

Product datasheet for **TP500018**

Atp5e (NM_025983) Mouse Recombinant Protein

Product data:

Product Type:	Recombinant Proteins
Description:	Purified recombinant protein of Mouse ATP synthase, H ⁺ transporting, mitochondrial F1 complex, epsilon subunit (Atp5e), with C-terminal MYC/DDK tag, expressed in HEK293T cells, 20ug
Species:	Mouse
Expression Host:	HEK293T
Expression cDNA Clone or AA Sequence:	>MR200018 protein sequence Red =Cloning site Green =Tags(s)
	MVAYWRQAGLSYIRFSQICAKAVRDALKTEFKANAETSGSSIKIVKVSKE
	TRTRPLEQKLISEEDLAANDILDYKDDDDKV
Tag:	C-MYC/DDK
Predicted MW:	5.8 kDa
Concentration:	>0.05 µg/µL as determined by microplate BCA method
Purity:	> 80% as determined by SDS-PAGE and Coomassie blue staining
Buffer:	25 mM Tris-HCl, 100 mM glycine, pH 7.3, 10% glycerol
Note:	For testing in cell culture applications, please filter before use. Note that you may experience some loss of protein during the filtration process.
Storage:	Store at -80°C after receiving vials.
Stability:	Stable for 12 months from the date of receipt of the product under proper storage and handling conditions. Avoid repeated freeze-thaw cycles.
RefSeq:	NP_080259
Locus ID:	67126
UniProt ID:	P56382 , Q545F5
RefSeq Size:	419
Cytogenetics:	2 H4
RefSeq ORF:	159



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Synonyms: 2410043G19Rik; ATPE; AV000645

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]