(0) ATP synthase or Complex V) produces ATP

from ADP in the presence of a proton gradient across the membrane which is generated by electron transport complexes of the respiratory chain. F-type ATPases consist of two structural domains, F(1) - containing the extramembraneous catalytic core, and F(0) -

containing the membrane proton channel, linked together by a central stalk and a peripheral stalk. During catalysis, ATP synthesis in the catalytic domain of F(1) is coupled via a rotary mechanism of the central stalk subunits to proton translocation. Part of the complex F(1) domain and of the central stalk which is part of the complex rotary element. Rotation of the central stalk against the surrounding alpha(3)beta(3) subunits leads to hydrolysis of ATP in three separate catalytic sites on the beta subunits (By similarity).[UniProtKB/Swiss-Prot

Function]