

Product datasheet for MR201389L3V

OriGene Technologies, Inc.

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Atp5d (NM_025313) Mouse Tagged ORF Clone Lentiviral Particle

Product data:

Product Type: Lentiviral Particles

Product Name: Atp5d (NM_025313) Mouse Tagged ORF Clone Lentiviral Particle

Symbol: Atp5d

Synonyms: 0610008F14Rik; 1500000I11Rik; AA960090; AI876556; AU020773; C85518

Mammalian Cell

Selection:

Puromycin

Vector: pLenti-C-Myc-DDK-P2A-Puro (PS100092)

Tag: Myc-DDK
ACCN: NM 025313

ORF Size: 507 bp

ORF Nucleotide

Sequence:

The ORF insert of this clone is exactly the same as(MR201389).

OTI Disclaimer: The molecular sequence of this clone aligns with the gene accession number as a point of reference only. However, individual transcript sequences of the same gene can differ through

naturally occurring variations (e.g. polymorphisms), each with its own valid existence. This clone is substantially in agreement with the reference, but a complete review of all prevailing

variants is recommended prior to use. More info

OTI Annotation: This clone was engineered to express the complete ORF with an expression tag. Expression

varies depending on the nature of the gene.

RefSeg: NM 025313.1

RefSeq Size: 931 bp
RefSeq ORF: 507 bp
Locus ID: 66043
UniProt ID: Q9D3D9
Cytogenetics: 10 C1







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 turnover 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.[UniProtKB/Swiss-Prot Function]