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Product datasheet

Recombinant Human ATP5A protein (His tag) ab235862

1 References 1 Image

Description

Product name Recombinant Human ATP5A protein (His tag)

Purity > 90 % SDS-PAGE.

Expression system Escherichia coli

Accession P25705-1

Protein length Full length protein

Animal free No

Nature Recombinant

Species Human

Sequence QKTGTAEMSSILEERILGADTSVDLEETGRVLSIGDGIARVH

GLRNVQAE

EMVEFSSGLKGMSLNLEPDNVGVVVFGNDKLIKEGDIVK

RTGAIVDVPVG

EELLGRVVDALGNAIDGKGPIGSKTRRRVGLKAPGIIPRISV

REPMQTGI

KAVDSLVPIGRGQRELIIGDRQTGKTSIAIDTIINQKRFNDGS

DEKKKLY

CIYVAIGQKRSTVAQLVKRLTDADAMKYTIVVSATASDAAP

LQYLAPYSG

CSMGEYFRDNGKHALIIYDDLSKQAVAYRQMSLLLRRPPG

REAYPGDVFY

LHSRLLERAAKMNDAFGGGSLTALPVIETQAGDVSAYIPTN

VISITDGQI

FLETELFYKGIRPAINVGLSVSRVGSAAQTRAMKQVAGTM

KLELAQYREV

AAFAQFGSDLDAATQQLLSRGVRLTELLKQGQYSPMAIEE

QVAVIYAGVR

GYLDKLEPSKITKFENAFLSHVVSQHQALLGTIRADGKISE

QSDAKLKEI VTNFLAGFEA

Predicted molecular weight 59 kDa including tags

Amino acids 44 to 553

Tags His tag N-Terminus

Additional sequence information N-terminal 6xHis-tagged. Full length mature chain without transit peptide.

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Specifications

Our Abpromise guarantee covers the use of ab235862 in the following tested applications.

The application notes include recommended starting dilutions; optimal dilutions/concentrations should be determined by the end user.

Applications SDS-PAGE

Form Liquid

Preparation and Storage

Stability and Storage Shipped at 4°C. Store at -20°C or -80°C. Avoid freeze / thaw cycle.

pH: 7.2

Constituents: Tris buffer, 50% Glycerol (glycerin, glycerine)

General Info

Function 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. Subunits alpha and beta form the catalytic core in F(1). 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. Subunit alpha does not

bear the catalytic high-affinity ATP-binding sites.

Tissue specificity Fetal lung, heart, liver, gut and kidney. Expressed at higher levels in the fetal brain, retina and

spinal cord.

Sequence similaritiesBelongs to the ATPase alpha/beta chains family.

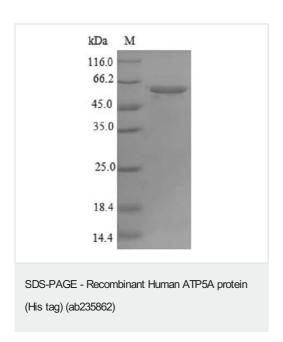
Post-translational

modifications

The N-terminus is blocked.

Cellular localization Mitochondrion inner membrane. Peripheral membrane protein.

Images



(Tris-Glycine gel) Discontinuous SDS-PAGE (reduced) with 5% enrichment gel and 15% separation gel analysis of ab235862.

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