

# Product datasheet for RC207908

### ATP5PD (NM\_006356) Human Tagged ORF Clone

### **Product data:**

#### OriGene Technologies, Inc.

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Product Type:	Expression Plasmids
Product Name:	ATP5PD (NM_006356) Human Tagged ORF Clone
Tag:	Myc-DDK
Symbol:	ATP5PD
Synonyms:	APT5H; ATP5H; ATPQ
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
ORF Nucleotide Sequence:	<pre>&gt;RC207908 ORF sequence Red=Cloning site Blue=ORF Green=Tags(s)</pre>
	TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC GCC <mark>GCGATCGC</mark> C
	ATGGCTGGGCGAAAACTTGCTCTAAAAACCATTGACTGGGTAGCTTTTGCAGAGATCATACCCCAGAACC AAAAGGCCATTGCTAGTTCCCTGAAATCCTGGAATGAGACCCTCACCTCCAGGTTGGCTGCTTTACCTGA GAATCCACCAGCTATCGACTGGGCTTACTACAAGGCCAATGTGGCCAAGGCTGGCT
	ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT ACAAGGATGACGACGATAAG <b>GTTTAA</b>
Protein Sequence:	<pre>&gt;RC207908 protein sequence Red=Cloning site Green=Tags(s)</pre>
	MAGRKLALKTIDWVAFAEIIPQNQKAIASSLKSWNETLTSRLAALPENPPAIDWAYYKANVAKAGLVDDF EKKFNALKVPVPEDKYTAQVDAEEKEDVKSCAEWVSLSKARIVEYEKEMEKMKNLIPFDQMTIEDLNEAF PETKLDKKKYPYWPHQPIENL
	TRTRPLEQKLISEEDLAANDILDYKDDDDKV
Chromatograms:	https://cdn.origene.com/chromatograms/mk6338_d01.zip



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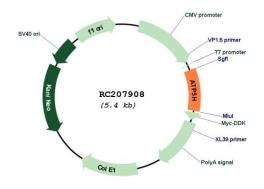
## **GRIGENE** ATP5PD (NM\_006356) Human Tagged ORF Clone – RC207908

ACCN: NM ORF Size: 483 OTI Disclaimer: The refe natu clore vari OTI Annotation: This vari Components: The com Reconstitution Method: 1. C 2. C 3. C 4. B	turally occurring variations (e.g. polymorphisms), each with its own valid existence. This ne is substantially in agreement with the reference, but a complete review of all prevailing
ACCN: NM ORF Size: 483 OTI Disclaimer: The refe natu clore vari OTI Annotation: This vari Components: The com Reconstitution Method: 1. C 2. C 3. C 4. B	<b>EVALUATE: EVALUATE: EVALUATE: EVALUAT: EVALUA</b>
CCN: NM PRF Size: 483 OTI Disclaimer: The referent other other omponents: The components: The components: 1. C 2. C 3. C 4. B	T CTG GCA GCA AAT GAT ATC CTG GAT TAC AAG GAT GAC GAC GAC GAC GAT AAG GTT TAA ACGGCCGGCC L A A N D I L D Y K D D D K V stop The bit codon before the Stop codon of the ORF A_006356 3 bp e molecular sequence of this clone aligns with the gene accession number as a point of ference only. However, individual transcript sequences of the same gene can differ through turally occurring variations (e.g. polymorphisms), each with its own valid existence. This ne is substantially in agreement with the reference, but a complete review of all prevailing
ACCN: NM DRF Size: 483 DTI Disclaimer: The refe nature Components: The components: The components: 1. C 2. C 3. C 4. B	1_006356 3 bp e molecular sequence of this clone aligns with the gene accession number as a point of erence only. However, individual transcript sequences of the same gene can differ through turally occurring variations (e.g. polymorphisms), each with its own valid existence. This ne is substantially in agreement with the reference, but a complete review of all prevailing
DRF Size: 483 DTI Disclaimer: The refe natu clor Vari DTI Annotation: This vari Components: The con Reconstitution Method: 1. C 2. C 3. C 4. B	3 bp e molecular sequence of this clone aligns with the gene accession number as a point of erence only. However, individual transcript sequences of the same gene can differ through turally occurring variations (e.g. polymorphisms), each with its own valid existence. This ne is substantially in agreement with the reference, but a complete review of all prevailing
DTI Disclaimer: The refe natu clore vari DTI Annotation: This vari components: The com econstitution Method: 1. C 2. C 3. C 4. B	e molecular sequence of this clone aligns with the gene accession number as a point of ference only. However, individual transcript sequences of the same gene can differ through turally occurring variations (e.g. polymorphisms), each with its own valid existence. This ne is substantially in agreement with the reference, but a complete review of all prevailing
refe natu clor vari TI Annotation: This vari omponents: The con econstitution Method: 1. C 2. C 3. C 4. B	erence only. However, individual transcript sequences of the same gene can differ through turally occurring variations (e.g. polymorphisms), each with its own valid existence. This ne is substantially in agreement with the reference, but a complete review of all prevailing
vari omponents: The con econstitution Method: 1. C 2. C 3. C 4. B	riants is recommended prior to use. <u>More info</u>
con econstitution Method: 1. C 2. C 3. C 4. B	is clone was engineered to express the complete ORF with an expression tag. Expression ries depending on the nature of the gene.
2. C 3. C 4. B	e ORF clone is ion-exchange column purified and shipped in a 2D barcoded Matrix tube ntaining 10ug of transfection-ready, dried plasmid DNA (reconstitute with 100 ul of water).
5. Si	Centrifuge at 5,000xg for 5min. Carefully open the tube and add 100ul of sterile water to dissolve the DNA. Close the tube and incubate for 10 minutes at room temperature. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid the bottom. Store the suspended plasmid at -20°C. The DNA is stable for at least one year from date of pping when stored at -20°C.
lote: Plas	ismids are not sterile. For experiments where strict sterility is required, filtration with 22um filter is required.
efSeq: <u>NM</u>	1 006356.3
efSeq Size: 628	8 bp
efSeq ORF: 486	6 hn

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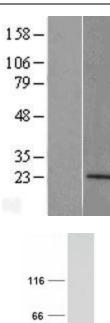
<b>GRIGENE</b> ATP5PD (NM_006356) Human Tagged ORF Clone – RC207908		
Locus ID:	10476	
UniProt ID:	<u>075947</u>	
Cytogenetics:	17q25.1	
Protein Pathways:	Alzheimer's disease, Huntington's disease, Metabolic pathways, Oxidative phosphorylation, Parkinson's disease	
MW:	18.5 kDa	
Gene Summary:	Mitochondrial 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 d subunit of the Fo complex. Alternatively spliced transcript variants encoding different isoforms have been identified for this gene. In addition, three pseudogenes are located on chromosomes 9, 12 and 15. [provided by RefSeq, Jun 2010]	

## Product images:



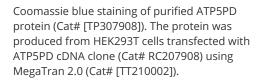
Circular map for RC207908

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35 -25 -18 = Western blot validation of overexpression lysate (Cat# [LY416696]) using anti-DDK antibody (Cat# [TA50011-100]). Left: Cell lysates from untransfected HEK293T cells; Right: Cell lysates from HEK293T cells transfected with RC207908 using transfection reagent MegaTran 2.0 (Cat# [TT210002]).



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